

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 18:41:36 ; Search time 1978 Seconds
(without alignments)
517.281 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18

Sequence: 1 ccacaccttatactc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_hlg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	357	10	G67590
2	18	100.0	418	6	CQ922146 Sequence
3	18	100.0	447	6	AX377240
4	18	100.0	496	6	CS071001 Sequence
5	18	100.0	559	6	CQ723247 Sequence
6	18	100.0	562	6	AR380655 Sequence
7	18	100.0	562	6	AX332734 Sequence
8	18	100.0	562	6	AX333340 Sequence
9	18	100.0	562	6	AX333743 Sequence
10	18	100.0	562	8	HUMPLA2A
11	18	100.0	569	6	E02268
12	18	100.0	600	6	AX377262 Sequence
13	18	100.0	644	6	BD209899 Human nuc
14	18	100.0	644	6	AX014213 Sequence
15	18	100.0	654	6	CS071209 Sequence
16	18	100.0	3375	8	HUMPLA2A1
17	18	100.0	8368	8	AY438977 Homo sapi
18	18	100.0	13612	6	AX377239 Sequence

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C 21	94.4	463	9	MMPAX83
C 22	94.4	7821	9	AY157583
C 23	94.4	150089	14	AC128066
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C 25	94.4	166465	9	AL732528
C 26	94.4	168648	5	BX571839
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C 28	94.4	190715	5	BX247878
C 29	94.4	203746	14	AC105464
C 30	94.4	213533	14	AC136410
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C 33	94.4	259335	14	AC095794
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C 91	85.6	433	2	AY552482

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AC078926 Homo sapi
X99593 M.musculus
AY157583 Mus muscu
AC128066 Rattus no
BX323576 Zebrafish
AL732528 Mouse DNA
BX571839 Zebrafish
AC099634 Mus muscu
BX247878 Zebrafish
AC105464 Rattus no
AC136410 Rattus no
AC119364 Rattus no
AC128521 Rattus no
AC095794 Rattus no
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AY135687 Mus muscu
AC151470 Xenopus t
AC006262 Homo sapi
Continuation (9 of
AY386265 Bovine pa
AC160234 Rhinolph
AC159925 Atelexix
AC160584 Atelexix
AC105201 Homo sapi
AC016373 Homo sapi
CR318635 Zebrafish
AL354997 Human DNA
AL359218 Human chr
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CR385076 Zebrafish
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AL596255 Mouse DNA
AX658289 Sequence
AE000659 Homo sapi
AC144457 Homo sapi
AC134770 Homo sapi
AC163904 Bos tauru
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AC139010 Homo sapi
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AL590677 Human DNA
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AC145793 Xenopus t
CR450821 Zebrafish
AC098698 Papio anu
AC055735 Homo sapi
AC144872 Pan trogl
CR847521 Danio rer
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AC068990 Homo sapi
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117	15.4	85.6	41883	2	U40800	U40800 Caenorhabdi
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135	15.4	85.6	91979	15	AC002510	AC002510 Arabidops
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137	15.4	85.6	97318	5	AL772382	AL772382 Zebrafish
138	15.4	85.6	99592	8	AF263284	AF263284 Homo sapi
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149	15.4	85.6	110000	14	TANN11_15	Continuation (16 o
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ALIGNMENTS

RESULT 1

G67590

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

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canpla2glb-pcr3-1

Human Homo sapiens STS genomic, sequence tagged site.

G67590

G67590.1

GI:12642952

STS.

Homo sapiens (human)

357 bp

DNA

linear

STS 31-JAN-2001

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

G67590

CO922146

Sequence 3346 from Patent WO2004097052.

CO922146

CO922146.1

GI:56212087

KEYWORDS

SOURCE

Homo sapiens (human)

418 bp

DNA

linear

PAT 23-NOV-2004

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 357)

AUTHORS

Wong,G.K.S., Yu,J., Yang,Z., Passey,D., Kibukawa,M., Paddock,M. and Olson,M.

TITLE

Gene based polymorphism discovery

JOURNAL

Unpublished (2000)

COMMENT

Contact: Gane Ka-Shu Wong

Genome Center

University of Washington

Fluke Hall, Box 352145, Seattle, WA 98195, USA

Tel: 206/685-7348

Fax: 206/685-7344

Email: gkew@u.washington.edu

Primer A: AAGCATCTTGGCGAAGTCAT

Primer B: AAGGAGACACTGCCAGAA

STS size: 357

PCR Profile:

Presoak: 92 degrees C for 1.00 minute

Denaturation: 92 degrees C for 0.16 minute

Annealing: 60-65 degrees C for 0.50 minute

Polymerization: 72 degrees C for 1.00 minute

PCR Cycles: 35

Thermal Cycler: Perkin Elmer TC

Protocol:

Template: 7 ng

Primer: each 0.5 uM

dNTPs: each 100 uM

Taq Polymerase: 0.025 units/ul

Total Vol: 10 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 8.3.

Location/Qualifiers

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/mol_type="genomic DNA"

/db_xref="taxon:9606"

/map="15q23-q24.1"

/clone_lib="Human"

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Best Local Similarity

100.0%; Pred. No. 60;

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Db

189 CCACACCTATTTCATCTC 206

RESULT 2

CO922146

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

CO922146

Sequence 3346 from Patent WO2004097052.

CO922146

CO922146.1

GI:56212087

KEYWORDS

SOURCE

Homo sapiens (human)

418 bp

DNA

linear

PAT 23-NOV-2004

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Burczynski, M.E., Twine, N.C., Slonim, D.K., Trepicchio, W.L.,
Strahs, A., Immerman, F. and Dorner, A.J.
TITLE Methods for prognosis and treatment of solid tumors
JOURNAL Patent: WO 2004097052-A 3346 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)

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LOCUS AX377240 447 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 2 from Patent WO0212562.
ACCESSION AX377240
VERSION AX377240.1 GI:19573529
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Kazemi, A., Kliem, S.E. and Koshy, B.
TITLE Haplotypes of the pla2g1b gene
JOURNAL Patent: WO 0212562-A 2 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)

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/mol_type="unassigned DNA"
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CS071001/c
LOCUS CS071001 496 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 164 from Patent WO2001032927.
ACCESSION CS071001
VERSION CS071001.1 GI:63088405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Sornasse, T., Seilhamer, J.J. and Watson, G.A.
TITLE Tissue specific genes of diagnostic import

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Burczynski, M.E., Twine, N.C., Slonim, D.K., Trepicchio, W.L.,
Strahs, A., Immerman, F. and Dorner, A.J.
TITLE Methods for prognosis and treatment of solid tumors
JOURNAL Patent: WO 2004097052-A 3346 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)

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source Location/Qualifiers
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RESULT 3
AX377240
LOCUS AX377240 447 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 2 from Patent WO0212562.
ACCESSION AX377240
VERSION AX377240.1 GI:19573529
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Kazemi, A., Kliem, S.E. and Koshy, B.
TITLE Haplotypes of the pla2g1b gene
JOURNAL Patent: WO 0212562-A 2 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)

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source Location/Qualifiers
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/mol_type="unassigned DNA"
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LOCUS CS071001 496 bp DNA linear PAT 05-MAY-2005
DEFINITION Sequence 164 from Patent WO2001032927.
ACCESSION CS071001
VERSION CS071001.1 GI:63088405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Sornasse, T., Seilhamer, J.J. and Watson, G.A.
TITLE Tissue specific genes of diagnostic import

JOURNAL Patent: WO 2001032927-A 164 10-MAY-2001;
Incyte Genomics, Inc. (US)

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source Location/Qualifiers
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RESULT 5
CQ723247
LOCUS CQ723247 559 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 9181 from Patent WO02068579.
ACCESSION CQ723247
VERSION CQ723247.1 GI:42284104
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 9181 06-SEP-2002;
PE Corporation (NY) (US)

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AR380655
LOCUS AR380655 562 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1200 from patent US 6607879.
ACCESSION AR380655
VERSION AR380655.1 GI:40088289
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 562)
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
TITLE Compositions for the detection of blood cell and immunological
response gene expression
JOURNAL Patent: US 6607879-A 1200 19-AUG-2003;
Incyte Corporation; Palo Alto, CA

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AX332734
LOCUS      AX332734          562 bp      DNA      linear      PAT 09-JAN-2002
DEFINITION Sequence 3243 from Patent WO0194629.
ACCESSION  AX332734
VERSION     AX332734.1 GI:18123368
KEYWORDS   . Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE       Cancer gene determination and therapeutic screening using signature
            gene sets
JOURNAL     Patent: WO 0194629-A 3243 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES    source
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Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
    |||||
Db 313 CCACACCTATTTCATCTC 330

RESULT 8
AX333340
LOCUS      AX333340          562 bp      DNA      linear      PAT 09-JAN-2002
DEFINITION Sequence 3849 from Patent WO0194629.
ACCESSION  AX333340
VERSION     AX333340.1 GI:18123974
KEYWORDS   . Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE       Cancer gene determination and therapeutic screening using signature
            gene sets
JOURNAL     Patent: WO 0194629-A 3849 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES    source
            1..562
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
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ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
    |||||
Db 313 CCACACCTATTTCATCTC 330

RESULT 9
AX333743
LOCUS      AX333743          562 bp      DNA      linear      PAT 09-JAN-2002
DEFINITION Sequence 4252 from Patent WO0194629.
ACCESSION  AX333743
VERSION     AX333743.1 GI:18124462
KEYWORDS   . Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE       Cancer gene determination and therapeutic screening using signature
            gene sets
JOURNAL     Patent: WO 0194629-A 4252 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES    source
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            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
    |||||
Db 313 CCACACCTATTTCATCTC 330

RESULT 10
HUMPLA2RA
LOCUS      HUMPLA2RA          562 bp      mRNA      linear      PRI 03-JUN-1994
DEFINITION Human lung phospholipase A-2 (PLA-2) mRNA, complete cds, clone
            lung-1(hcDNA).
ACCESSION  M21054 M14965
VERSION     M21054.1 GI:190012
KEYWORDS   phospholipase A2.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 562)
AUTHORS     Seilhamer,J.J., Randall,T.L., Yamanaka,M. and Johnson,L.K.
TITLE       Pancreatic phospholipase A2: isolation of the human gene and cDNAs
            from porcine pancreas and human lung
JOURNAL     DNA 5 (6), 519-527 (1986)
PUBMED     3028739
COMMENT     Original source text: Homo sapiens lung cDNA to mRNA.
FEATURES    source
            1..562
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
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            38..484
            /EC_number="3.1.1.4"
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            /product="phospholipase"

CDS

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/protein_id="AAA36450.1"
/db_xref="GI:190013"
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ORIGIN

Query Match 100.0%; Score 18; DB 8; Length 562;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 313 CCACACCTATTTCATCTC 330

RESULT 11

E02268 LOCUS 569 bp RNA linear PAT 29-SEP-1997
DEFINITION cDNA encoding human phospholipase A2.
ACCESSION E02268

VERSION E02268.1 GI:2170505
KEYWORDS JP 1990065781-A/1.
SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 569)
Tamaki,M., Takimoto,N., Nakamura,E., Teraoka,H., Ogawa,M. and
Matsubara,K.

TITLE

PRODUCTION OF PHOSPHOLIPASE A2 OF HUMAN PANCREAS

JOURNAL Patent: JP 1990065781-A 1 06-MAR-1990;

SHIONOGI & CO LTD

COMMENT

OS Homo sapiens
PN JP 1990065781-A/1
PD 06-MAR-1990
PF 29-AUG-1988 JP 1988214666
PI TAMAKI MIKIO, TAKIMOTO NORIKO, NAKAMURA ETSUO, TERAOKA
HIROSHI, PI OGAWA MICHIO, MATSUBARA KENICHI
PC C12N9/18/C12N15/55, (C12N9/18, C12R1.865);
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
CC *source: tissue type=pancreas;
CC *source: clone=HplII;
FH Key Location/Qualifiers

FT CDS 25..471
FT sig_peptide 25..90
FT mat_peptide 91..468
FT peptide' /product='human phospholipase A2 precursor' FT

FT 5'UTR 1..24
FT polyA_signal 503..508.

FEATURES

source 1..569
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
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Db 300 CCACACCTATTTCATCTC 317

RESULT 12

AX377262

LOCUS 600 bp DNA linear PAT 18-MAR-2002

DEFINITION Sequence 24 from Patent WO0212562.

ACCESSION AX377262

VERSION AX377262.1 GI:19573550

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1

REFERENCE

AUTHORS Kazami,A., Kliehm,S.E. and Koshy,B.

TITLE Haplotypes of the pla2g1b gene

JOURNAL Patent: WO 0212562-A 24 14-FEB-2002;

Genaissance Pharmaceuticals, Inc. (US)

FEATURES

source 1..600
Location/Qualifiers

variation 30

misc_feature 61..120

variation 150

misc_feature 181..240

variation 270

misc_feature 301..360

variation 390

misc_feature 421..480

variation 510

misc_feature 541..600

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 600;

Best Local Similarity 100.0%; Pred. No. 58;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 372 CCACACCTATTTCATCTC 389

RESULT 13

BD209899

LOCUS 644 bp DNA linear PAT 17-JUL-2003

DEFINITION Human nucleic acid sequence originating in normal pancreas.

ACCESSION BD209899

VERSION BD209899.1 GI:33019669

KEYWORDS JP 2002512022-A/3.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 644)
Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and
Rosenthal,A.

TITLE Human nucleic acid sequence originating in normal pancreas

JOURNAL Patent: JP 2002512022-A 3 23-APR-2002;

METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH

OS Homo sapiens (human)

PN JP 2002512022-A/3


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Query Match      100.0%; Score 18; DB 8; Length 3375;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACTATTTCATCTC 18
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Db      3304 CCACACTATTTCATCTC 3321

RESULT 17
AY438977
LOCUS      AY438977      8368 bp      DNA      linear      PRI 29-OCT-2003
DEFINITION Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B) gene,
            complete cds.
ACCESSION      AY438977
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE      1 (bases 1 to 8368)
AUTHORS      Rieder,M.J., Livingston,R.J., Daniels,M.R., Chung,M.-W.,
            Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
            Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
TITLE      Direct Submission
JOURNAL      Submitted (16-OCT-2003) Genome Sciences, University of Washington,
            1705 NE Pacific, Seattle, WA 98195, USA
COMMENT      To cite this work please use: NIEHS-SNPs, Environmental Genome
            Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
            (URL: http://egp.gs.washington.edu).
FEATURES
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                /codon_start=1
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                /db_xref="GI:37953285"
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            2194..2319
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4347. .4634
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4386. .4723
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5779. .6083
/rpt_family="Alu"
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100.0%; Score 18; DB 8; Length 8368;

Query Match
Best Local Similarity 100.0%; Pred. No. 48;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 3684 CCACACCTATTTCATCTC 3701
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RESULT 18
AX377239 13612 bp DNA linear PAT 18-MAR-2002
LOCUS Sequence 1 from Patent WO212562.
DEFINITION AX377239
ACCESSION AX377239
VERSION AX377239.1 GI:19573528
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1
AUTHORS Kazemi,A., Kliehm,S.E. and Koshy,B.
TITLE Haplotypes of the pla2glb gene
JOURNAL Patent: WO 0212562-A 1 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES
source
1..13612
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
variation
/note="PS1: polymorphic base G or A"
variation
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variation
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variation
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variation
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ORIGIN
Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 13612;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 6826 CCACACCTATTTCATCTC 6843
|||||

RESULT 19
AC003982 122302 bp DNA linear PRI 18-MAR-1999
LOCUS Homo sapiens PAC clone 166H1 from 12q, complete sequence.
DEFINITION AC003982
ACCESSION AC003982
VERSION AC003982.1 GI:2769695
SOURCE HTG.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 122302)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 9847074
REFERENCE 2 (bases 1 to 122302)
AUTHORS Bradshaw,H., Wu,X. and Ozersky,P.
TITLE The sequence of Homo sapiens PAC clone 166H1
JOURNAL Unpublished (1999)
REFERENCE 3 (bases 1 to 122302)
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/rpt_family="Alu"
repeat_region 11568..11705
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repeat_region 11737..12032
/rpt_family="Alu"
repeat_region 12034..12066
/rpt_family="7SLRNA"
repeat_region 12075..12372
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repeat_region 12448..12753
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Query Match 100.0%; Score 18; DB 8; Length 122302;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 25978 CCACACCTATTTCATCTC 25961

RESULT 20
AC078926/c
LOCUS AC078926 220384 bp DNA linear HTG 26-MAR-2002
DEFINITION Homo sapiens chromosome 12 clone RP11-836M11, WORKING DRAFT
SEQUENCE, 11 unordered pieces.
ACCESSION AC078926
VERSION AC078926.23 GI:19718703
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 220384)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Amaraltinge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falle,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
Hombi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
Jacobson,B., Jia,Y., Johnson,R., Jollivet,S., Joudan,S.,
Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Louseged,H.,
Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
Moser,M., Neal,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N.,
Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogih,M., Okwuonu,G.,
Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
Rives,M., Rojas,A., Rojubokan,I., Roife,M., Ruiz,S., Savery,G.,
Scherer,S., Scott,G., Shen,H., Shoostari,N., Sisson,I.,
Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
Sutton,A., Svatek,A., Tabot,P., Tamerisa,A., Tamerisa,K., Tang,H.,
Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S.,
Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 220384)
Worley,K.C.
Direct Submission
Submitted (11-AUG-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 220384)
Worley,K.C.
Direct Submission
Submitted (26-MAR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 26, 2002 this sequence version replaced gi:18449664.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: HCAPM
Center clone name: RP11-836M11
----- Summary Statistics
Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-primer Bodipy: 47% of reads
Chemistry: Dye-terminator Big Dye: 53% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 234783 bases at least Q40
Consensus quality: 241821 bases at least Q30
Consensus quality: 245671 bases at least Q20
Estimated insert size: 219187, sum-of-contigs estimation
Quality coverage: 8.9x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docx/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2156: contig of 2156 bp in length
* 2157 2256: gap of unknown length
* 2257 7112: contig of 4856 bp in length

```


7113	7212: gap of unknown length	9205117	PUBMED
7213	13283: contig of 6071 bp in length	2	(bases 1 to 463)
13283	13383: gap of unknown length	Okladnova,O.	REFERENCE
20660	20660: contig of 7277 bp in length	Direct Submission	TITLE
20761	20760: gap of unknown length	Submitted (18-JUL-1996)	JOURNAL
34473	34473: contig of 13713 bp in length	Uni Muenster, Vesaliusweg 12-14, D- 48149 Muenster, Germany, FRG	
34474	34573: gap of unknown length	Location/Qualifiers	FEATURES
44394	44394: contig of 9821 bp in length	1. .463	source
44395	44494: gap of unknown length	/organism="Mus musculus"	
57127	57126: contig of 12632 bp in length	/mol_type="genomic DNA"	
57227	57226: gap of unknown length	/db_xref="taxon:10090"	
80267	80366: contig of 23040 bp in length	/chromosome="2B"	
80367	80366: gap of unknown length	112. .277	gene
109398	109398: contig of 29032 bp in length	/gene="Pax-8"	
109499	109498: gap of unknown length	112. .277	exon
149812	149812: contig of 40314 bp in length	/gene="Pax-8"	
149813	149812: gap of unknown length	/usedin=X99592:pax8 cds	
220384	220384: contig of 70472 bp in length.	/usedin=X99592:pax8_mrna	
Location/Qualifiers		/label=ex3	
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/organism="Homo sapiens"			
/mol_type="genomic DNA"			
/db_xref="taxon:9606"			
/chromosome="12"			
/clone="RP11-836M11"			
2157. .2256			
/estimated_length=unknown			
7113. .7212			
/estimated_length=unknown			
13284. .13383			
/estimated_length=unknown			
20661. .20760			
/estimated_length=unknown			
34474. .34573			
/estimated_length=unknown			
44395. .44494			
/estimated_length=unknown			
57127. .57226			
/estimated_length=unknown			
80267. .80366			
/estimated_length=unknown			
109399. .109498			
/estimated_length=unknown			
149813. .149912			
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ORIGIN			
Query Match	100.0%; Score 18; DB 14; Length 220384;		
Best Local Similarity	100.0%; Pred. No. 38;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CCACACCTATTCATCTC 18		
Db	71201 CCACACCTATTCATCTC 71184		
RESULT 21			
MMPAX83			
LOCUS	M.musculus Pax-8 gene, exon 3.		
DEFINITION	M.musculus Pax-8 gene, exon 3.		
ACCESSION	X99593		
VERSION	X99593.1 GI:1850884		
KEYWORDS	Pax-8 gene		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1		
AUTHORS	Okladnova,O., Poleev,A., Fantes,J., Lee,M., Plachov,D. and Horst,J.		
TITLE	The genomic organization of the murine Pax 8 gene and characterization of its basal promoter		
JOURNAL	Genomics 42 (3), 452-461 (1997)		
7113	7212: gap of unknown length	9205117	PUBMED
7213	13283: contig of 6071 bp in length	2	(bases 1 to 463)
13283	13383: gap of unknown length	Okladnova,O.	REFERENCE
20660	20660: contig of 7277 bp in length	Direct Submission	TITLE
20761	20760: gap of unknown length	Submitted (18-JUL-1996)	JOURNAL
34473	34473: contig of 13713 bp in length	Uni Muenster, Vesaliusweg 12-14, D- 48149 Muenster, Germany, FRG	
34474	34573: gap of unknown length	Location/Qualifiers	FEATURES
44394	44394: contig of 9821 bp in length	1. .463	source
44395	44494: gap of unknown length	/organism="Mus musculus"	
57127	57126: contig of 12632 bp in length	/mol_type="genomic DNA"	
57227	57226: gap of unknown length	/db_xref="taxon:10090"	
80267	80366: contig of 23040 bp in length	/chromosome="2B"	
80367	80366: gap of unknown length	112. .277	gene
109398	109398: contig of 29032 bp in length	/gene="Pax-8"	
109499	109498: gap of unknown length	112. .277	exon
149812	149812: contig of 40314 bp in length	/gene="Pax-8"	
149813	149812: gap of unknown length	/usedin=X99592:pax8 cds	
220384	220384: contig of 70472 bp in length.	/usedin=X99592:pax8_mrna	
Location/Qualifiers		/label=ex3	
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/organism="Homo sapiens"			
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/chromosome="12"			
/clone="RP11-836M11"			
2157. .2256			
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7113. .7212			
/estimated_length=unknown			
13284. .13383			
/estimated_length=unknown			
20661. .20760			
/estimated_length=unknown			
34474. .34573			
/estimated_length=unknown			
44395. .44494			
/estimated_length=unknown			
57127. .57226			
/estimated_length=unknown			
80267. .80366			
/estimated_length=unknown			
109399. .109498			
/estimated_length=unknown			
149813. .149912			
/			

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exon      3063. .3228
           /number=3
exon      457. .4854
           /number=4
exon      6114. .6202
           /number=5
exon      6591. .6716
           /number=6
exon      6979. .7154
           /number=7

ORIGIN
Query Match      94.4%; Score 17; DB 9; Length 7821;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
   |||||
Db 2975 CACACCTATTCATCTC 2991

RESULT 23
AC128066/c
LOCUS      Rattus norvegicus clone CH230-465J23, WORKING DRAFT SEQUENCE.
DEFINITION AC128066
VERSION    AC128066.3 GI:25139719
KEYWORDS  HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
           Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS  Muzny,D,Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
           Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
           Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
           Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
           Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
           Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
           Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
           Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
           Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
           Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
           Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Diyya,K.,
           Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
           Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
           Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
           Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
           Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
           Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
           Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
           Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogue,M.,
           Hollins,B., Howells,S., Hulvik,S., Hume,J., Idlebird,D., Jackson,A.,
           Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
           Karkathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
           Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
           Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
           Lorensuhewa,L., Loulseg,H., Lozado,R.J., Lu,X., Ma,J.,
           Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
           Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
           Mathew,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
           Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
           Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Naik,L.,
           Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
           Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
           Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
           Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
           Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reich,R.,
           Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
           Rives,C., Rodkey,T., Rojass,A., Rose,M., Rose,R., Ruiz,S.J.,
           Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
           Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,

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Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,P., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 150089)
Worley,K.C.
Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 150089)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23665247.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GZRZ
Center clone name: CH230-465J23
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 142316 bases at least Q40
Consensus quality: 143836 bases at least Q30
Consensus quality: 14418 bases at least Q20
Estimated insert size: 147956; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved
* 1 150089: contig of 150089 bp in length.
* Location/Qualifiers
  1..150089
    /organism="Rattus norvegicus"
    /mol_type="genomic DNA"
    /db_xref="taxon:10116"
    /clone="CH230-465J23"
  1..1354
    /note="wgs_end_extension

FEATURES
source
misc_feature

```

```

misc_feature      clone_end:Sp6"
4927. .5761
/notes="clone boundary
clone_end:Sp6"
site:
end_sequence:RXBNK60TVB"
4927. .5712
/notes="clone boundary
clone_end:Sp6"
site:
end_sequence:RXBNK60TV"
complement(146702. .147615)
/notes="clone boundary
clone_end:T7
site:
end_sequence:RXBNK60TJB"

ORIGIN
Query Match      94.4%; Score 17; DB 14; Length 150089;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCTC 18
|||||
Db      54484 CACACCTATTTCATCTC 54468

RESULT 24
BX323576      163069 bp DNA linear VRT 27-AUG-2004
LOCUS
DEFINITION
Zebrafish DNA sequence from clone DKEYP-77A12 in linkage group 7,
complete sequence.
ACCESSION      BX323576
VERSION      BX323576.9 GI:51591805
KEYWORDS      HTG.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 163069)
Johnson,C.
Direct Submission
Submitted (27-AUG-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 27, 2004 this sequence version replaced gi:50724700.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em., EMBL; Sw., SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information
on the WormPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
Zebrafish pUC subclones occasionally display inconsistencies over the

```

```

length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.
Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhirong Bao and Sean Eddy, submitted), and those
beginning 'drr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEYP-77A12
is from a Zebrafish BAC library
VECTOR: pIndigoBAC-5
Location/Qualifiers
1..163069
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEYP-77A12"
/clone_lib="Daniokeypilot"

FEATURES
source
Query Match      94.4%; Score 17; DB 5; Length 163069;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCTC 18
|||||
Db      100672 CACACCTATTTCATCTC 100688

RESULT 25
AL732528      166465 bp DNA linear ROD 07-SEP-2002
LOCUS
DEFINITION
Mouse DNA sequence from clone RP23-218B17 on chromosome 2, complete
sequence.
ACCESSION      AL732528
VERSION      AL732528.12 GI:22798098
KEYWORDS      HTG.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 166465)
Oliver,K.
Direct Submission
Submitted (06-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 12, 2002 this sequence version replaced gi:22213682.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em., EMBL; Sw.,
SWISSPROT; Tr., TrEMBL; Wp., WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
RP23-218B17 is
from the RPCI-23 Mouse PAC Library

```

constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.

FEATURES

source

Location/Qualifiers

```
1. .166465
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /db_xref="taxon:10090"
   /chromosome="2"
   /clone="RP23-218B17"
   /clone_lib="RPCI-23"
```

ORIGIN

Query Match 94.4%; Score 17; DB 9; Length 166465;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18

|||||

Db 125209 CACACCTATTTCATCTC 125193

RESULT 26

BX571839/c

LOCUS

DEFINITION BX571839 168648 bp DNA linear VRT 21-JUL-2004
Zebrafish DNA sequence from clone DKEY-259P7 in linkage group 16,
complete sequence.

ACCESSION

BX571839

VERSION BX571839.8 GI:50470903

KEYWORDS

HTG.

SOURCE

ORGANISM

Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 168648)

AUTHORS

TITLE

JOURNAL

COMMENT

Direct Submission
Submitted (20-JUL-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfsh-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 21, 2004 this sequence version replaced gi:50399659.

Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfsh-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30);
an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a VAC.

The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Emi., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WormPEP; Information
on the WormPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived
Zebrafish pUC subclones occasionally display inconsistency over the
length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhirong Bao and Sean Eddy, submitted), and those

beginning 'drr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-259P7
is from a Zebrafish BAC library
VECTOR: pindigoBAC-5.

FEATURES

source

Location/Qualifiers

```
1. .168648
   /organism="Danio rerio"
   /mol_type="genomic DNA"
   /db_xref="taxon:7955"
   /clone="DKEY-259P7"
   /clone_lib="DanioKey"
```

ORIGIN

Query Match 94.4%; Score 17; DB 5; Length 168648;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18

|||||

Db 100066 CACACCTATTTCATCTC 100050

RESULT 27

AC099634

LOCUS

DEFINITION

AC099634 177551 bp DNA linear HTG 14-JUN-2003
Mus musculus clone RP24-126P14, WORKING DRAFT SEQUENCE, 19
unordered pieces.

ACCESSION

AC099634

VERSION

AC099634.2 GI:31745422

KEYWORDS

HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.

SOURCE

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 177551)

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Unpublished

2 (bases 1 to 177551)

Birren, B., Linton, L., Nussbaum, C., and Lander, E.

Mus musculus, clone RP24-126P14

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B.,
Choepel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
Cooke, P., DeArelano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrum, J.,
Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 3 (bases 1 to 177551)

Birren, B., Nussbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collamore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S.,

Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrum,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,W., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
Submitted (14-JUN-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 14, 2003 this sequence version replaced gi:16947881.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

TITLE JOURNAL

COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L17389
Center clone name: 126_P14
----- Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 171576 bases at least Q40
Consensus quality: 173582 bases at least Q30
Consensus quality: 174212 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 175751; sum-of-contigs
Quality coverage: 6.9 in Q20 bases; agarose-fp
Quality coverage: 6.9 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 9555: contig of 9555 bp in length
* 9556 9555: gap of 100 bp
* 9556 10295: contig of 640 bp in length
* 10296 10395: gap of 100 bp
* 10396 11093: contig of 698 bp in length
* 11094 11193: gap of 100 bp
* 11194 12358: contig of 1165 bp in length
* 12359 12459: gap of 100 bp
* 12459 13510: contig of 1052 bp in length
* 13511 13610: gap of 100 bp
* 13611 16664: contig of 3054 bp in length
* 16665 16764: gap of 100 bp
* 16665 19485: contig of 2721 bp in length
* 19486 19585: gap of 100 bp
* 19586 23382: contig of 3797 bp in length
* 23383 23482: gap of 100 bp
* 23483 25198: contig of 1716 bp in length
* 25199 25298: gap of 100 bp
* 25299 31520: contig of 6222 bp in length
* 31521 31620: gap of 100 bp
* 31621 39389: contig of 7769 bp in length
* 39390 39489: gap of 100 bp
* 39490 47996: contig of 8507 bp in length
* 47997 48096: gap of 100 bp

* 48097 59411: contig of 11315 bp in length
* 59412 59511: gap of 100 bp
* 59512 70527: contig of 11016 bp in length
* 70528 70627: gap of 100 bp
* 70628 80578: contig of 9951 bp in length
* 80579 80678: gap of 100 bp
* 80679 94343: contig of 13665 bp in length
* 94344 94443: gap of 100 bp
* 94444 106090: contig of 11647 bp in length
* 106091 106190: gap of 100 bp
* 106191 129001: contig of 22811 bp in length
* 129002 129101: gap of 100 bp
* 129102 177551: contig of 48450 bp in length.
FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-126P14"
/clone_lib="RPC1-24 Male Mouse BAC"
misc_feature
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/note="assembly_fragment"
clone_end:SP6
vector_side:left
9556..9655
/estimated_length=100
9656..10255
/note="assembly_fragment"
10296..10395
/estimated_length=100
10396..11093
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11094..11193
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13511..13610
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23483..25198
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39490..47996
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48097..59411
/note="assembly_fragment"
59412..59511

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misc_feature      /estimated length=100
59512..70527
/note="assembly_fragment"
gap              70528..70627
/estimated length=100
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Query Match      94.4%; Score 17; DB 14; Length 177551;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
Db 48878 CACACCTATTTCATCTC 48894
|||||

RESULT 28
BX247878/c
LOCUS      BX247878      190715 bp      DNA      linear      VRT 25-DEC-2003
DEFINITION Zebrafish DNA sequence from clone CH211-26605 in linkage group 7,
complete sequence.
ACCESSION  BX247878
VERSION     BX247878.5 GI:40363411
KEYWORDS   HTG.
SOURCE     Danio rerio (zebrafish)
ORGANISM   Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 190715)
Woodmansey R.
Direct Submission
Submitted (25-DEC-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Dec 25, 2003 this sequence version replaced gi:38091208.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C_elegans/wormpep
Zebrafish pUC subclones occasionally display inconsistency over the
length of mononucleotide A/T runs and conserved TA repeats. Where
this is found the longest good quality representation will be
submitted.
Repeat names beginning 'Dr' were identified by the Recon repeat
discovery system (Zhiron Bao and Sean Eddy, submitted), and those
beginning 'dr' were identified by Rick Waterman (Stephen Johnson
lab, WashU). For further information see
http://www.sanger.ac.uk/projects/D_rerio/fishmask.shtml CH211-26605
is from a CHORI-211 BAC library
VECTOR: pTARBAC2.1.
FEATURES
```

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1. 190715
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="CH211-26605"
/clone_lib="CHORI-211"

Query Match      94.4%; Score 17; DB 5; Length 190715;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
Db 88799 CACACCTATTTCATCTC 88783
|||||

RESULT 29
AC105464/c
LOCUS      AC105464      203746 bp      DNA      linear      HTG 13-NOV-2002
DEFINITION Rattus norvegicus clone CH230-25001, WORKING DRAFT SEQUENCE.
ACCESSION  AC105464
VERSION     AC105464.4 GI:24942074
KEYWORDS   HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
1 (bases 1 to 203746)
Muzny D.Marie., Metzker M.Lee., Abramzon S., Adams C., Alder J.,
Allen C., Allen H., Alebrooks S., Amin A., Anguiano D.,
Anyalebechi V., Aoyagi A., Ayodeji M., Baca E., Baden H.,
Baldwin D., Bandaranaike D., Barber M., Barnstead M., Benahmed F.,
Biswal K., Blair J., Blankenburg K., Blyth P., Brown M.,
Bryant N., Buhay C., Burch P., Burrell K., Calderon E.,
Cardenas V., Carter K., Cavazos I., Ceasar H., Center A.,
Chacko J., Chavez D., Chen G., Chen Y., Chen Y., Chen J.,
Cleveland C., Cockrell R., Cox C., Coyle M., Cree A., D'Souza L.,
Davila M.L., Davis C., Davy-Carroll L., De Anda C., Dederich D.,
Delgado O., Denson S., Deramo C., Ding Y., Dinh H., Divya K.,
Draper H., Dugan-Rocha S., Dunn A., Durbin K., Duval B., Eaves K.,
Egan A., Escotto M., Eugene C., Evans C.A., Falls T., Fan G.,
Fernandez S., Finley M., Flagg N., Forbes L., Foster M., Foster P.,
Frazer C.M., Gabisi A., Ganta R., Garcia A., Garner T., Garza M.,
Gebregeorgis E., Geer K., Gill R., Grady M., Guerra M., Guevara W.,
Gunaratne P., Haaland W., Hamil C., Hamilton C., Hamilton K.,
Harvey Y., Havlak P., Hawes A., Henderson N., Hernandez J.,
Hernandez R., Hines S., Hladun S.L., Hodgson A., Hogues M.,
Hollins B., Howells S., Hulyk S., Hume J., Idlebird D., Jackson A.,
Jackson L., Jacob L., Jiang H., Johnson B., Johnson R., Jolivet A.,
Karpathy S., Kelly S., Kelly S., Khan Z., King L., Kovar C.,
Kowis C., Kraft C.L., Lebow H., Levan J., Lewis L., Li Z., Liu J.,
Liu J., Liu W., Liu Y., London P., Longacre S., Lopez J.,
Lorensuwa L., Louisedge H., Lozado R.J., Lu X., Ma J.,
Maheshwari M., Mahindratne M., Mahmoud M., Malloy K., Mangum A.,
Mangum B., Mapua P., Martin K., Martin R., Martinez E.,
Mawhinney S., McLeod M.P., McNeill T.Z., Meenen E.,
Milosavljevic A., Miner G., Minja E., Montemayor J., Moore S.,
Morgan M., Morris K., Morris S., Munidasa M., Murphy M., Nair L.,
Nankervis C., Neal D., Newton N., Nguyen N., Norris S.,
Nwaekelimeh O., Okwunnu G., Olarnpunsagoon A., Pal S., Parks K.,
Pasternak S., Paul H., Perez A., Perez L., Pfankoch C.,
Plopper F., Poindexter A., Popovic D., Primus E., Pu L.-L.,
Puzo M., Quiroz J., Rachlin E., Reeves K., Regier M.A., Reigh R.,
Reilly B., Reilly M., Ren Y., Reuter M., Richards S., Riggs F.,
Rivers C., Rodkey T., Rojas A., Rose M., Rose R., Ruiz S.J.,
Sanders W., Savery G., Scherer S., Scott G., Shatsman S., Shen H.,
Shetty J., Shvartsbeyn A., Sisson I., Sitter C.D., Smajs D.,
Sneed A., Sodergren E., Song X.-Z., Sorelle R., Sosa J.,
Steimle M., Strong R., Sutton A., Svatek A., Taber P., Taylor C.,
Taylor T., Thomas N., Thomas S., Tingey A., Trejos Z., Usmani K.,
Valas R., Vera V., Villasana D., Waldron L., Walker B., Wang J.,
```

Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstein,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 203746)
Worley K.C.

TITLE JOURNAL

REFERENCE

TITLE JOURNAL

Submitted (09-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 203746)
Rat Genome Sequencing Consortium.

REFERENCE AUTHORS JOURNAL

Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:23101651.

COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GNAB

Center clone name: CH230-25001

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 195938 bases at least Q40

Consensus quality: 197488 bases at least Q30

Consensus quality: 198349 bases at least Q20

Estimated insert size: 202264; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 203746: contig of 203746 bp in length.

Location/Qualifiers

1. .203746

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone="CH230-25001"

2746. .3484

/note="clone_boundary"

clone_end:T7

site:

FEATURES source

misc_feature

misc_feature

/note="clone_boundary
clone_end:Sp6
site:
end_sequence:BZ215948"
195142. .197124
/note="wgs_end_extension
clone_end:Sp6"
200690. .203746
/note="wgs_end_extension
clone_end:Sp6"

misc_feature

misc_feature

ORIGIN

Query Match 94.4%; Score 17; DB 14; Length 203746;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18

DB 7055 CACACCTATTTCATCTC 7039

RESULT 30

AC136410

LOCUS

DEFINITION

AC136410.3 GI:51948542

HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus;
1 (bases 1 to 213533)

REFERENCE

AUTHORS

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allien,H., Albrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Gear,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Healand,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Haviak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorenshewa,L., Louised,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapa,P., Martin,K., Martin,R., Martinez,E., Mawhney,S., McLeod,M., McNeill,T., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackeleme,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindeux,A., Popovic,D., Primus,E., Pu,L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A.,

Sisson, I., Sitter, C.D., Smajcs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorrelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Trejos, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

TITLE

JOURNAL

REFERENCE

AUTHORS

CONSRMT

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished

2 (bases 1 to 213533)

Rat Genome Sequencing Consortium

Direct Submission

Submitted (01-NOV-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 213533)

Worley, K.C.

Direct Submission

Submitted (15-SEP-2004) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

On Sep 9, 2004 this sequence version replaced gi:25188275.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help.tmc.edu

----- Project Information

Center project name: KAIJ

Center clone name: CH230-489H14

----- Summary Statistics

Sequencing vector: Plasmid;

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.990329

Consensus quality: 322827 bases at least Q40

Consensus quality: 326270 bases at least Q30

Consensus quality: 328526 bases at least Q20

Estimated insert size: 372074; sum-of-contigs estimation

Quality coverage: 8x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone

* The sequence data in this record represents an 'enhanced' version

of a Phase 2 submission. The indicated order and orientation of

each sequence has been established using one or more of the

following: read-pair data from individual subclones, overlaps

with neighboring clones, alignment with available reference

sequence (e.g., human), and/or confirmation by PCR testing.

* NOTE: This is a 'working draft' sequence. It currently

consists of 5 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces

is believed to be correct as given, however the sizes

of the gaps between them are based on estimates that have

been provided by the submitter.

* This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

* 1 28444: contig of 28444 bp in length

* 28445 30144: gap of 1700 bp

* 30145 79409: contig of 49265 bp in length

* 79410 80509: gap of 1100 bp

* 80510 92987: contig of 12488 bp in length

* 92988 94297: gap of 1300 bp

* 94298 185713: contig of 91416 bp in length

* 185714 187713: gap of 2000 bp

* 187714 213533: contig of 25820 bp in length.

FEATURES

source

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/db_xref="taxon:10116"
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/note="assembly_name:Contig148"
28445. 30144
/note="assembly_name:gap"
28445. 30144
/estimated_length=1700
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/note="assembly_name:Contig150"
79410. 80509
/note="assembly_name:gap"
79410. 80509
/estimated_length=1100
80510. 92997
/note="assembly_name:Contig152"
92998. 94297
/note="assembly_name:gap"
92998. 94297
/estimated_length=1300
94298. 185713
/note="assembly_name:Contig153"
185714. 187713
/note="assembly_name:gap"
185714. 187713
/estimated_length=2000
187714. 213533
/note="assembly_name:Contig149"

ORIGIN

Query Match 94.4%; Score 17; DB 14; Length 213533;

Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACT 17

Db 87350 CCACACCTATTCTACT 87366

RESULT 31

AC119364/C

LOCUS

DEFINITION

AC119364

AC119364

AC119364.5

HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

KEYWORDS

Rattus norvegicus (Norway rat)

SOURCE

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Murioidea; Muridae; Murinae; Rattus.

REFERENCE

1 (bases 1 to 213533)

AUTHORS

Murphy D.Marie, Metzker M.Lee, Abramson S., Adams C., Alder J.,

Allen C., Allen H., Alsbrooks S., Amin A., Anguiano D.,

Anyalebechi V., Ayodeji A., Ayodeji M., Baca E., Baden H.,

Baldwin D., Bandaranaike D., Barber M., Barnstead M., Benahmed F.,

Biswal K., Blair J., Blankenburg K., Blyth P., Brown M.,

Bryant N., Buhay C., Burch P., Burrell K., Calderon E.,

Cardenas V., Carter K., Cavazos I., Ceasar H., Center A.,

Chacko J., Chavez D., Chen G., Chen R., Chen Y., Chen Z., Chu J.,

Cleveland C., Cockrell R., Cox C., Coyle M., Crea A., D'Souza L.,

Davila M.L., Davis C., Davy-Carroll L., De Anda C., Dederich D.,

Delgado O., Denson S., Deramo C., Ding Y., Dinh H., Divya K.,

Draper H., Dugan-Rocha S., Dunn A., Durbin K., Duval B., Eaves K.,

Egan A., Escotto M., Eugene C., Evans C.A., Falls T., Fan G.,

Fernandez S., Finley M., Flagg N., Forbes L., Foster M., Foster P.,

Fraser C.M., Gabisi A., Ganta R., Garcia A., Garner T., Garza M.,

Georgiev B., Geer K., Gill R., Grady M., Guerra W., Guevara W.,

Gunaratne P., Haaland W., Hamil C., Hamilton C., Hamilton K.,

Harvey Y., Havlak P., Hawes A., Henderson N., Hernandez J.,

Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hoques, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kellow, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levay, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhea, L., Louseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaekemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Prannokun, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzao, M., Qunroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajis, D., Sneed, A., Sodergren, E., Song, X.-Z., Soreller, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taborz, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wluczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederthausen, A., Weiss, R., Weinstock, G., Smith, H.O., Weinstock, G. and Gibbs R.A.

TITLE	JOURNAL	REFERENCE
Direct Submission	Unpublished	2 (bases 1 to 234063)

JOURNAL Submitted (26-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 234063)

REFERENCE
AUTHORS
3 (bases 1 to 234063)
Rat Genome Sequencing

TITLE
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza Houston, TX 77030, USA

COMMENT

On Nov 15, 2002 this sequence version replaced gi:32659754. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GVGG
Center Clone name: CH230-179F6

```

* -----
* NOT: Estimated insert size may differ from sequence length
*       (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOT: This is a 'working draft' sequence. It currently
*       consists of 2 contigs, the true order of the pieces
*       is not known and their order in this sequence record is
*       arbitrary. Gaps between the contigs are represented as
*       runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*

```

be preserved.

*	1	229273:	contig of 229273 bp in length
*		229274	229373: gap of unknown length
*		229374	234063: contig of 4690 bp in length.

FEATURES
SOURCE

```

1. 234063
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-179F6"

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misc feature

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1. .1040
/note="wgs_end_extension
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misc feature

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clone_end:Sp6
17876. .18364
/note="clone_boundary
clone end:Sp6
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clone_end:sp3
site:
end_sequence:BH301784"
complement(222098..222893)
/note="clone_boundary
clone end:T7
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site:
end_sequence:BH301783"
226417. 227431

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clone end: T7"
227933. .229273
/note="wgs end extension

```

gan

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clone_end:17
229274. .229373
/estimated length=unknown
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ORIGIN

Query Match	94.4%	Score 17;	DB 14;	Length 234063;
Best Local Similarity	100.0%;	pred. No. 1.4e+02;		
Matches 17;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

Qy 2 CACACCTATTCATACTC 18
|||
Db 177485 CACACCTATTCATACTC 177469

RESULT 32	AC128521/c	AC128521	250548 bp	DNA	linear	HTG 09-OCT-2002
LOCUS		Rattus norvegicus clone CH230-29N17,				
DEFINITION		***, 2 unordered pieces.				*** SEQUENCING IN PROGRESS

AC128521	GI:22855063
AC128521.2	GI:22855063
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED	
Rattus norvegicus (Norway rat)	
Rattus norvegicus	

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE
AUTHORS

1. (Pages 1 to 250548)
Murny D. Marie, Metzker M. Lee., Abramson S., Adams C., Alder, J., Allen C., Allen H., Alsbrooks, S., Amin, A., Angulano, D., Anylebechi, V., Ayvagi A., Ayodeji M., Baca E., Baden H., Baldwin, D., Bandaranaika D., Barber M., Barnstead, M., Benahmed, F., Biswalo, K., Blair J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas V., Carter, K., Cavazos, I., Ceasar, H., Center A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gegeorgis, E., Geer, K., Gill, R., Garcia, A., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulvik, S., Hume, J., Idelbird, D., Jackson, A., Jacob, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kowar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulaeged, H., Lozada, R.J., Lu, X., Ma, J., Maheeshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nait, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokeme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Fu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C.D., Smajis, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 250548)
Worley, K.C.

Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 250548)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21903266.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYRL
Center clone name: CH230-29N17
----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 235756 bases at least Q40
Consensus quality: 237808 bases at least Q30
Consensus quality: 239171 bases at least Q20
Estimated insert size: 257025; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 249385: contig of 249385 bp in length
* 249386 249485: gap of unknown length
* 249486 250548: contig of 1063 bp in length.

FEATURES

source
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-29N17"
misc_feature
245412..247253
/note="wgs contig"
misc_feature
247780..249385
/note="wgs contig"
gap
249386..249485
/estimated_length=unknown

ORIGIN

Query Match 94.4%; Score 17; DB 14; Length 250548;
Best Local Similarity 100.0%; Pred. No. 1.4e-02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
|||||

DB 234445 CACACCTATTCATCTC 234429

RESULT 33

AC095794
Rattus norvegicus clone CH230-9f15, *** SEQUENCING IN PROGRESS ***,
5 unordered pieces.

AC095794 5 GI:24940895 linear HTG 13-NOV-2002

HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Rattus.

1 (bases 1 to 259335)

Muzny, D., Marie, Metzker, M., Lee, A., Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Haves, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louseged, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathew, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelme, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, P., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shwartzbeyn, A., Sisson, I., Sitter, C. D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasaana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G., and Gibbs, R. A.

Direct Submission
Unpublished
2 (bases 1 to 259335)
Worley, K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 259335)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 13, 2002 this sequence version replaced gi:22773035.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKKK
Center clone name: CH230-9F15
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 234689 bases at least Q40
Consensus quality: 238072 bases at least Q30

Consensus quality: 240241 bases at least Q20
Estimated insert size: 241666; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 245368: contig of 245368 bp in length
* 245369 245468: gap of unknown length
* 245469 254303: contig of 8835 bp in length
* 254304 254403: gap of unknown length
* 254404 256377: contig of 1974 bp in length
* 256378 256477: gap of unknown length
* 256478 257611: contig of 1134 bp in length
* 257612 257711: gap of unknown length
* 257712 259335: contig of 1624 bp in length.

FEATURES
source
1..259335
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-9F15"
1..1341
/note="wgs end extension
clone_end:Sp6"
6828..7544
/note="clone boundary
clone_end:Sp6
site:
end sequence:BH340872"
135172..136506
/note="wgs contig"
245369..245468
/estimated_length=unknown
245469..247036
/note="wgs contig"
254304..254403
/estimated_length=unknown
256378..256477
/estimated_length=unknown
257612..257711
/estimated_length=unknown

ORIGIN
Query Match 94.4%; Score 17; DB 14; Length 259335;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CACACCTATTTCATCTC 18
Db 93238 CACACCTATTTCATCTC 93254
|||||
RESULT 34
DQ097951
LOCUS DQ097951 2005 bp DNA linear PFI 23-JUL-2005
DEFINITION Homo sapiens nonfunctional T cell receptor alpha variable 8-5
ACCESSION DQ097951
VERSION DQ097951
KEYWORDS DQ097951.1 GI:70913413
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 2005)
AUTHORS Mackelprang,R., Livingston,R.J., da Ponte,S.H., Rieder,M.J., Yi,Q.,
Subrahmanyam,L., Montoya,M. and Nickerson,D.A.
TITLE Direct Submission
JOURNAL Submitted (17-JUN-2005) Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
COMMENT This work was supported by the National Institutes of Health
(AI45278) and a Program for Genomic Applications (HL66682 and
HL66642) (URL: <http://chum.gs.washington.edu/>).
FEATURES
source
1..2005
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/germline
51
variation
/frequency="0.49"
/replace="g"
95
variation
/frequency="0.47"
/replace="a"
196
variation
/frequency="0.08"
/replace="a"
303
variation
/frequency="0.49"
/replace="t"
328
variation
/frequency="0.21"
/replace="a"
339..1559
gene
/gene="TRAV8-5"
339..1559
misc_feature
/notes="TRAV8-5"
/notes="nonfunctional T cell receptor alpha variable 8-5
due to premature stop codon"
339..1559
variation
/gene="TRAV8-5"
532
/genes="TRAV8-5"
/frequency="0.46"
/replace="a"
720
variation
/gene="TRAV8-5"
/frequency="0.47"
/replace="g"
950
variation
/genes="TRAV8-5"
/frequency="0.40"
/replace="g"
1006
variation
/gene="TRAV8-5"
/frequency="0.47"
/replace="a"
1016
variation
/gene="TRAV8-5"
/frequency="0.16"
/replace="t"
1033
variation
/genes="TRAV8-5"
/frequency="0.01"
/replace="t"
1386
variation
/genes="TRAV8-5"
/frequency="0.50"
/replace="a"
1398
variation
/genes="TRAV8-5"
/frequency="0.48"

variation
/replace="c"
1399
/gene="TRAV8-5"
/frequency="0.48"
/replace="t"
ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 2005;
Best Local Similarity 94.4%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTCATCTC 18
|||||
Db 1432 CCACACCTATTCATACAC 1449
RESULT 35
AY135687
LOCUS Mus musculus argonaute 1 protein (Agol) gene, partial cds.
DEFINITION
ACCESSION AY135687
AY135687.1 GI:26449032
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 64211)
AUTHORS Carmell,M.A., Xuan,Z., Zhang,M.Q. and Hannon,G.J.
TITLE The Argonaute family: tentacles that reach into RNAi, developmental
control, stem cell maintenance, and tumorigenesis
JOURNAL Genes Dev. 16 (21), 2733-2742 (2002)
PUBMED 12414724
REFERENCE 2 (bases 1 to 64211)
AUTHORS Adams,M. and Mural,R.
TITLE Direct Submission
JOURNAL Submitted (24-JUL-2002) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
FEATURES
source
1..64211
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
11710..11763
gap /estimated_length=54
15643..15790
gap /estimated_length=148
<2001..>44211
gene /gene="Agol"
/note="Agol"
mRNA join(<20001..20245,22112..22232,22824..23005,23408..23544,
23776..23910,24044..24131,24655..24802,29574..29693,
30050..30172,30307..30440,35046..35230,40779..40983,
41113..41203,41936..42130,42708..42842,43588..43689,
44012..>44211)
/gene="Agol"
/product="argonaute 1 protein"
CDS join(20001..20245,22112..22232,22824..23005,23408..23544,
23776..23910,24044..24131,24655..24802,29574..29693,
30050..30172,30307..30440,35046..35230,40779..40983,
41113..41203,41936..42130,42708..42842,43588..43689,
44012..>44211)
/gene="Agol"
/codon_start=1
/product="argonaute 1 protein"
/protein_id="AA075579.1"
/db_xref="GI:26449033"
/translation="MSDGRRLPDSVLGTGVFVTAAGAYLPPLQVFOAPRRPGIGTV
GKPKLLANYFEVDIPKIDVHYEVDIKDKCPRVNREVVEVMYQHFQPIFGDRKP
YDGGKNITVTALPIGHERVDFTVIGEGKDRIFKVISIKWLAIVSWMLHEALVSG
QIPVPLESVQALDVAIRHLSMRITPVGRSFPSPPEGYTHPLGGREVMFGHQSVRP
AMWKMLNIDVSATFYKAQPVIEFMCEVLDIRNIDQPKPLTDSQRVFTKEIKGLK

```

VEVTHCGQMKRYRVCNTRRSPASHQTFPQLQESGQVETVAQFKQKYNLQKYPH
LPCLOVQSQKHLYPLEVCNI VAGORCIKKLTNDOTNKIATARSAPDROEESRL
MKNASVLPYQIEFGIKVKDDMTVTGRVLPAPILQYGRNRATNPQWDMRGK
QFYNGLEIKWATACAPQKQCEEBVLKNFTQDLRKISKDAGMPQGGPCFKYAGGA
DSVEPNRHLKNTYSGQLIIVLPKTPVIAEVRVGGDTLLGMATQCQVQKNNVKTS
POTLSNLCINKVLGGINNLI VPHORYERLLALSPPGESAVFQOPVIFLGADVT
HPGAGKGPSTAVVGSMDAHPSCYCATVRQPRQEIIEDLSYVRELLIQFYKST
RFPKTRIIIFRQGVPEGQLPQILHYELLAIRQDACIKLEKDYQFGITYI VVQKRHHTRL
FCADKNERIGKSGNI PAGTTVDNTNI THPEFDFYLCSHAGIOGTSRPSHYVLWDDNR
FPADELQIILTQOLCHTYVTRSVSPAPAYVARLVAFPRARHLVDKHDH"
25228.. .52547
/estimated_length=20
43039.. .43264
/estimated_length=226

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ORIGIN

```

Query Match      91.1%; Score 16.4; DB 9; Length 64211;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CCACACCTATTTCATCTC 18
Db 63505 CCACACCTATTTCATCTC 63522

```

RESULT 36

```

AC151470      68792 bp      DNA      linear      HTG 02-SEP-2004
Xenopus tropicalis, WORKING DRAFT SEQUENCE, 5 ordered pieces.

```

```

AC151470
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

Xenopus tropicalis (Silurana tropicalis)

```

```

Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Silurana.

```

```

1 (bases 1 to 68792)

```

```

Tindall A.J., Pownall M.E., Morris I.D. and Isaacs H.V.

```

```

The Xenopus tropicalis peroxidase gene is expressed within the
developing neural tube and pronephric kidney

```

```

Dev. Dyn. (2004) In press

```

```

2 (bases 1 to 68792)

```

```

DOE Joint Genome Institute.

```

```

Direct Submission

```

```

Submitted (02-SEP-2004) Production Genomics Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive B100, Walnut Creek, CA
94598-1698, USA

```

COMMENT

```

* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

```

```

1 5364: contig of 5364 bp in length

```

```

5365 5464: gap of unknown length

```

```

5465 6272: contig of 808 bp in length

```

```

6273 6372: gap of unknown length

```

```

6373 66225: contig of 59853 bp in length

```

```

66226 66325: gap of unknown length

```

```

66326 67110: contig of 785 bp in length

```

```

67111 67210: gap of unknown length

```

```

67211 68792: contig of 1582 bp in length.

```

```

Location/Qualifiers

```

```

1. .68792

```

FEATURES

```

source

```

```

/organism="Xenopus tropicalis"

```

```

/mol_type="genomic DNA"

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```

/db_xref="taxon:8364"

```

```

5365..5464

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```

/estimated_length=unknown

```

```

/clone="CTC-297N14"

```

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gap      6273.. .6372
/estimated_length=unknown
gap      66226.. .66325
/estimated_length=unknown
gap      67111.. .67210
/estimated_length=unknown

```

ORIGIN

```

Query Match      91.1%; Score 16.4; DB 14; Length 68792;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CCACACCTATTTCATCTC 18
Db 9134 CCACCTCTATTTCATCTC 9151

```

RESULT 37

```

AC006262/c

```

```

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

```

```

AC006262

```

```

AC006262.2 GI:15718550

```

```

HTG.

```

```

Homo sapiens (human)

```

```

Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

```

```

Hominidae; Homo.

```

```

1 (bases 1 to 106320)

```

```

Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Briler A., Christensen M., Georgescu A., Avila J.,
Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
Krommiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S.,
Kobayashi A., Olsen A.S. and Cartano A.V.

```

```

Sequence analysis of a 1.9 Mb region in 19q13.2 between APOE and
D19S412

```

```

Unpublished

```

```

2 (bases 1 to 107573)

```

```

Lamerdin J.E.

```

```

Direct Submission

```

```

Submitted (30-DEC-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

```

```

3 (bases 1 to 106320)

```

```

Lamerdin J.E.

```

```

Direct Submission

```

```

Submitted (30-DEC-1998) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

```

```

4 (bases 1 to 107573)

```

```

Lamerdin J.E.

```

```

Direct Submission

```

```

Submitted (21-SEP-2001) Joint Genome Institute, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA

```

```

On Sep 21, 2001 this sequence version replaced gi:4079612.

```

```

Map and sequence oriented from centromere to q telomere. BC264576
overlaps BC282485 (CTC-344H19, AC007785) to the left from bases 1
to 20,296 of this accession, and overlaps BC82621 (CTB-139A18,
AC007193) to the right from bases 106,317 to 107,573 of this
accession. This sequence does not represent the entire insert of
BC264576. Additional chromosome 19 map and sequence information may
be obtained at: http://www-bio.llnl.gov/bbrp/genome/genome.html.

```

```

Location/Qualifiers

```

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1. .107573

```

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/organism="Homo sapiens"

```

```

/mol_type="genomic DNA"

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/db_xref="taxon:9606"

```

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/chromosome="19"

```

```

/map="19q13.2 between APOE and D19S412"

```

```

/clone="CTC-297N14"

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/cell_line="9785X"
/cell_type="Fibroblast"
/notes="LNL clone name: BC264576 BAC library obtained
from Research Genetics."
354. .567
misc_feature
/notes="DPS similarity to AA456254 zx99d06.r1 Soares
NHMPuS1 Homo sapiens cDNA clone 811883 5'; (3. .215); 100%
identity."
repeat_region
complement(669. .800)
/rpt_family="AluJb"
/rpt_family="AluJb"
repeat_region
complement(829. .953)
/rpt_family="GGAJn"
/rpt_family="GGAJn"
repeat_region
complement(1035. .2017)
/rpt_family="L1MB7"
/rpt_family="L1MB7"
repeat_region
complement(2014. .2202)
/rpt_family="L1MA7"
/rpt_family="L1MA7"
repeat_region
complement(2206. .2495)
/rpt_family="AluJo"
/rpt_family="AluJo"
repeat_region
complement(2497. .2728)
/rpt_family="L1MA7"
/rpt_family="L1MA7"
repeat_region
complement(2730. .3133)
/rpt_family="L1MB7"
/rpt_family="L1MB7"
repeat_region
3158. .3447
/rpt_family="AluJb"
/rpt_family="AluJb"
repeat_region
complement(3448. .3803)
/rpt_family="L1MB7"
/rpt_family="L1MB7"
repeat_region
complement(3805. .4108)
/rpt_family="AluJo"
/rpt_family="AluJo"
repeat_region
complement(4110. .4801)
/rpt_family="L1MB7"
/rpt_family="L1MB7"
repeat_region
complement(4826. .5069)
/rpt_family="L1M1"
/rpt_family="L1M1"
repeat_region
complement(5338. .5369)
/rpt_family="AluJb"
/rpt_family="AluJb"
repeat_region
complement(5370. .5708)
/rpt_family="TA)n"
/rpt_family="TA)n"
repeat_region
complement(5974. .6277)
/rpt_family="L1PA8"
/rpt_family="L1PA8"
repeat_region
complement(7059. .7080)
/rpt_family="AluJb"
/rpt_family="AluJb"
repeat_region
complement(7150. .7485)
/rpt_family="L1"
/rpt_family="L1"
repeat_region
complement(7527. .7646)
/rpt_family="FLAM C"
/rpt_family="FLAM C"
repeat_region
complement(7661. .7916)
/rpt_family="L1"
/rpt_family="L1"
repeat_region
7938. .9725
/rpt_family="L1"
/rpt_family="L1"
repeat_region
complement(9736. .10038)
/rpt_family="AluSg"
/rpt_family="AluSg"
misc_feature
/notes="predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 75.000"
repeat_region
11326. .11517
/rpt_family="AluJb"
/rpt_family="AluJb"
misc_feature
/notes="DPS similarity to AA456254 zx99d06.r1 Soares
NHMPuS1 Homo sapiens cDNA clone 811883 5'; (216. .269);
100% identity."
12144. .12411
/rpt_family="AluJb"
/rpt_family="AluJb"
misc_feature
/notes="DPS similarity to overlapping ESTs:
(12144. .12398) AA456254 zx99d06.r1 Soares NHMPuS1 Homo
sapiens cDNA clone 811883 5'; (270. .523); 99%
identity.~(12182. .12411) AI081371 ox76g10.x1
Soares NHMPuS1 Homo sapiens cDNA clone IMAGE:1662306 3';
(454. .225); 100% identity.~(12173. .12411) AA456254
zx99d06.r1 Soares NHMPuS1 Homo sapiens cDNA clone 811883
3'; (455. .217); 100% identity.~(12144. .12411) AA760247
vv74e06.r1 Stragene mouse skin (#937313) Mus musculus
cDNA clone 1228162 5'; (119. .380); 69% identity."
complement(12536. .12614)
/notes="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 90.000"
misc_feature
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/notes="DPS similarity to overlapping ESTs:
(12603. .12818) AA456254 zx99d06.r1 Soares NHMPuS1 Homo
sapiens cDNA clone 811883 3'; (216. .1); 99%
identity.~(12600. .12823) AI081371 ox76g10.x1
Soares NHMPuS1 Homo sapiens cDNA clone IMAGE:1662306 3';
(224. .1); 98% identity.~(12600. .12656) AA760247 vv74e06.r1
Stragene mouse skin (#937313) Mus musculus cDNA clone
1228162 5'; (381. .432); 76% identity."
complement(12967. .16062)
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/rpt_family="L1P5"
misc_feature
/notes="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 58.000"
complement(17695. .18620)
/rpt_family="MER11B"
/rpt_family="MER11B"
repeat_region
19151. .19519
/rpt_family="MLT1B"
/rpt_family="MLT1B"
repeat_region
complement(19592. .19754)
/rpt_family="AluJo"
/rpt_family="AluJo"
repeat_region
complement(19767. .19870)
/rpt_family="MER65A"
/rpt_family="MER65A"
repeat_region
complement(20427. .20481)
/rpt_family="CA)n"
/rpt_family="CA)n"
repeat_region
20546. .20751
/rpt_family="AluJo"
/rpt_family="AluJo"
repeat_region
21128. .21397
/rpt_family="AluSx"
/rpt_family="AluSx"
repeat_region
21768. .22798
/rpt_family="MER11A"
/rpt_family="MER11A"
misc_feature
complement(23050. .23194)
/notes="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 50.000"
complement(24023. .24141)
/rpt_family="FLAM A"
/rpt_family="FLAM A"
repeat_region
complement(24258. .24429)
/rpt_family="AluJb"
/rpt_family="AluJb"
repeat_region
complement(24910. .25309)
/rpt_family="MSTB"
/rpt_family="MSTB"
repeat_region
25325. .25464
/rpt_family="HERVL"
/rpt_family="HERVL"
repeat_region
25732. .25881
/rpt_family="MER45"
/rpt_family="MER45"
repeat_region
complement(26586. .26613)
/rpt_family="AT_rich"
/rpt_family="AT_rich"
repeat_region
complement(26677. .26941)
/rpt_family="MIR"
/rpt_family="MIR"
repeat_region
complement(27078. .27369)
/rpt_family="AluSx"
/rpt_family="AluSx"
repeat_region
complement(27374. .27682)
/rpt_family="AluSg"
/rpt_family="AluSg"
repeat_region
27743. .28177
/rpt_family="L1M1/2"
/rpt_family="L1M1/2"
repeat_region
28646. .28929
/rpt_family="AluSx"
/rpt_family="AluSx"
repeat_region
28987. .29070
/rpt_family="TA)n"
/rpt_family="TA)n"
misc_feature
29085. .29241
/notes="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 50.000"
29332. .29526
/rpt_family="MER4D"
/rpt_family="MER4D"
repeat_region
29527. .29826
/rpt_family="AluSg"
/rpt_family="AluSg"
repeat_region
29827. .29870
/rpt_family="MER4D"
/rpt_family="MER4D"
repeat_region
29870. .30491
/rpt_family="MER4D"
/rpt_family="MER4D"
repeat_region
30523. .30611
/rpt_family="GA)n"
/rpt_family="GA)n"
repeat_region
31175. .31465
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Query Match	91.1%;	Score 16.4;	DB 8;	Length 107573;
Best Local Similarity	94.4%;	Pred. No. 3.2e+02;		
Matches 17;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1	CCACACCTATTTCATCTC	18	
DB	17921	CCACACCTATTTCATACAC	17904	
RESULT 38				
AE017349 08/c				
WPCOMMENT				
Sequence split into 12 fragments LOCUS AE017349 Accession AE017349				
Fragment Name		Begin	End	
AE017349_00		1	110000	
AE017349_01		100001	210000	
AE017349_02		200001	310000	
AE017349_03		300001	410000	
AE017349_04		400001	510000	
AE017349_05		500001	610000	
AE017349_06		600001	710000	
AE017349_07		700001	810000	
AE017349_08		800001	910000	
AE017349_09		900001	1010000	
AE017349_10		1000001	1110000	
AE017349_11		1100001	1178688	
Continuation (9 of 12) of AE017349 from base 800001 (AE017349 Cryptococcus neoformans va				
Query Match	91.1%;	Score 16.4;	DB 15;	Length 110000;
Best Local Similarity	94.4%;	Pred. No. 3.1e+02;		
Matches 17;	Conservative	0;	Mismatches 1;	Indels 0; Gaps 0;
QY	1	CCACACCTATTTCATCTC	18	
DB	70977	CCACACCTTTTCATCTC	70960	
RESULT 39				
AY386265				
LOCUS				
AY386265				
Bovine papular stomatitis virus strain BV-AR02, complete genome.				
ACCESSION				
AY386265.1 GI:40019124				
VERSION				
AY386265.1				
KEYWORDS				
Bovine papular stomatitis virus				
SOURCE				
Bovine papular stomatitis virus				
ORGANISM				
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae; Parapoxvirus.				
REFERENCE				
1 (bases 1 to 134431)				
AUTHORS				
Delhon,G., Tulman,E.R., Afonso,C.L., Lu,Z., de la				
Concha-Bermejo,A., Lehmkuhl,H.D., Piccone,M.E., Kutish,G.F. and				
Rock,D.L.				
Genomes of the Parapoxviruses Orf Virus and Bovine Papular				
Stomatitis Virus				
J. Virol. 78 (1), 168-177 (2004)				
PUBMED				
14671098				
REFERENCE				
2 (bases 1 to 134431)				
AUTHORS				
Kutish,G.F.				
Direct Submission				
Submitted (08-SEP-2003) African Swine Fever Research, Plum Island				
Animal Disease Center, U.S. Department of Agriculture, Agricultural				
Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA				
JOURNAL				
Location/Qualifiers				
FEATURES				
source				
1. .134431				
/organism="Bovine papular stomatitis virus"				
/mol_type="genomic DNA"				
/strain="BV-AR02"				
/isolate="ORFB"				
/isolation_source="three week old calf with oral lesions,				
then passaged in primary lamb kidney cells"				
/db_xref="taxon:129727"				
/country="USA: Arkansas"				

CDS	complement(513..956)	/codon_start=1	/evidence=not experimental	/product="ORF001 hypothetical protein"	/protein_id="AAR98359.1"	/db_xref="GI:41018754"	/translation="MSALRLAAALVALGILLGFPAAPALPAAFVFCGPARAD	/note="similar to Vaccinia virus strain Copenhagen M1L"
CDS	complement(1097..2587)	/codon_start=1	/product="ORF003 ankyrin repeat protein"	/protein_id="AAR98360.1"	/db_xref="GI:41018755"	/translation="MESALRYDYFFTRGPDVRASEVROLLSLGADVNFTGFGNTALHT	/note="similar to Vaccinia virus strain Copenhagen M1L"	
CDS	complement(2656..4215)	/codon_start=1	/product="ORF004 ankyrin repeat protein"	/protein_id="AAR98361.1"	/db_xref="GI:41018756"	/translation="MDHPVEDVADVEDGVEALYNYFCICPRVSARAVRTLKMGADV	/note="similar to Vaccinia virus strain Copenhagen M1L"	
CDS	complement(4331..4627)	/codon_start=1	/evidence=not experimental	/product="ORF005 hypothetical protein"	/protein_id="AAR98362.1"	/db_xref="GI:41018757"	/translation="MSGIPRYGMYDQGNKYGTANDPGGACRPHSLSSGGSSDSSG	/note="similar to Vaccinia virus strain Copenhagen F2L"
CDS	complement(4904..5362)	/codon_start=1	/product="ORF006 vascular endothelial growth factor"	/protein_id="AAR98363.1"	/db_xref="GI:41018758"	/translation="MKCLIVCMQWSLALLCLQCVMQMAFTSGNHNHEVKSVDVY	/note="similar to Vaccinia virus strain Copenhagen B4R"	
CDS	complement(5458..5949)	/codon_start=1	/product="ORF007 dUTPase"	/protein_id="AAR98364.1"	/db_xref="GI:41018759"	/translation="MKCLIVCMQWSLALLCLQCVMQMAFTSGNHNHEVKSVDVY	/note="similar to Vaccinia virus strain Copenhagen B4R"	
CDS	complement(6025..7581)	/codon_start=1	/product="ORF008 ankyrin repeat protein"	/protein_id="AAR98365.1"	/db_xref="GI:41018760"	/translation="MLSRSSVFSFSSHEDLLFRYLETGSPVDLDVVRALVATDADVNFRG	/note="similar to Vaccinia virus strain Copenhagen B4R"	

EVGRPTLHLCLVARNACADIVETILLEAGADVARNADVCVYTPLHCYVQHDYVQLRVV
ETMLAAGAEVRETEGGVFYDNLVLSFLASCGSTGSEADIVRVLIIRAGADVRESDAYDM
TALHVVARNPAARPDPVLGLMEAGADVDRAMDRGHVTPPLAVLISSTGVDNELVAMMLRA
GADPRADMDGRTLHLHLATVPRAKESIMRTLIVDSGCCDPAGIDTGGNTALHYVMAYGT
CRRPVVFLLEKGLMDRONDRAGQALYRAAVFNPAAACRRLLIQMGADLAPVAYTFCFA
VAEVPFRNDPKSAALLERKPPIDILLVRAVATATNNGFFPDSEAAALICVHSLVARGA
GERVRAEVLGYKADAVRECAEIRAMREVRNCADTTLDDLRADESA KAVHPVNAL
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/notes="similar to Vaccinia virus strain Copenhagen F11L
and Molluscum contagiosum virus MC018L"
/codon_start=1
/evidence=not_experimental
/product="ORF009 hypothetical protein"
/protein_id="AAR98366.1"
/db_xref="GI:41018761"
/translation="MTWCGLARMSFSLFRLLSYGRSSCVPTGCMPMRRPRIKNSD
EDSEYDNNVPGDPSDAAAPVARPLVLTVPGASRPVLVDSVFERIIPDVSALVTH
LGEWTEIRLFESFPFRAPVCRVLARIYDAEMFEVKDCQALKLRHGEWYMRQKV
SPDMASFVALICIRNEGVAALAVNNTKYLNTITVGSALVFFPAVRGMFLPHIGGAE
YIILTPMTQDLDDQDYVSPSQDQAIQTASAAETKRACVLSLDLITURIELEE
CYHRICKLMIVTSEFGDLYSNVAKMITEVDIAIKMGSDVGVGENCEVDGASAVA
LCRRASSRRRPVSVSMNRSHSLNIGLNNLFAMPAOCANGTTPHDSLMARMEKDLQ
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GGGYRLTSGSGEVPV"
complement(9147..11078)
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and Molluscum contagiosum virus MC019L"
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FQAQSVRDAIIVPLSKSTRTCTFVDPHRDALDPPAASTQRFATVSRDDPACYTIPES
SGPFLDIRREDEPELLAAFEENIPKAPARSIDELNQLSDAGLHLRMVSTDAVR
RLGTPVRKQTLIDNNVCYGVVIAWPKDPAVTRPDTTEVLAHDARTAAQASWQAPH
LHSPSTCVANFCRCGGDRVQLHSIVMTGMVPRGFSARMVRELLMLWLTCKEH
MTVYGFSFSDVIFPFDNALAGKQTRLSLNLKGNRVTFVDLARFAPGLFSEYIC
EFWGGCAVPEPDIPEVDNPAVEDAAVAQAALMDAARSHQAALARIFPCCDWAA
NGLRVMWGNAGCAGCACHSHSALDMVNAALFIEAGANPAPADARCFRLSPPLREA
ASKRYPAGKPHFVTELTGLLSIALCEVERSEVIRPVLFPDDEDLQRLFSVVLTSVD
IFETANRLKCYIRVIAALEWGESEVLTGIEAQAATRELAIPTOTSNLMSIASMPL
PLDPSSPGSRASVRAFAASYCRSTIHSILSERVDSHFSGNFVRHGYDRFWDRV
AKHLGVSQIEVLPVAVAR"
complement(11155..12291)
/notes="similar to Vaccinia virus strain Copenhagen F13L
and Molluscum contagiosum virus MC021L"
/codon_start=1
/product="ORF011 EVV phospholipase"
/protein_id="AAR98368.1"
/db_xref="GI:41018763"
/translation="MMPFESIPVGAECRVVETLPARVSSLQVNMKSTFECSAIVESA
TKFLYIASPCNLGSRVDVNDKCLTKLAGSVNVTVLVDVQSDKRDABEELREAGVN
YVKVYSGRDVNDNLGSPWISNAGOWYVGSALTGCSISNTKNLGYSTNRLHATDL
MRRYNTFYSMIEPKVPFSLCCAMITPTATDFLHDAGGVFFSDAPKEFLGFVRTL
DEDLVHRIDSANKSIDLSLSPVIRHADRVVWPRMDALLRAIDRSVRVRVIV
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ANNDGTHYKHAFVSNVSKGDIVNLQSAVFERDMRSQYCKPIN"
complement(12312..12569)
/codon_start=1
/evidence=not_experimental
/product="ORF012 hypothetical protein"
/protein_id="AAR98369.1"
/db_xref="GI:41018764"
/translation="MRVHGARNLDEVIDQLDDMQIDGIDIFPEVPDCTPEDVVDALD
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12910..13131
/codon_start=1
/evidence=not_experimental
/product="ORF013 hypothetical protein"
/protein_id="AAR98370.1"
/db_xref="GI:41018765"

/translation="MCLGICFPCEAMLVRRVNRLLIIVRRRVGGEPAYVSVVQACDD
YFTDEPDAQSQSVSLLRAGAEAAPIARV"
complement(13212..13493)
/note="similar to Molluscum contagiosum virus MC026L"
/codon_start=1
/product="ORF014 modified RING finger protein"
/protein_id="AAR98371.1"
/db_xref="GI:41018766"
/translation="MPIKVKSWKVAVKSLACPPVCYICSKKASEGCLNAACPGACPF
VVMCGHYRHRGUGPANTDVCVFSVLQKADIDPETASDAVIREFML"
complement(13500..15110)
/note="similar to Molluscum contagiosum virus MC027L"
/codon_start=1
/evidence=not_experimental
/product="ORF015 hypothetical protein"
/protein_id="AAR98372.1"
/db_xref="GI:41018767"
/translation="MDEBILILLGFAMPDSEMPLSHMNKLRLRLTKLRMNSFAVIMCLR
EAILRKAWLPFGSILGTISDDVRLLEFVSEVDSARENIPEYLVTVQWTHNADIFDE
CMRAMEALFGDSVQRLAMGVVESRYPHLVAERCNSCLAALMPEDASVRFVNAILRYS
GNMAGAVDRREAGSHELADMWVQQHASKIRMPRVVGVAVRVVENDIEGLTKYC
Query Match 91.1%; Score 16.4; DB 13; Length 134431;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
||| ||||| ||||| |||||
Db 96522 CCACACCTATTATACTC 96539
RESULT 40
AC160234/c
LOCUS
AC160234 Rhinolphus ferrumequinum clone VMC7-248B22, WORKING DRAFT
SEQUENCE, 4 ordered pieces.
AC160234
AC160234.2 GI:63055136
HTG; HTGS_PHASE2; HTGS_DRAFT.
Rhinolphus ferrumequinum
Rhinolphus ferrumequinum
Rhinolphus ferrumequinum
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;
Rhinolphidae; Rhinolophinae; Rhinolophus.
1 (bases 1 to 138685)
Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
Engle,J., Fukeenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G.,
Hurle,B., Idol,J.R., Kwong,P., Latic,P., Larson,S., Lee-Lin,S.-Q.,
Legaspi,R., Madden,M., Maduro,Q.L., McDowell,J., Mojidi,H.A., Mullikin,J.C.,
Masello,C., Maskeri,B., Maduro,V.B., Margulies,E.H.,
Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O.,
Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantrupop,S., Stephen,E., Taye,A., Thomas,J.W., Thomas,P.J.,
Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and
Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 138685)
Green,E.D.
Direct Submission
Submitted (20-APR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 138685)
Green,E.D.
Direct Submission
Submitted (06-MAY-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On May 6, 2005 this sequence version replaced gi:62751232.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC

Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: ipi
Center clone name: 248B22

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 137930 bases at least Q40
Consensus quality: 138141 bases at least Q30
Consensus quality: 138305 bases at least Q20
Insert size: 167000; agarose-fp
Quality coverage: 8.50x in Q20 bases; agarose-fp
Quality coverage: 10.26x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 27052: contig of 27052 bp in length
* 27053 27152: gap of unknown length
* 27153 105879: contig of 78727 bp in length
* 105880 105979: gap of unknown length
* 105980 130171: contig of 24192 bp in length
* 130172 130271: gap of unknown length
* 130272 138685: contig of 8414 bp in length.

FEATURES

source

1. .138685
/organism="Rhinolophus ferrumequinum"
/mol_type="genomic DNA"
/db_xref="taxon:59479"
/clone="VMRC7-248B22"
/clone_lib="VMRC7"
/note="BAC resource: <http://bacpac.chori.org/>"

misc_feature

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/note="assembly_fragment
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vector_side:left"

gap

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27153. .105879

misc_feature

83540. .138685
/note="assembly_fragment"

/note="clone overlaps with GenBank Accession Number
AC160240 clone VMRC7-88J4 (center project name ipj)"

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105980. .130171

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/note="assembly_fragment"
130172. .130271

gap

/estimated_length=unknown
130272. .138685

misc_feature

/note="assembly_fragment"

clone_end:SP6
vector_side:right"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 138685;
Best Local Similarity 94.4%; Pred. No. 3.1e-02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18

Db 8910 CCACACCTATTTCATCTC 8893

RESULT 41

AC159925

LOCUS

AC159925 149184 bp DNA linear HTG 06-MAY-2005
Atelerix albiventris clone LB4-257D11, WORKING DRAFT SEQUENCE, 7
ordered pieces.

ACCESSION

AC159925

KEYWORDS

HTG; HTGS PHASE2; HTGS DRAFT.

SOURCE

Atelerix albiventris (Middle-African hedgehog)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
Erinaceinae; Atelerix.

REFERENCE

1 (bases 1 to 149184)

AUTHORS

Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,
Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,
Engle,J., Fukukenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,
Haghghi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G.,
Hurlb,B., Idol,J.R., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,
Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,
Masello,C., Maskeri,B., McDowell,J., Mojidi,H.A., Mullikin,J.C.,
Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O.,
Reddi-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stratipop,S., Stephen,E., Tave,A., Thomas,J.W., Thomas,P.J.,
Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and
Green,E.D.

NISC Comparative Sequencing Initiative

TITLE

Unpublished

REFERENCE

2 (bases 1 to 149184)

AUTHORS

Green,E.D.

TITLE

Direct Submission

JOURNAL

Submitted (14-APR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA

REFERENCE

3 (bases 1 to 149184)

AUTHORS

Green,E.D.

TITLE

Direct Submission

JOURNAL

Submitted (06-MAY-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA

COMMENT

On May 6, 2005 this sequence version replaced gi:62543316.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: <http://www.nisc.nih.gov>
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: kdw
Center clone name: 257D11

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----
 Sequencing vector: plasmid; n/a; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.990319
 Consensus quality: 147467 bases at least Q40
 Consensus quality: 147906 bases at least Q30
 Consensus quality: 148268 bases at least Q20
 Insert size: 145000; agarose-fp
 Inert size: 148584; sum-of-contigs
 Quality coverage: 7.95x in Q20 bases; agarose-fp
 Quality coverage: 7.76x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 7 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 54387: contig of 54387 bp in length
 * 54388 54487: gap of unknown length
 * 54488 82572: contig of 28085 bp in length
 * 82573 82672: gap of unknown length
 * 82673 95830: contig of 13158 bp in length
 * 95831 95930: gap of unknown length
 * 95931 101313: contig of 5383 bp in length
 * 101314 101413: gap of unknown length
 * 101414 128146: contig of 26733 bp in length
 * 128147 128246: gap of unknown length
 * 128247 132000: contig of 3754 bp in length
 * 132001 132100: gap of unknown length
 * 132101 149184: contig of 17084 bp in length.

FEATURES

source	1. .149184 /organism="Atelerix albiventris" /mol_type="genomic DNA" /db_xref="taxon:9368" /clone="LB4-257D11" /clone_lib="LB4" /notes="BAC resource: http://bacpac.chori.org/"
misc_feature	1. 54387 /note="assembly_fragment clone_end:17 vector_side:left"
misc_feature	26261. .149184 /notes="clone overlaps with GenBank Accession Number AC160584 clone LB4-23009 (center project name kdx)"
gap	54388. .54487 /estimated_length=unknown
misc_feature	54488. .82572 /notes="assembly_fragment"
gap	82573. .82672 /estimated_length=unknown
misc_feature	82673. .95830 /notes="assembly_fragment"
gap	95831. .95930 /estimated_length=unknown
misc_feature	95931. .101313 /notes="assembly_fragment"
gap	101314. .101413 /estimated_length=unknown
misc_feature	101414. .128146 /notes="assembly_fragment"
gap	128147. .128246 /estimated_length=unknown
misc_feature	128247. .132000 /notes="assembly_fragment"
gap	132001. .132100 /estimated_length=unknown
misc_feature	132101. .149184 /notes="assembly_fragment"

clone_end:SP6
 vector_side:right"

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 149184;
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 100334 CAACACCTATTTCATCTC 100351

RESULT 42

AC160584

LOCUS

DEFINITION

AC160584 150567 bp DNA linear HTG 05-MAY-2005

Atelerix albiventris clone LB4-23009, WORKING DRAFT SEQUENCE, 2

ordered pieces.

AC160584

AC160584.2 GI:63028190

HTG; HTGS_PHASE2; HTGS_DRAFT.

KEYWORDS

SOURCE

ORGANISM

Atelerix albiventris (middle-African hedgehog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;

Erinaceinae; Atelerix.

1 (bases 1 to 150567)

Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A.,

Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H.,

Engle,J., Fuksenko,T., Gestole,M., Greene,A., Guan,X., Gupta,J.,

Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hunter,G.,

Hurle,B., Idol,J.R., Kwong,P., Laric,P., Larson,S., Lee-Lin,S.-Q.,

Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H.,

Mastaglio,C., Maskeri,B., McDowell,J., Mojidi,H.A., Mullikin,J.C.,

Oestreicher,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O.,

Reddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,

Stantropop,S., Stephen,E., Tave,A., Thomas,J.W., Thomas,P.J.,

Tsipouri,V., Ung,L., Vogt,J.L., Wetherby,K.D., Young,A. and

Green,E.D.

NISC Comparative Sequencing Initiative

Unpublished

2 (bases 1 to 150567)

Green,E.D.

Direct Submission

Submitted (28-APR-2005) NIH Intramural Sequencing Center, 5625

Fishers Lane, Rockville, MD 20852, USA

3 (bases 1 to 150567)

Green,E.D.

Direct Submission

Submitted (05-MAY-2005) NIH Intramural Sequencing Center, 5625

Fishers Lane, Rockville, MD 20852, USA

On May 5, 2005 this sequence version replaced gi:62945479.

----- Genome Center

Center: NIH Intramural Sequencing Center

Center code: NISC

Web site: http://www.nisc.nih.gov

Contact: nisc.zoo@nhgri.nih.gov

----- Project Information

Center project name: kdx

Center clone name: 230009

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

```

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 149914 bases at least Q40
Consensus quality: 150134 bases at least Q30
Consensus quality: 150306 bases at least Q20
Insert size: 148000; agarose-fp
Insert size: 150467; sum-of-contigs
Quality coverage: 8.80x in Q20 bases; agarose-fp
Quality coverage: 8.66x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 27872: contig of 27872 bp in length
* 27873 150567: contig of 122595 bp in length.
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ORIGIN
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Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
Db 73641 CAACACCTATTCTACTC 73658

RESULT 43
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DEFINITION Homo sapiens chromosome 18, clone RP11-244M2, complete sequence.
ACCESSION AC105201
VERSION AC105201.3 GI:18653689
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 151032)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11-244M2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 151032)

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AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferrelira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
Jones,C., Kamat,A., Karatas,A., Kells,C., LaRoque,K.,
Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrum,J.,
Meneus,L., Mihova,T., Mlenga,V., Murphy,T., O'Donnell,P., O'Neill,D.,
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R.,
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 151032)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
Ferrelira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamazares,R.,
Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C.,
McEwan,P., McKernan,K., Meldrum,J., Meneus,L., Mihova,T.,
Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schuback,R., Seaman,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (02-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Feb 13, 2002 this sequence version replaced gi:18483543.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIER
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Project Information
Center project name: L22966
Center clone name: 244_M_2
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/db_xref="taxon:9606"
/chromosome="18"
/map="18"
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/clone_lib="RPCI-11 Human Male BAC"

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repeat_region 3819. .4110
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Query Match 91.1%; Score 16.4; DB 8; Length 151032;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 71375 CCACACCTATTTCATAC 71358

RESULT 44
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LOCUS Homo sapiens clone RP11-13M18, WORKING DRAFT SEQUENCE, 13 unordered
DEFINITION pieces.
ACCESSION AC016373
VERSION AC016373.3 GI:7341913
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 152106)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome, clone RP11-13M18
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 152106)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boquelavkiy L., Boukhgalter,B.,
Brown,A., Casale,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., DeArelano,K., Dewart,K., Domino,M., Donegan,L., Doyle,M.,
Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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VERSION KEYWORDS SOURCE ORGANISM	CR318635.8 GI:63094294 HTG. Danio rerio (zebrafish) Danio rerio Aukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 154312) Heath, P. Direct Submission Submitted (12-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk zfish-help@sanger.ac.uk On May 7, 2005 this sequence version replaced gi:62954551.
REFERENCE AUTHORS TITLE JOURNAL	----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk -----
COMMENT	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-309H8 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACE3.6 ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: vegas@sanger.ac.uk -----
FEATURES source	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Location/Qualifiers 1..156077 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="13" /clone="RP11-309H8" /clone_lib="RPCI-11.2" 1 /note="Clone left_end: RP11-309H8" complement(10967) complement(11000..11005) join(complement(32931..33002), complement(AL353635.17:28148..28173), complement(AL353635.17:27186..27323), complement(AL353635.17:25849..25909), complement(AL353635.17:22461..22941)) /locus_tag="RP11-143O10.1-001" join(complement(32931..33002), complement(AL353635.17:28148..28173), complement(AL353635.17:27186..27323), complement(AL353635.17:25849..25909), complement(AL353635.17:22461..22941)) /locus_tag="RP11-143O10.1-001" /note="match: ESTs: BG183515 BG183515.1 BG189865 BG189865.1 BG191871 BG191871.1" complement(44930..46212) /locus_tag="RP11-309H8.2-001" /pseudo complement(44930..46212) /locus_tag="RP11-309H8.2-001"
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CDS	1

REFERENCE AUTHORS TITLE JOURNAL	CR318635.8 GI:63094294 HTG. Danio rerio (zebrafish) Danio rerio Aukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. 1 (bases 1 to 154312) Heath, P. Direct Submission Submitted (12-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: clonerequest@sanger.ac.uk zfish-help@sanger.ac.uk On May 7, 2005 this sequence version replaced gi:62954551.
COMMENT	During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em.; EMBL; Sw.; SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-309H8 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBACE3.6 ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk -----
FEATURES source	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. Location/Qualifiers 1..154312 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="CH211-253D2" /clone_lib="CHORI-211" 1 /note="Clone left_end: RP11-309H8" complement(10967) complement(11000..11005) join(complement(32931..33002), complement(AL353635.17:28148..28173), complement(AL353635.17:27186..27323), complement(AL353635.17:25849..25909), complement(AL353635.17:22461..22941)) /locus_tag="RP11-143O10.1-001" join(complement(32931..33002), complement(AL353635.17:28148..28173), complement(AL353635.17:27186..27323), complement(AL353635.17:25849..25909), complement(AL353635.17:22461..22941)) /locus_tag="RP11-143O10.1-001" /note="match: ESTs: BG183515 BG183515.1 BG189865 BG189865.1 BG191871 BG191871.1" complement(44930..46212) /locus_tag="RP11-309H8.2-001" /pseudo complement(44930..46212) /locus_tag="RP11-309H8.2-001"
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polyA_site	complement(10967)
polyA_signal	complement(11000..11005)
gene	join(complement(32931..33002), complement(AL353635.17:28148..28173), complement(AL353635.17:27186..27323), complement(AL353635.17:25849..25909), complement(AL353635.17:22461..22941))
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CDS	1

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74442..74460
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/note="Weak data."
97179..97234
/note="Sequence from AC027145, sequenced by Whitehead.
Assembly confirmed by restriction digest data."
134856..134919
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Assembly confirmed by restriction digest data."
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/note="Clone_left_end: RP11-114G1"

ORIGIN
Query Match          91.1%; Score 16.4; DB 8; Length 156077;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 39509 CCACACCTATTTCATCAC 39526

RESULT 47
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LOCUS          160718 bp DNA linear PRI 01-JUN-2001
DEFINITION    Human chromosome 14 DNA sequence BAC R-55G7 of library RPCI-11 from
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ACCESSION     AL359218.4 GI:14329664
VERSION       HTGS_ACTIVEFIN.
KEYWORDS      HTG; HTGS_ACTIVEFIN.
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
               Homnidae; Homo.
REFERENCE     1 (bases 1 to 160718)
AUTHORS       Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
               Brottier,P., Cattolico,L., Barbe,V., Pelletier,B., Artiguenave,F.,
               Levy,M., Eckenberg,R., Brule,T., deBerardinis,V., Cruaud,C.,
               Gyapay,G., Saurin,W. and Weissensbach,J.
               Sequencing of the human chromosome 14
               Unpublished
               Genoscope.
TITLE         Direct Submission
AUTHORS       Submitted (31-MAY-2001) Genoscope - Centre National de Sequencage :
               BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
               - Web : www.genoscope.cns.fr)
JOURNAL       On Jun 8, 2001 this sequence version replaced gi:12580647.
               ----- Genome Center
               Center: Genoscope / Centre National de Sequencage
               Center code: GS
               Web site: http://www.genoscope.cns.fr/
               Contact: SeqRef@genoscope.cns.fr
               -----
               The following BAC sequence is oriented from the T7 to the SP6 end.
               Upstream BAC (overlapping the T7 end) : R-98N22 (AC=AL163152)
               Downstream BAC (overlapping the SP6 end) : C-2335L22
               ----- Summary Statistics
               Assembly program: Phrap; version 2.0
               Quality coverage: 7.46x in Q20 bases; sum-of-contigs
               -----

```

```

-----quality chart :
Range : bases
0 :
1 - 9 : 1
10 - 19 : 12
20 - 29 : 69
30 - 39 : 98
40 - 49 : 976
50 - 59 : 3761
60 - 69 : 6619
70 - 79 : 18798
80 - 89 : 45434
90 - 99 : 84950
-----
Percentage of bases with a quality value >= 40 : 99 %.

FEATURES
source
Location/Qualifiers
1..160718
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="R-55G7"
/clone_lib="RPCI-11"

ORIGIN
Query Match          91.1%; Score 16.4; DB 8; Length 160718;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||
Db 132546 CCACACCTATTTCACATC 132529

RESULT 48
AC103218
LOCUS          163443 bp DNA linear HTG 03-OCT-2002
DEFINITION    Rattus norvegicus clone CH230-47A7, *** SEQUENCING IN PROGRESS ***,
               12 unordered pieces.
ACCESSION     AC103218.4 GI:23120606
VERSION       HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE        Rattus norvegicus (Norway rat)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
               Sciurognathi; Murioidea; Muridae; Murinae; Rattus.
REFERENCE     1 (bases 1 to 163443)
AUTHORS       Muzny,D.Marie., Metsker,M.Lee., Abranzon,S., Adams,C., Alder,J.,
               Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
               Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
               Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
               Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
               Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
               Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
               Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
               Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
               Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
               Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
               Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
               Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
               Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
               Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
               Gregegeorgis,B., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
               Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
               Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
               Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
               Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
               Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
               Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
               Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
               Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,

```

Lorensuhewa, L., Louleaged, H., Lozado, R. J., Lu, X., Ma, J.,
 Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
 Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
 Mawhney, S., McLeod, M. P., McNeill, T. Z., Meenen, B.,
 Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
 Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
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 Nwakoemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
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 Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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 Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
 Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
 Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
 Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J.,
 Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
 Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K.,
 Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
 Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von
 Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,
 Weinstock, G. and Gibbs, R. A.
 Direct Submission
 Unpublished
 2 (bases 1 to 163443)
 Worley, K. C.
 Direct Submission
 Submitted (24-NOV-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 163443)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (03-OCT-2002) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On Sep 18, 2002 this sequence version replaced gi:21731181.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the
 sequence may extend beyond the ends of the clone and there may be
 contigs that consist entirely of whole genome shotgun sequence
 reads. Both end sequences and whole genome shotgun sequence only
 contigs will be indicated in the feature table.
 ----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GJMN
 Center clone name: CH230-47A7
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 145314 bases at least Q40
 Consensus quality: 148176 bases at least Q30
 Consensus quality: 149375 bases at least Q20
 Estimated insert size: 230087; sum-of-contigs estimation
 Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 12 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 25280: contig of 25280 bp in length
 * 25281 25380: gap of unknown length
 * 25381 36275: contig of 10895 bp in length
 * 36276 36375: gap of unknown length
 * 36376 48643: contig of 12268 bp in length
 * 48644 48743: gap of unknown length
 * 48744 142879: contig of 94136 bp in length
 * 142880 142979: gap of unknown length
 * 142980 144304: contig of 1325 bp in length
 * 144305 144404: gap of unknown length
 * 144405 145001: contig of 1197 bp in length
 * 145002 145701: gap of unknown length
 * 145702 146935: contig of 1234 bp in length
 * 146936 147035: gap of unknown length
 * 147036 149375: contig of 2940 bp in length
 * 149376 150075: gap of unknown length
 * 150076 152399: contig of 2324 bp in length
 * 152400 152499: gap of unknown length
 * 152500 156007: contig of 3508 bp in length
 * 156008 156107: gap of unknown length
 * 156108 159786: contig of 3679 bp in length
 * 159787 159886: gap of unknown length
 * 159887 163443: contig of 3557 bp in length.

FEATURES

source

1..163443
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-47A7"
 25281..25380
 /estimated_length=unknown
 36276..36375
 /estimated_length=unknown
 48644..48743
 /estimated_length=unknown
 142880..142979
 /estimated_length=unknown
 144305..144404
 /estimated_length=unknown
 145602..145701
 /estimated_length=unknown
 146936..147035
 /estimated_length=unknown
 149976..150075
 /estimated_length=unknown
 152400..152499
 /estimated_length=unknown
 156008..156107
 /estimated_length=unknown
 159787..159886
 /estimated_length=unknown

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 163443;
 Best Local Similarity 94.4%; Pred. No. 3.1e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCACACCTTATTCATCTC 18
 ||| |||||
 Db 47763 CCATCTCTTATTCATCTC 47780

RESULT 49

AC007785/c 166500 bp DNA linear PRI 11-JUN-1999
 LOCUS Homo sapiens chromosome 19, BAC 282485 (CIT-B-344H19), complete
 DEFINITION sequence.
 ACCESSION AC007785
 VERSION AC007785.1 GI:5042403
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE AUTHORS

1 (bases 1 to 166500)
Lamerdin, J.E., McCreedy, P.M., Richardson, P., Sakaldasis, G., Burkhardt-Schultz, K., Gordon, L., Scott, D., Johnson, G., Stiilwagen, S., Phan, H., Velasco, N., Do, B., Regala, W., Terry, A., Danganan, L., Erler, A., Christensen, M., Georgescu, A., Avila, J., Attix, C., Andreise, T., Anico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Krommiller, B., Arellano, A., Sanders, C., Ow, D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V.

Sequence analysis of a 2.5 Mb region in 19q13.2-13.3 between APOE and CSRI

JOURNAL REFERENCE AUTHORS

2 (bases 1 to 166500)
Lamerdin, J.E.

TITLE JOURNAL

Submitted (11-JUN-1999) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
Map and sequence oriented from q centromere to telomere. BAC 282485 overlaps cosmid R30477 to the left from bases 1 to 4,419 of this accession, and overlaps BAC 264576 (CIT-B-297N14; AC006262) from bases 146,203 to 166,500. Additional chromosome 19 map and sequence information may be obtained at:
<http://www-bio.lnl.gov/bbrp/genome/genome.html>.

FEATURES source

1..166500
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosomes="19"
/map="19q13.3 between DM and c5r1"
/clone="CIT-B-344H19"
/clone_lib="Cal Tech CIT-B BAC library"
/note="LLNL clone name: BC282485"

repeat_region

repeat_region

repeat_region

CDS

Join<746..904,1157..1239,4294..4451,5875..6036,12784..12994,13080..13162,13903..13958,14053..14128,14429..14568,14726..14804,14982..15039,15813..15885,16025..16122)
/note="Hypothetical arginine-rich gene product;
Hypothetical CDS constructed from overlapping ESTs and Xgrail predictions. EST coverage is lacking for some portions of the CDS. Gene may be alternatively spliced, as multiple transcripts map into this region; alternatively, these individual clones may represent artifactual events during RT and cDNA creation"

/codon_start=3
/evidence=not_experimental
/product="BC282485_1"
/protein_id="AAD38244.1"
/db_xref="GI:5042405"

/translation="TLMNDQAGLQVDYVFRGVEHVRVWVSGVLEVEDRWTDQ WKRGFDAGIELTHGNFKQNFCHMLESALTQSSSVTLDDLTYYDLSLRNK MGRPGSLAPRSQAQNSKRYLILYISVEFDRIHYPLPYQKGPVVLQGIIRLKE ELGRQLQDQNTROTREINWHLREQVSRLSASEKLEAQLGRSREALAGRAARQE AEARGLRGLLELRQERGLRVRAGRGQDCRLAKLEBEAKSRERLARLKTLT SELALYKKGSGRGRGSRPARPSPPTGRRALRFDPTAFVKAKERKOREIQMKQOQRN RLGGSGDGPVSVSRQTPPAALTGRGDAPNRNRSVSSVDSFRSCSSASSGSDL EFPSSLSRGHRRKQKPSPTPWGSGNSKSPVSRSHHQKSLANSGGWVPVKEYSSE HQAADAEDIDAKLQKQYMNRLMRS"
746..904
/note="DDS similarity to overlapping ESTs:
N39722 yx92e04.r1 Homo sapiens cDNA clone 269214 5';
(12..170); 99% identity.-AA283147 zt14d07.r1 NCI CGAP_GCB1
Homo sapiens cDNA clone IMAGE:713101 5'; (6..163); 99%
identity.-AA143160 z149d07.r1 Soares pregnant uterus NBHPU
Homo sapiens cDNA clone 505261 5'; (1..43); 100%

misc_feature

identity.-AA142881 z149d07.s1 Soares pregnant uterus NBHPU
Homo sapiens cDNA clone 505261 3'; (570..527); 64%
identity."

misc_feature

1157..1239
/note="predicted exon, program: grrail2exons_human_1.3,
frame: 0, quality: good, score: 62.000-DDS similarity to
overlapping ESTs:
N39722 yx92e04.r1 Homo sapiens cDNA clone 269214 5';
(171..255); 95% identity.-AA283147 zt14d07.r1
NCI CGAP_GCB1 Homo sapiens cDNA
clone IMAGE:713101 5'; (164..247); 92% identity.-AA143160
z149d07.r1 Soares pregnant uterus NBHPU Homo sapiens cDNA
clone 505261 5'; (44..126); 100% identity.-N28707
yx66d11.r1 Homo sapiens cDNA clone 266709 5'; (1..66); 98%
identity.-AA142881 z149d07.s1 Soares pregnant uterus NBHPU
Homo sapiens cDNA clone 505261 3'; (526..438); 82%
identity."

repeat_region

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repeat_region 9456..9520
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complement(9539..9841)
/rpt_family="AluX"
9909..9944
/rpt_family="MER5B"
10095..10401
/rpt_family="AluX"
complement(10587..10752)
/rpt_family="AluJ"
complement(10753..11057)
/rpt_family="AluX"
complement(11065..11191)
/rpt_family="AluJ"
11322..11619
/rpt_family="AluSg"
11775..11814
/rpt_family="AT rich"
complement(11864..11885)
/rpt_family="AT rich"
complement(11914..11976)
/rpt_family="AluS"
complement(12055..12088)
/rpt_family="AT rich"
complement(12186..12327)
/rpt_family="LIM1"
complement(12334..12384)
/rpt_family="LINE2"
12784..12994
/notes="Predicted exon, program: grail2exons_human_1.3,
frame: 1, quality: excellent, score: 92.000"
12847..12908
/rpt_family="GC rich"
12895..12994
/notes="DPS similarity to AA765166 nz79c05.s1 NCI CGAP GCBI
Homo sapiens cDNA clone IMAGE:1301672; (222..123); 97%
identity."
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/rpt_family="GC rich"
13080..13162
/notes="Predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 100.000-DDS
similarity to AA765166 nz79c05.s1 NCI CGAP GCBI Homo
sapiens cDNA clone IMAGE:1301672; (122..48); 100%
identity."
Query Match 91.1%; Score 16.4; DB 8; Length 166500;
Best Local Similarity 94.4%; Pred. No. 3.le+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTATCTC 18
|||||
Db 164125 CCACACCTATTCTATCAC 164108

RESULT 50
AL358792/c
LOCUS
DEFINITION
Human DNA sequence from clone RP11-280M4 on chromosome 9 Contains
the 5' end of the ASTN2 gene for astrotactin2 (KIAA0364) and a CpG
island, complete sequence.
ACCESSION AL358792 166931 bp DNA linear PRI 18-MAY-2005
VERSION AL358792.24 GI:16030128
KEYWORDS HTG; ASTN2; CpG island; KIAA0634.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 166931)
REFERENCE
AUTHORS Corby,N.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,

COMMENT
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Oct 10, 2001 this sequence version replaced gi:15705207.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr9
RP11-280M4 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
FEATURES
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1..166931
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-280M4"
/clone_lib="RPCI-11.1"
misc_feature 1
/note="Clone left end: RP11-280M4"
gene
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complement(AL355608.11:56896..57280),
complement(AL354981.41:54070..54177),
complement(AL392085.12:91070..155827),
complement(AL157829.24:4108..142070),
complement(AL133284.13:52027..85496),
complement(AL137024.27:148000..148860))
/genes="ASTN2"
/locus_tag="RP11-45A16.2-001"
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complement(AL355608.11:56896..57280),
complement(AL354981.41:54070..54177),
complement(AL392085.12:155681..155827),
complement(AL392085.12:13954..124121),
complement(AL392085.12:92563..92647),
complement(AL392085.12:91976..92050),
complement(AL392085.12:91070..91207),
complement(AL157829.24:141920..142070),
complement(AL157829.24:98954..99120),
complement(AL157829.24:83969..84157),
complement(AL157829.24:11736..11860),
complement(AL157829.24:7329..7433),
complement(AL157829.24:4108..4287),
complement(AL133284.13:85231..85496),
complement(AL133284.13:54013..54146),
complement(AL133284.13:52027..52175),
complement(AL133282.15:51488..51629),
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complement(AL133282.15:4738..4921),
complement(AL137024.27:148000..148860))
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/locus_tag="RP11-45A16.2-001"
/product="astrotactin 2"

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/notes="match: ESTs: AA099036.1 AA371047.1 AA430277.1
AA677654.1 AI499778 AL079991 AU133297.1 AW347402
AW347402.1 AW409774.1 BE751213.1 BF315314 BF315314.1
BF338569 BF338569.1 B1197478.1 CA357296.1 H09468 H11271
H11271.1 T09839.1 T12623.1 T19257
match: cDNAs: AB006627 AB014534 AB014534.1 AF116573
AF116573.1 AF116574 AF116574.1 U48797
join(complement(126444..126985),complement(3274..3461),
complement(AL335608.11:56896..57280),
complement(AL335498.1:41:54070..54177),
complement(AL3392085.12:155681..155827),
complement(AL332085.12:123954..124121),
complement(AL3392085.12:92563..92647),
complement(AL3392085.12:91976..92050),
complement(AL3392085.12:91070..91207),
complement(AL157829.24:141920..142070),
complement(AL157829.24:98954..99120),
complement(AL157829.24:83969..84157),
complement(AL157829.24:11736..11860),
complement(AL157829.24:7329..7433),
complement(AL157829.24:4108..4287),
complement(AL133284.13:85231..85496),
complement(AL133284.13:54013..54146),
complement(AL133284.13:52027..52175),
complement(AL133282.15:51488..51629),
complement(AL133282.15:6582..6682),
complement(AL133282.15:4738..4921),
complement(AL137024.27:148623..148860))
/genes="ASTN2"
/locus_tag="RP11-45A16.2-001"
/standard_name="OTTHUMP00000022742"
/notes="match: proteins: O14525 O60799 O75129 O75998 Q61137
Q9QY74 Q9UHW6"
/codon_start=1
/product="ascrotactin 2"
/protein_id="CAH71966.1"
/db_xref="GI:55664465"
/db_xref="GOA:O5VXG8"
/db_xref="InterPro:IPR001862"
/db_xref="InterPro:IPR003961"
/db_xref="UniProt/TREMBL:O5VXG8"
/translation="MAAAGARSLPGSGGLRGRPLCRPHGPPPLPLLLFLLLPLP
PPLLAGATAAREDPSPCKRTVTVTLPALRESDIDGWSGARAGAGTAGTGAGAAAA
ASPGSPGASGASRLRLVFNELPGRIAVQDDLDNTLPEFTLEMSGTAADISLVH
WQOQLENTLVFHVMSSSGOLAQATPTLQEPSEIVQEHILHISVMGGLIALLL
LLLVLTVALYAGQRKRRIIPKQSAETHEIHYPSVLGPOARESFRSSRLQTH
NSVIGVPIRETILODIDCEDEEPPRANHVREDFGQVTHILDSLGHGPEEKVD
FKKGISFGRAGTSGSEADDETQTFYEQYRSRRRSKGLKSPVKNLTALIAVS
SCILAVCGSQMSCPLTVKVTILVPEHFIADGGSFVSESYLIDISDLNPAKLSLY
QINATSPVVRDLCCGQRTTACQOLCDPETGEGCHEGAPDPVHRHLVRSWDMQSEG
PWYTTLBERGYDLVTGEQAPEKILRSTFSLGOLMLPVSKSFVPPVELSINPLASCK
TDVLTEDPADVREAMLSYFETINDLLSSFGVPVDCSRNNGGCTRNPKVCSRDQVD
SSGCVPEELKPMKQSGCTDRSKGIDCSGDGNGGCEQLCQTLPLPYDATSTIFM
FCGVEEYKLAIDPGKSLMSDVCEGPKCLPKDFNDTLFGEMLHGYNNRTQHVNQ
QVQMTFRENNIFKDFPQALGLVILPLFVEECQGVLESEPLDQLLTGDIRYDEAM
GYPMQOVRNRLVYKLSLTTTLAGFTNVLKILTKESSREELLSFTQHGSHVIAE
DQLSGELTCIHFPSPKVOQWLQVQKETTGLSKKELKSMFFITYLSGLLTAOMLS
EAFKALMSVCSGSGVDVDDWCRLDSAFDANGLPNCSPULQVPLRSLPVEPSST
VYSLEWVDQPAIGTVSYIILQHKKYDEYTDLTLYTEGFLSFDLGLSGTSCVAA
GRSHGEVPEVSYIVFKCLEPDGLYKFTLYAVDTRGHSLSLTVTLRTACPLVDNKK
ABEIAKIVNLNGYVTSQEQOQMYNTLMEVSAFMLFRVOHHYNSHYEKFQDFVWRSE
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49154
/notes="Clone right_end: RP11-567J2"
123824..123876
/notes="Single clone region. Assembly confirmed by
restriction digest data."
126530..127179
/notes="Single clone region. Sequence from reads from a
short insert library derived from a single pUC clone.
Restriction digest data confirm the assembly."

misc_feature
misc_feature
misc_feature

misc_feature 164932
/note="Clone_left_end: RP11-388N2"
ORIGIN
Query Match 91.1%; Score 16.4; DB 8; Length 166931;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
|||||
Db 94228 CCACACCTAGTCATCTC 94211
|||||
RESULT 51
AL606976/c
LOCUS AL606976 169465 bp DNA linear ROD 20-JUN-2002
DEFINITION Mouse DNA sequence from clone RP23-113P22 on chromosome 4, complete
sequence.
ACCESSION AL606976
VERSION AL606976.25 GI:21537445
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 169465)
AUTHORS Pandian,R.
TITLE Direct Submission
JOURNAL Submitted (31-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Jun 21, 2002 this sequence version replaced gi:21213218.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; SW:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-113P22 is
from the RPI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBAC3.6.
FEATURES
source
1..169465
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RP23-113P22"
/clone_lib="RPI-23"
ORIGIN
Query Match 91.1%; Score 16.4; DB 9; Length 169465;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
|||||
Db 137483 CCACACCTATTTCATCTC 137466
|||||

RESULT 52	CR385076	172382 bp	DNA	linear	VRT 03-MAY-2005
LOCUS	Zebrafish DNA sequence from clone DKEY-230H18 in linkage group 2, complete sequence.				
DEFINITION	CR385076				
ACCESSION	CR385076.8	GI:62954692			
VERSION					
KEYWORDS	HTG.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1. (bases 1 to 172382)				
AUTHORS	Hunter, G.				
TITLE	Direct Submission				
JOURNAL	Submitted (03-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk				
COMMENT	On Apr 28, 2005 this sequence version replaced gi:62909866. ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk ----- During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted. Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml is from a Zebrafish BAC library VECTOR: pIndigoBAC-5 Location/Qualifiers 1. .172382 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="DKEY-230H18" /clone_lib="DanioKey"				
FEATURES	source				
ORIGIN	Query Match 91.1%; Score 16.4; DB 5; Length 172382; Best Local Similarity 94.4%; Pred. No. 3e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1 CCACACCTATTTCATCTC 18 				
Db	144941 CCACACCATTCATCTC 144958 				

RESULT 53
AC024399
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC024399 185323 bp DNA linear HTG 04-JUN-2000
Homo sapiens clone RP11-516D7, WORKING DRAFT SEQUENCE, 12 unordered pieces.

AC024399 3 GI:8247873

HTG: HTGS_PHASE1; HTGS_DRAFT.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1. (bases 1 to 185323)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-516D7

Unpublished

2. (bases 1 to 185323)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Bedalov, F., Boguslavsky, L.,

Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,

Choe, Y., Colangelo, M., Collins, S., Collins, S., Collymore, A., Cooke, P.,

DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M.,

Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., Landers, T., Larcocque, K., Lehoczy, J., Levine, R.,

Li, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,

McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J.,

Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,

Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivari, T. M.,

Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,

Riley, K., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,

Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,

Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,

Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B.,

Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and

Zody, M.

Direct Submission

Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 4, 2000 this sequence version replaced gi:7342078.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WISR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L6755

Center clone name: 516.D.7

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 174909 bases at least Q40

Consensus quality: 180249 bases at least Q30

Consensus quality: 182452 bases at least Q20

Insert size: 188000; agarose-ef

Insert size: 184223; sum-of-contigs

Quality coverage: 4.7 in Q20 bases; agarose-ef

Quality coverage: 4.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1520: contig of 1520 bp in length
 * 1521 1520: gap of 100 bp
 * 1621 4220: contig of 2600 bp in length
 * 4221 4320: gap of 100 bp
 * 4321 6884: contig of 2564 bp in length
 * 6885 6984: gap of 100 bp
 * 6985 10741: contig of 3757 bp in length
 * 10742 10841: gap of 100 bp
 * 10842 14568: contig of 3727 bp in length
 * 14569 14669: gap of 100 bp
 * 14669 22794: contig of 8126 bp in length
 * 22795 22894: gap of 100 bp
 * 22895 31230: contig of 8336 bp in length
 * 31231 31330: gap of 100 bp
 * 31331 45469: contig of 14139 bp in length
 * 45470 45569: gap of 100 bp
 * 45570 65126: contig of 19557 bp in length
 * 65127 65226: gap of 100 bp
 * 65227 92039: contig of 26813 bp in length
 * 92040 92139: gap of 100 bp
 * 92140 128331: contig of 36192 bp in length
 * 128332 128431: gap of 100 bp
 * 128432 185323: contig of 56892 bp in length.

FEATURES

Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="RP11-516D7"
 /clone_lib="RPCI-11 Human Male BAC"
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 1521..1620
 /estimated_length=100
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 1621..4220
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 gap
 4221..4320
 /estimated_length=100
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 4321..6884
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 6985..10741
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 10742..10841
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 10842..14568
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 14569..14668
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 14669..22794
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 22795..22894
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 22895..31230
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 31231..31330
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 65227..92039
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 misc_feature
 92140..128331
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 clone_end:SP6
 vector_side:left"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 14; Length 185323;
 Best Local Similarity 94.4%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
 |||||
 DB 87585 CCACACCTATTCACATC 87602

RESULT 54
 AL671173/c
 LOCUS
 DEFINITION Mouse DNA sequence from clone RP23-426N4 on chromosome 4, complete sequence.
 ACCESSION AL671173
 VERSION AL671173.12 GI:21955531
 KEYWORDS HTG.
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.
 1 (bases 1 to 201741)
 Leongamornlert,D.
 Direct Submission
 Submitted (25-JUL-2002) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
 On Jul 25, 2002 this sequence version replaced gi:21738473.
 ----- Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk

 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >=
 30); an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em: EMBL; Sw:
 SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-426N4 is
 from the RPCI-23 Mouse PAC Library
 constructed by the group of Pieter de Jong.
 For further details see <http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACe3.6
 Location/Qualifiers
 1..201741
 /organism="Mus musculus"
 /mol_type="genomic DNA"

FEATURES
 source
 1..201741
 /organism="Mus musculus"
 /mol_type="genomic DNA"


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/notes="clone_boundary
clone_end:Sp6
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end_sequence:BH277959"
misc_feature 16474..18153
/notes="wgs_contig"
gap 182366..182465
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gap 208007..208106
/estimated_length=unknown

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 209355;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservativity 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACTATTCTATCTC 18
DB 203249 CCACACCCATTCATCTC 203266

RESULT 56
AC118365/c
LOCUS AC118365 212446 bp DNA linear HTG 08-OCT-2002
DEFINITION Rattus norvegicus clone CH230-273H4, *** SEQUENCING IN PROGRESS
***
ACCESSION AC118365
VERSION AC118365.3 GI:22856535
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 212446)

REFERENCE
AUTHORS Muzny,D., Marie., Metzker,M., Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Derano,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowig,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,X., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuewa,L., Loulseghe,H., Lozodo,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindarne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapa,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Naif,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokeleneh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,R., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,X., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 212446)
Worley,K.C.
Direct Submission
Submitted (17-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 212446)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (08-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Sep 14, 2002 this sequence version replaced gi:21745733.
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GTT
Center clone name: CH230-273H4
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 183516 bases at least Q40
Consensus quality: 186007 bases at least Q30
Consensus quality: 187853 bases at least Q20
Estimated insert size: 196344; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 212446: contig of 212446 bp in length.
Location/Qualifiers
1..212446
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-273H4"
misc_feature 1..1081
source
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misc_feature 134812. .136879 /note="wgs_contig"
misc_feature 210901. .212446 /note="wgs_contig"
ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 212446;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 93985 CCACACCTATTTCATCTC 93968

RESULT 57
AC097131
LOCUS
DEFINITION
AC097131 221055 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-49P11, *** SEQUENCING IN PROGRESS
***, 4 unordered pieces.
AC097131
VERSION
HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 221055)
Muzny,D.Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blythe,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoques,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Louieged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,M., Martinez,E.,
Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaelumeh,O., Okwuonu,G., Olarnpungsoo,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Prannkoeh,C.,
Plopper,F.S., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajis,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steinle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
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Wang Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willison, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission
Unpublished
2 (bases 1 to 221055)
Worley, K.C.
Direct Submission
Submitted (11-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 221055)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25091251.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GHXP
Center clone name: CH230-49P11
----- Summary Statistics
Assembly program: Atlas 3.0:
Consensus quality: 197551 bases at least Q40
Consensus quality: 200898 bases at least Q30
Consensus quality: 202942 bases at least Q20
Estimated insert size: 205057; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 42645: contig of 42645 bp in length
* 42646 42745: gap of unknown length
* 42746 173337: contig of 130592 bp in length
* 173338 173437: gap of unknown length
* 173438 218952: contig of 45415 bp in length
* 218953 218952: gap of unknown length
* 218953 221055: contig of 2103 bp in length.
Location/Qualifiers
1..221055
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-49P11"
3702..4811
misc_feature

gap /notes="wgs_contig"
 42646..42745
 /estimated_length=unknown
 misc_feature 51725..52966
 /notes="wgs_contig"
 gap 173338..173437
 /estimated_length=unknown
 gap 218853..218952
 /estimated_length=unknown

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 221055;
 Best Local Similarity 94.4%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18

Db 168698 CCACACCTATTCTACTC 168715

RESULT 58

AC113290/c

LOCUS AC113290 221392 bp DNA linear HTG 03-APR-2004
 DEFINITION Mus musculus chromosome 17 clone RP23-416K3 map 17, *** SEQUENCING
 IN PROGRESS ***, 11 unordered pieces.

ACCESSION AC113290

VERSION AC113290.5 GI:46195547

KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEPIN.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 221392)

Birren,B., Nusbbaum,C. and Lander,E.

Mus musculus chromosome 17, clone RP23-416K3

Unpublished

2 (bases 1 to 221392)

Birren,B., Linton,L., Nusbbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cook,A.,
 Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,
 Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
 Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
 Kamat,A., Karatas,A., Kells,C., Lakocque,K., Lamazares,R.,
 Landers,T., Lehoczy,J., Levine,R., Liu,G., MacLean,C.,
 MacDonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M.,
 McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T.,
 Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C.,
 Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J.,
 Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
 Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
 Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
 Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (28-FEB-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 221392)

Birren,B., Nusbbaum,C., Lander,E., Abouelleil,A., Allen,N.,
 Anderson,M., Anderson,S., Arachchi,H.M., Barna,N., Bastien,V.,
 Bloom,T., Boguslavskiy,L., Boukhgalter,B., Camarata,J., Chang,J.,
 Choepel,Y., Collymore,A., Cook,A., Cooke,P., Corum,B.,
 DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L.,
 Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D.,
 Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N.,
 Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I.,
 Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., Landers,T.,

Levine,R., Lindblad-Toh,K., Liu,G., Liu,X., Lui,A., Mabbitt,R.,
 MacLean,C., MacDonald,P., Major,J., Manning,J., Matthews,C.,
 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nguyen,T., Nicol,R., Norbu,C.,
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Rachupka,A., Ramasamy,U., Raymond,C.,
 Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R.,
 Seaman,S., Severy,P., Smith,C., Spencer,B., Stange-Thomann,N.,
 Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J.,
 Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R.,
 Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J., Zembek,L.,
 Zimmer,A. and Zody,M.

Direct Submission

Submitted (03-APR-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 3, 2004 this sequence version replaced gi:44886440.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@broad.mit.edu

----- Project Information

Center project name: L22740

Center clone name: 416_K_3

* NOTE: This is a 'working draft' sequence. It currently

* consists of 11 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1 26029: contig of 26029 bp in length

* 26030 26129: gap of 100 bp

* 26130 35243: contig of 9114 bp in length

* 35244 35343: gap of 100 bp

* 35344 44075: contig of 8732 bp in length

* 44076 44175: gap of 100 bp

* 44176 58702: contig of 14527 bp in length

* 58703 58802: gap of 100 bp

* 58803 122564: contig of 63862 bp in length

* 12265 122764: gap of 100 bp

* 122765 130126: contig of 7362 bp in length

* 130127 130226: gap of 100 bp

* 130227 133955: contig of 3729 bp in length

* 133956 134055: gap of 100 bp

* 134056 186673: contig of 52618 bp in length

* 186674 186773: gap of 100 bp

* 186774 198183: contig of 11410 bp in length

* 198184 198283: gap of 100 bp

* 198284 219225: contig of 20942 bp in length

* 219226 219325: gap of 100 bp

* 219326 221392: contig of 2067 bp in length.

Location/Qualifiers

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/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="17"

/map="17"

/clone="RP23-416K3"

/clone_lib="RPC1-23 Female Mouse BAC"

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/estimated_length=100

35244..35343

/estimated_length=100

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58703..58802

FEATURES

source

gap

gap

gap

gap

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130127..130226
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186674..186773
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219226..219325
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ORIGIN

Query Match      91.1%; Score 16.4; DB 14; Length 221392;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTATTTCATCTC 18
Db 134193 CCACCTATTTCATACC 134176

RESULT 59
AC098768/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-184P12, WORKING DRAFT SEQUENCE, 2
unordered pieces.
ACCESSION
AC098768
VERSION
HTG; HTGS PHASB1; HTGS DRAFT; HTGS_FULLTOP.
KEYWORDS
Rattus norvegicus (Norway rat)
SOURCE
Rattus norvegicus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 221397)
Muzny,D.,Marie., Metzker,M.Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Caesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregiorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hughes,M.,
Hollins,B., Howells,S., Huliy,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensheua,L., Loulsegad,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhinney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokelenah,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,

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Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Soosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Ugmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 221397)
Worley,K.C.
Direct Submission
Submitted (01-NOV-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 221397)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23268156.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIRW
Center clone name: CH230-184P12
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 198467 bases at least Q40
Consensus quality: 201844 bases at least Q30
Consensus quality: 203826 bases at least Q20
Estimated insert size: 20357; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 11412: contig of 11412 bp in length
* 11413 11512: gap of unknown length
* 11513 221397: contig of 203885 bp in length.
Location/Qualifiers
1..221397
/organism="Rattus norvegicus"
FEATURES
source

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/db_xref="taxon:10116"
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1670. .2134
/notes="clone_boundary
clone_end:Sp6
site:EcoRI
end sequence:BH261431"
7248. .9324
/notes="wgs_contig"
11413. .11512
/estimated_length=unknown
11513. .13645
/notes="wgs_contig"
complement(205657. .206268)
/notes="clone_boundary
clone_end:T7
site:EcoRI
end sequence:BH261429"
218210. .221397
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clone_end:T7"

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Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||
DB 146811 CCACACCTATTCATCTC 146794

RESULT 60
AC162180          226160 bp DNA linear ROD 30-JUL-2005
LOCUS             Mus musculus BAC clone RP23-126K16 from chromosome 9, complete
DEFINITION
sequence.
AC162180 AC113972
VERSION           AC162180.2 GI:715333498
KEYWORDS          HTG.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 226160)
Kanchi,K., Kozlowicz,A., Levy,A., Bielicki,L. and Haglund,K.
The sequence of Mus musculus BAC clone RP23-126K16
Unpublished (2001)
2 (bases 1 to 226160)
Wilson,R.K.
Direct Submission
Submitted (25-MAY-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 226160)
Wilson,R.K.
Direct Submission
Submitted (30-JUL-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jul 30, 2005 this sequence version replaced gi:66571672.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BA0126K16
Drafting center: WIBR

```

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e. phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone, fosmid clone or direct clone walk sequence. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to obtain the consensus sequence. The assembly was confirmed by restriction digest.

This finishing standard has slightly changed from the previous Human standard. Specifically, standards for regions of low sequence complexity (such as dinucleotide repeats and small unit tandem repeats) have been relaxed. These regions are very prevalent in the mouse genome, and the return on extended finishing efforts is minimal.

If a sequence meets the criteria of the above statement, it needs no comments or tags. If the criteria are not met, such as ambiguous bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:

The BAC library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (<http://www.chori.org>) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>

This sequence is the entire insert of the clone.

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FEATURES
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            /mol_type="genomic DNA"
            /db_xref="taxon:10090"
            /chromosome="9"
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            /clone_size="63467"
            /note="Sequence derived from PCR product of project DNA"
        161629. .161909
            /note="Unresolved simple sequence repeat."
        220317. .220375
            /note="Sequence derived from PCR product of project DNA"
        220785. .221239
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        222901. .223213
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ORIGIN

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Query Match          91.1%; Score 16.4; DB 9; Length 226160;
Best Local Similarity 94.4%; Pred. No. 3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CCACACCTATTCATCTC 18
|||||

```

```

DB 121803 CCACACATATTCATCTC 121820
|||||

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Search completed: May 10, 2006, 19:26:09
Job time : 1996 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 02:29:57 ; Search time 672 Seconds
(without alignments)
178.519 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18

Sequence: 1 ccacaccttatactc 18

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

N Geneseq_21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	12	ADJ135111
2	18	100.0	18	12	ADJ10012
3	18	100.0	224	6	ABV98192
4	18	100.0	224	6	ABV98533
5	18	100.0	224	6	ABV97702
6	18	100.0	224	6	ABV98622
7	18	100.0	224	6	ABV97592
8	18	100.0	224	6	ABV98196
9	18	100.0	418	13	ADU12907
10	18	100.0	445	3	AAC99186
11	18	100.0	447	6	ABK47377
12	18	100.0	447	14	ADV43454
13	18	100.0	496	4	AAS7324
14	18	100.0	562	3	AAA35100
15	18	100.0	562	3	AAF21222
16	18	100.0	562	6	ABL64906
17	18	100.0	562	6	ABL65512
18	18	100.0	562	6	ABL65915
19	18	100.0	562	10	ABZ96916

20	18	100.0	562	11	ADI31874
21	18	100.0	562	11	ABD20765
22	18	100.0	562	13	ADS83941
23	18	100.0	585	12	ADO28598
24	18	100.0	630	3	AAC98824
25	18	100.0	644	2	AAZ41391
26	18	100.0	654	4	AAH57532
27	18	100.0	654	5	AAH576099
28	18	100.0	742	13	ACN42348
29	18	100.0	3375	3	AAA35101
30	18	100.0	3375	3	AAF21223
31	18	100.0	3375	10	ABZ96917
32	18	100.0	3375	11	ABD20766
33	18	100.0	6771	3	AAA35103
34	18	100.0	6771	3	AAF21225
35	18	100.0	6771	10	ABZ96919
36	18	100.0	6771	11	ABD20768
37	18	100.0	12174	12	ADI35082
38	18	100.0	12174	12	ADJ09983
39	18	100.0	13612	6	ABK47376
40	16	88.9	224	6	ABV95110
41	15.4	85.6	611	13	ACN46442
42	15.4	85.6	1733	13	ADR60118
43	15.4	85.6	3093	6	ABZ13765
44	15.4	85.6	3093	7	ADZ75114
45	15.4	85.6	3120	10	ABE52630
46	15.4	85.6	8528	2	AAQ46249
47	15.4	85.6	17934	6	ABL33718
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49	15.4	85.6	11877	12	ADP44620
50	15	83.3	544	6	ABQ28339
51	15	83.3	544	6	ABQ28338
52	15	83.3	3951	12	ADQ63331
53	14.8	82.2	362	3	AAK69655
54	14.8	82.2	466	6	ABZ08767
55	14.8	82.2	506	8	ACC62584
56	14.8	82.2	584	12	ACH91848
57	14.8	82.2	591	6	ABQ20739
58	14.8	82.2	591	6	ABQ20738
59	14.8	82.2	601	6	ABQ26403
60	14.8	82.2	601	6	ABQ26402
61	14.8	82.2	619	6	ABQ46422
62	14.8	82.2	619	6	ABQ46423
63	14.8	82.2	621	6	ABQ50029
64	14.8	82.2	621	6	ABQ50028
65	14.8	82.2	834	9	ADA28759
66	14.8	82.2	907	6	ADA40514
67	14.8	82.2	1293	6	ABQ72697
68	14.8	82.2	1597	13	ADX15056
69	14.8	82.2	1719	6	ADA40519
70	14.8	82.2	1835	11	ADM02866
71	14.8	82.2	2009	4	AAH17000
72	14.8	82.2	2500	14	ADV98063
73	14.8	82.2	2582	4	ABL23978
74	14.8	82.2	2698	4	ABL16108
75	14.8	82.2	2841	4	ABL23980
76	14.8	82.2	2965	4	AAS26099
77	14.8	82.2	2965	8	ABX73440
78	14.8	82.2	2970	8	ABZ62029
79	14.8	82.2	2984	8	ABX73370
80	14.8	82.2	2984	6	ABA01095
81	14.8	82.2	3237	10	ADB62874
82	14.8	82.2	3692	4	AAC89368
83	14.8	82.2	3692	14	ADZ49774
84	14.8	82.2	3725	4	AAH17635
85	14.8	82.2	3725	6	ABZ11378
86	14.8	82.2	3725	12	ADM43896
87	14.8	82.2	4345	12	ADQ24757
88	14.8	82.2	4456	6	ABZ73865
89	14.8	82.2	6141	4	ABZ07105
90	14.8	82.2	6141	4	AAK89317
91	14.8	82.2	7500	6	ABL33114
92	14.8	82.2	13831	4	ABK42498

C	93	14.8	82.2	13831	9	ADB60654	Connectiv
C	94	14.8	82.2	13832	4	ABK42497	Genomic s
C	95	14.8	82.2	13832	9	ADB60653	Connectiv
C	96	14.8	82.2	15743	6	ABK28395	DNA trans
C	97	14.8	82.2	18001	14	ABE95154	Mouse eIF
C	98	14.8	82.2	28974	4	AAK69977	Human imm
C	99	14.8	82.2	28974	4	AAK69977	Human gen
C	100	14.8	82.2	29360	12	ADQ97189	Human gen
C	101	14.8	82.2	46765	6	AA599306	DNA encod
C	102	14.8	82.2	70549	12	ADQ97436	Mouse can
C	103	14.8	82.2	85873	10	ADH10008	Human chr
C	104	14.8	82.2	99544	14	ADZ13273	Human can
C	105	14.8	82.2	99588	11	ACN45034	Human gen
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C	109	14.8	82.2	126990	12	ADP13332	Renal cel
C	110	14.8	82.2	140152	12	ADP03002	Human hou
C	111	14.8	82.2	140152	13	AD88500	Human hou
C	112	14.8	82.2	140152	13	ADU60105	Housekeep
C	113	14.8	82.2	158417	13	AD536461	Human gen
C	114	14.8	82.2	165043	13	ADL08127	Human gen
C	115	14.8	82.2	199868	12	ADQ97831	Mouse can
C	116	14.8	82.2	201143	6	ABK83568	Human DNA
C	117	14.8	82.2	227448	13	ABD32841	Mouse can
C	118	14.8	82.2	277616	13	ABD32602	Human can
C	119	14.4	80.0	100	10	ADG70411	CLLD7 SNP
C	120	14.4	80.0	204	6	ABS72727	Human gen
C	121	14.4	80.0	317	2	AAT22909	Human gen
C	122	14.4	80.0	337	6	ABL78789	Human ova
C	123	14.4	80.0	342	6	ABL82353	Human ova
C	124	14.4	80.0	377	3	AAF21688	Human bre
C	125	14.4	80.0	377	8	ABZ56640	Aspergill
C	126	14.4	80.0	401	9	ACH31727	Human bon
C	127	14.4	80.0	477	6	ABV95161	Human pan
C	128	14.4	80.0	549	4	AHL15500	Human cdn
C	129	14.4	80.0	628	10	ADF50179	Salmonell
C	130	14.4	80.0	640	5	AAH8067	Peppermin
C	131	14.4	80.0	739	10	ADF50162	Salmonell
C	132	14.4	80.0	825	4	AL23514	Human bre
C	133	14.4	80.0	1428	13	ADS8395	Bacterial
C	134	14.4	80.0	1476	5	AA579679	DNA encod
C	135	14.4	80.0	1677	8	ACA44458	Prokaryot
C	136	14.4	80.0	1728	10	ADF03105	Bacterial
C	137	14.4	80.0	1953	10	ADG77038	Human nuc
C	138	14.4	80.0	2316	10	ADG70165	Human CIL
C	139	14.4	80.0	2480	12	ADP56492	Human bre
C	140	14.4	80.0	2902	4	AHL14457	Human cdn
C	141	14.4	80.0	3152	8	ABT17714	Aspergill
C	142	14.4	80.0	3154	10	ADB61996	Human cdn
C	143	14.4	80.0	3790	8	AD50838	Pig BAC 8
C	144	14.4	80.0	4015	11	ADMO2730	Human cdn
C	145	14.4	80.0	4037	6	ABS78715	Human cdn
C	146	14.4	80.0	4434	12	ADO60128	Human TFA
C	147	14.4	80.0	4590	8	AD50839	Pig BAC 9
C	148	14.4	80.0	5900	8	ACC50312	Breast ca
C	149	14.4	80.0	7179	2	AAZ21006	Salmonell
C	150	14.4	80.0	7443	13	ADR84285	Aspergill

PLA2G1B; fat deposition; leanness; single nucleotide polymorphism;
non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;
hypertension; glucose intolerance; dyslipidemia; hypercoagulability;
microalbuminuria; ss; SNP.

Homo sapiens.
Synthetic.

WO2004002295-A2.

08-JAN-2004.

27-JUN-2003; 2003WO-US020830.

27-JUN-2002; 2002US-0392361P.

(SEQU-) SEQUENOM INC.

Adam GIR, Langdown ML;
WPI; 2004-082843/08.

Diagnosing a predisposition to fat deposition or leanness, useful for
diagnosing a predisposition to e.g. diabetes or hypertension, comprises
detecting the presence of a polymorphism in the PLA2G1B nucleic acid from
the subject.

Claim 8; Page 63; 91pp; English.

The invention relates to diagnosing a predisposition to fat deposition or leanness in a subject comprising detecting the presence or absence of a polymorphic variation associated with fat deposition at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, where the presence of the polymorphic variation indicates a predisposition to fat deposition in the subject. The polymorphic variation is a guanine at position 7328 or thymine at position 9182 of the present sequence. The method is useful for diagnosing a predisposition to fat deposition or leanness in a subject, and consequently for diagnosing a predisposition to non-insulin dependent diabetes mellitus (NIDDM) in a subject and conditions such as hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia, hypercoagulability, or microalbuminuria, which can lead to early prescripation of preventive measures. Sequences AD135104-AD135113 represent exemplary extension oligonucleotides that hybridize to a region of the PLA2G1B sequence that is adjacent to the polymorphic variation.

Sequence 18 BP: 5 A: 8 C: 0 G: 5 T: 0 U: 0 Other:

ALIGNMENTS

RESULT 1
ADI35111
ID ADI35111 standard: DNA: 18 BP.

XX	
XX	ADI35111;
AC	
XX	22-APR-2004 (first entry)
DT	
XX	Human PLA2G1B fragment hybridising extension oligonucleotide.
DE	
XX	
XX	


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PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
PA
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 4030; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 68 C; 37 G; 51 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTTATTCATCTC 18
DB 5 CCACACCTTATTCATCTC 22
RESULT 7
ABV97592
ID ABV97592 standard; cDNA; 224 BP.
XX
XX ABV97592;
AC
XX
XX 14-JAN-2003 (first entry)
DT
XX
XX Human pancreatic cancer expressed cDNA SEQ ID NO 3000.
DE
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200260317-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR
XX 31-JAN-2001; 2001US-0265682P.
PR
XX 09-FEB-2001; 2001US-0267568P.
PR
XX 21-MAR-2001; 2001US-0278651P.
PR
XX 28-APR-2001; 2001US-0287112P.
PR
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PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX (CORI-) CORIXA CORP.
PA
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 3000; 300pp + Sequence Listing; English.
XX
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 69 C; 37 G; 50 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTTATTCATCTC 18
DB 5 CCACACCTTATTCATCTC 22
RESULT 8
ABV98196
ID ABV98196 standard; cDNA; 224 BP.
XX
XX ABV98196;
AC
XX
XX 14-JAN-2003 (first entry)
DT
XX
XX Human pancreatic cancer expressed cDNA SEQ ID NO 3604.
DE
XX
XX Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200260317-A2.
PN
XX
XX 08-AUG-2002.
PD
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX
XX 30-JAN-2001; 2001US-0265305P.
PR
XX 31-JAN-2001; 2001US-0265682P.
PR
XX 09-FEB-2001; 2001US-0267568P.
PR
XX 21-MAR-2001; 2001US-0278651P.
PR
XX 28-APR-2001; 2001US-0287112P.
PR
```

PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX
XX (CORI-) CORIXA CORP.
XX Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
PI
XX WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX
PS Claim 1; SEQ ID NO 3604; 300pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 224 BP; 68 A; 68 C; 37 G; 51 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 224;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db |||||
5 CCACACCTATTTCATCTC 22

RESULT 9
ADU12907
ID ADU12907 standard; DNA; 418 BP.
XX
XX AC ADU12907;
XX
XX DT 27-JAN-2005 (first entry)
XX
XX DE Solid tumour prognosis gene seqid 3346.
XX
XX KW cytostatic; gene therapy; expression profile; solid tumour;
KW peripheral blood mononuclear cell; PMBC; prognosis; ds.
XX
XX OS Unidentified.
XX
XX PN WO2004097052-A2.
XX
XX PD 11-NOV-2004.
XX
XX PF 29-APR-2004; 2004WO-US013587.
XX
XX PR 29-APR-2003; 2003US-0466067P.
XX
XX PR 23-JAN-2004; 2004US-0538246P.
XX
XX XX (AMHP) WYETH.
XX
XX PA (STRA/) STRAHS A.
XX
XX PI Strahs A, Trepicchio WL, Burczynski ME, Twine NC, Slonim DK;

PI Immerman F, Dorner AJ;
XX
XX DR WPI; 2004-804779/79.
XX
XX
PT A method, useful for prognosing and treating solid tumor, comprises
PT comparing an expression profile of a gene expressed in peripheral blood
PT mononuclear cells to a reference expression profile of a gene.
XX
XX Disclosure; Page; 111pp; English.
XX
XX The invention describes a method comprising comparing an expression
CC profile of at least one gene in a peripheral blood sample of a patient to
CC at least one reference expression profile of the at least one gene, where
CC the patient has a solid tumour, and each of the gene is differentially
CC expressed in peripheral blood mononuclear cells (PBMCs) of a first class
CC of patients as compared to PBMCs of a second class of patients, where
CC both the first and second classes of patients have the solid tumour, and
CC each of the first and second classes is a subcluster formed by an
CC unsupervised clustering analysis of gene expression profiles in PBMCs of
CC a population of patients who have the solid tumour, and where the
CC majority of the first class of patients has a first clinical outcome, and
CC the majority of the second class of patients has a second clinical
CC outcome. Also described are: a system comprising (i) a memory or a
CC storage medium including data that represent an expression profile of at
CC least one gene in a peripheral blood sample of a patient who has a solid
CC tumour, (ii) at least another storage medium including data that
CC represent at least one reference expression profile of the gene, (iii) a
CC program capable of comparing the expression profile to the reference
CC expression profile, and (iv) a processor capable of executing the
CC program, where expression levels of the gene in peripheral blood
CC mononuclear cells of patients who have the solid tumour correlate with
CC clinical outcomes of the patients; and a nucleic acid or protein array
CC comprising concentrated probes for solid tumour prognosis genes, where
CC each of the solid tumour prognosis genes is differentially expressed in
CC PBMCs of a first class of patients as compared to PBMCs of a second class
CC of patients, where both the first and second classes of patients have a
CC solid tumour, and where the first class of patients has a first clinical
CC outcome, and the second class of patients has a second clinical outcome.
CC The method, system, and array are useful for prognosing and treating
CC solid tumours. This sequence represents a solid tumour prognosis gene of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 418 BP; 105 A; 125 C; 104 G; 84 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 13; Length 418;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db |||||
275 CCACACCTATTTCATCTC 292

RESULT 10
AAC99186
ID AAC99186 standard; cDNA; 445 BP.
XX
XX AC AAC99186;
XX
XX DT 09-MAR-2001 (first entry)
XX
XX DE Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:414.
XX
XX KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW diagnosis; identification; cytostatic; neuroprotective; nontropic;
KW immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic; neural;
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW cardiovascular; renal; proliferative; ss.
XX

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OS Homo sapiens.
PN WO200055320-A1.
XX
XX
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 200WO-US005989.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-579444/54.
DR P-PSDB; AAB54421.
XX
XX New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition.
PT
XX
PS Claim 1; Page 848; 1379pp; English.
XX
XX AAC98773 to AAC9231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,
CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
CC gynaecological, cardiant and antiinflammatory activities, and can be used
CC in gene therapy. The polynucleotide and proteins can be used for
CC preventing, treating, or ameliorating a medical condition or in assays
CC for diagnosing a pathological condition or a susceptibility to one in a
CC subject. Binding partners to the proteins and the activity of the
CC proteins can be identified. The pancreatic cancer antigens can be used to
CC detect, treat or prevent pancreatic disorders, especially cancer.
CC Agonists and antagonists to the antigens can be screened for. The
CC pancreatic cancer antigen polynucleotides can be used to design nucleic
CC acid hybridisation probes that can be used in chromosome mapping, linkage
CC analysis, tissue identification and/or typing and a variety of forensic
CC and diagnostic methods. The proteins can be used to generate antibodies
CC which are used to purify, detect and target the polypeptides, including
CC both in vivo and in vitro diagnostic and therapeutic methods. The
CC proteins can be used to treat or prevent neural, immune system, muscular,
CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
CC proliferative disorders. AAC9232 to AAC99240 and AAB54467 represent
CC sequences used in the exemplification of the present invention
XX
XX Sequence 445 BP; 111 A; 135 C; 94 G; 96 T; 0 U; 9 Other;
SQ
Query Match 100.0%; Score 18; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
Db 282 CCACACCTATTTCATCTC 299
|||||
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RESULT 11
ABK47377
ID ABK47377 standard; cDNA; 447 BP.
XX
XX AC ABK47377;
XX
XX 18-JUN-2002 (first entry)
XX
XX Human Phospholipase A2, group1B (PLA2G1B) cDNA.
XX
XX Human; ss; gene; SNP; single nucleotide polymorphism; pancreatitis;
KW pancreatic cancer; Phospholipase A2 group1B; PLA2G1B; gene therapy;
KW haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening.
XX
XX Homo sapiens.
OS
XX

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PH Key Location/Qualifiers
FT CDS 1..447
FT /*tag= a
FT /product= "Pla2G1B"
FT replace(294,A)
FT /*tag= h
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT variation
FT /*tag= j
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
XX
XX WO200212562-A2.
PN
XX
XX 14-PEB-2002.
PD
XX
XX 06-AUG-2001; 2001WO-US024663.
PF
XX
XX 04-AUG-2000; 2000US-0223179P.
PR
XX
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX
XX Kazemi A, Kilem SE, Koshiy B;
PI
XX WPI; 2002-303982/34.
XX P-PSDB; AAU78667.
DR
XX
XX Novel isolated human Phospholipase A2, Group 1B pancreas polynucleotide,
PT for therapeutic purposes, for studying expression and function of the
PT polynucleotide and for expressing the phospholipase protein.
PT
XX
XX Claim 27; Fig 2; 51pp; English.
XX
XX The invention relates to an isolated human Phospholipase A2, Group 1B
CC (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a
CC polymorphic variant for a reference sequence for the PLA2G1B gene or its
CC fragment, or a polymorphic variant of a reference sequence for a PLA2G1B
CC cDNA or its fragment. Also included are haplotyping/genotyping the
CC PLA2G1B gene of an individual, predicting the haplotype pair for the
CC PLA2G1B gene of an individual, identifying an association between a trait
CC and at least one haplotype or haplotype pair of the PLA2G1B gene, an
CC isolated genotyping oligonucleotide for detecting a polymorphism in the
CC PLA2G1B gene, a recombinant non-human organism transformed or transfected
CC with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein
CC encoded by the first nucleotide sequence or by the polymorphic variant
CC sequence, an isolated polypeptide comprising a sequence which is a
CC polymorphic variant of a reference sequence for the PLA2G1B protein or
CC its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs
CC targeting PLA2G1B, a computer system for storing and analysing
CC polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B
CC gene. The PLA2G1B variant is useful in studying the expression and
CC function of PLA2G1B, and in expressing PLA2G1B protein for use in
CC screening for candidate drugs to treat diseases related to PLA2G1B
CC activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic
CC purposes. The transgenic organism is useful for studying expression of
CC the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against PLA2G1B protein, and for testing the efficacy of
CC therapeutic agents and compounds in a biological system. The antibody is
CC useful for studying the effect of the variation on the biological
CC activity of PLA2G1B as well as on the binding affinity of candidate drugs
CC targeting PLA2G1B. The PLA2G1B gene is located on chromosome 12q23-q24.1.
CC The present sequence is the cDNA encoding PLA2G1B
XX
XX Sequence 447 BP; 116 A; 128 C; 112 G; 91 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 6; Length 447;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
Db 276 CCACACCTATTTCATCTC 293
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RESULT 12
ADV43454
ID ADV43454 standard; cDNA; 447 BP.
XX
AC ADV43454;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human psychoneuroendocrinimmune expressed sequence tag SEQ ID NO 1082.
XX
KW microarray; psychoneuroendocrinimmune; chronic fatigue;
KW non-insulin dependent diabetes; allergy; immune disorder; inflammation;
KW cancer; neoplasm; infection; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN WO2004108899-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017686.
XX
PR 04-JUN-2003; 2003US-0475915P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Nicholson A, Vernon SD;
XX
DR WPI; 2005-031682/03.
XX
New microarray comprising probes for genes involved in
PT psychoneuroendocrinimmune (PNI) activity, useful in diagnosing a
PT condition associated with PNI activity, e.g., inflammatory or infectious
PT diseases.
XX
PS Claim 1; SEQ ID NO 1082; 254pp; English.
XX
The invention relates to a new microarray which comprises probes for
CC genes involved in psychoneuroendocrinimmune (PNI) activity. The
CC microarray is useful in diagnosing a condition associated with PNI
CC activity, such as CFS, type-2 diabetes, allergic condition, inflammation,
CC cancer and infection. The present sequence represents a
CC psychoneuroendocrinimmune gene expressed sequence tag. Note the
CC specificatio mentions SEQ ID NO of up to 3314 but only sequences up to
CC SEQ ID NO 1829 are provided.
XX
SQ Sequence 447 BP; 116 A; 128 C; 112 G; 91 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 14; Length 447;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db |||||
276 CCACACCTATTTCATCTC 293

RESULT 13
AAH57324/C
ID AAH57324 standard; cDNA; 496 BP.
XX
AC AAH57324;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human pancreas specific cDNA sequence SEQ ID NO:164.
XX
Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX
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XX Homo sapiens.
OS
XX WO200132927-A2.
XX
PD 10-MAY-2001.
XX
PF 02-NOV-2000; 2000WO-US030396.
XX
PR 04-NOV-1999; 99US-0163508P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Sornasse T, Seilhamer JJ, Watson GA;
XX
DR WPI; 2001-291057/30.
XX
New cell and tissue specific polynucleotides useful for diagnosis,
PT prognosis or monitoring of treatments for disorders where the gene is
PT associated with a cancer, immunopathology or neuropathology.
XX
PS Claim 1; Page 126; 327pp; English.
XX
AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and
CC neuroprotective activities, and can be used in gene therapy. (I) and
CC proteins (II) encoded by then are used in high throughput screening
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
CC mimetics, peptides, proteins, agonists, antagonists, drug compounds and pharmaceutical
CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
CC agents. Expression of (I) in a sample indicates the differentiation of
CC embryonic stem cells into a tissue selected from brain, heart, kidney,
CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
CC to produce an expression profile that defines a metabolic or
CC developmental process, treatment, condition, disease or disorder. The
CC gene profile can be used for diagnosis, prognosis or monitoring of
CC treatments and for investigating a predisposition to a disorder where the
CC gene is associated with a cancer, immunopathology or neuropathology
XX
SQ Sequence 496 BP; 102 A; 120 C; 142 G; 127 T; 0 U; 5 Other;

Query Match 100.0%; Score 18; DB 4; Length 496;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db |||||
209 CCACACCTATTTCATCTC 192

RESULT 14
AAA35100
ID AAA35100 standard; DNA; 562 BP.
XX
AC AAA35100;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2789.
XX
Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
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PD 24-FEB-2000.
XX
XX PF 03-AUG-1999; 99WO-US017712.
XX
XX PR 03-AUG-1998; 98US-0095212P.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX
XX NYce JW;
XX
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
XX Disclosure; Page 1056; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytosstatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA3992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
XX Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 3; Length 562;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
DB 313 CCACACCTTATTCATCTC 330

RESULT 15
ID AAF21222
XX
XX AC AAF21222;
XX
XX DT 14-MAR-2001 (first entry)
XX
XX Human low adenosine antisense oligonucleotide related sequence #2789.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyrostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

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KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200062736-A2.
XX
XX PD 26-OCT-2000.
XX
XX PF 24-MAR-2000; 2000WO-US008020.
XX
XX PR 06-APR-1999; 99US-0127958P.
XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX
XX PA (NYCE/) NYCE J W.
XX
XX NYce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX PS Disclosure; Page 1135; 1592pp; English.
XX
XX CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
XX Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 3; Length 562;
XX Best Local Similarity 100.0%; Pred. No. 15;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
DB 313 CCACACCTTATTCATCTC 330

RESULT 16
ABL64906
ID ABL64906 standard; DNA; 562 BP.
XX
XX ABL64906;

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XX DT 15-MAY-2002 (first entry)
XX DE Lung cancer related gene sequence SEQ ID NO:3243.
XX KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US010838.
XX PR 05-JUN-2000; 2000US-0209473P.
XX PR 05-JUN-2000; 2000US-0209531P.
XX PR 18-SEP-2000; 2000US-0233133P.
XX PR 18-SEP-2000; 2000US-0233617P.
XX PR 20-SEP-2000; 2000US-0234009P.
XX PR 20-SEP-2000; 2000US-0234034P.
XX PR 20-SEP-2000; 2000US-0234052P.
XX PR 22-SEP-2000; 2000US-0234509P.
XX PR 22-SEP-2000; 2000US-0234567P.
XX PR 25-SEP-2000; 2000US-0234923P.
XX PR 25-SEP-2000; 2000US-0234924P.
XX PR 25-SEP-2000; 2000US-0234924P.
XX PR 25-SEP-2000; 2000US-0235077P.
XX PR 25-SEP-2000; 2000US-0235082P.
XX PR 25-SEP-2000; 2000US-0235134P.
XX PR 25-SEP-2000; 2000US-0235280P.
XX PR 26-SEP-2000; 2000US-0235637P.
XX PR 26-SEP-2000; 2000US-0235638P.
XX PR 27-SEP-2000; 2000US-0235711P.
XX PR 27-SEP-2000; 2000US-0235720P.
XX PR 27-SEP-2000; 2000US-0235840P.
XX PR 27-SEP-2000; 2000US-0235863P.
XX PR 28-SEP-2000; 2000US-0236028P.
XX PR 28-SEP-2000; 2000US-0236032P.
XX PR 28-SEP-2000; 2000US-0236033P.
XX PR 28-SEP-2000; 2000US-0236034P.
XX PR 28-SEP-2000; 2000US-0236109P.
XX PR 28-SEP-2000; 2000US-0236111P.
XX PR 29-SEP-2000; 2000US-0236842P.
XX PR 29-SEP-2000; 2000US-0236891P.
XX PR 02-OCT-2000; 2000US-0237172P.
XX PR 02-OCT-2000; 2000US-0237173P.
XX PR 02-OCT-2000; 2000US-0237278P.
XX PR 02-OCT-2000; 2000US-0237294P.
XX PR 02-OCT-2000; 2000US-0237295P.
XX PR 02-OCT-2000; 2000US-0237316P.
XX PR 03-OCT-2000; 2000US-0237425P.
XX PR 03-OCT-2000; 2000US-0237598P.
XX PR 03-OCT-2000; 2000US-0237604P.
XX PR 03-OCT-2000; 2000US-0237606P.
XX PR 03-OCT-2000; 2000US-0237608P.
XX PR 01-NOV-2000; 2000US-0244867P.
XX PR 01-NOV-2000; 2000US-0245084P.
XX PA (AVAL-) AVALON PHARM.
XX PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX PI Soppet DR, Weaver Z;
XX XX WPI; 2002-188264/24.
XX PT Screening for anti-neoplastic agent involves exposing cells to a chemical
XX PT agent to be tested for anti-neoplastic activity, and determining a change
XX PT in expression of a gene of a signature gene set.
XX PS Claim 1; SEQ ID NO 3243; 44pp; English.

XX CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX CC
XX CC Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
XX CC
XX CC Query Match 100.0%; Score 18; DB 6; Length 562;
XX CC Best Local Similarity 100.0%; Pred. No. 15;
XX CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX CC 1 CCACACCTATTTCATCTC 18
XX CC ||||||||||||||||
XX CC 313 CCACACCTATTTCATCTC 330
XX CC
XX CC
XX CC RESULT 17
XX CC ABL65512
XX CC ID ABL65512 standard; DNA; 562 BP.
XX CC AC ABL65512;
XX CC DT 15-MAY-2002 (first entry)
XX CC DE Lung cancer related gene sequence SEQ ID NO:3849.
XX CC
XX CC Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
XX CC stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
XX CC cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX CC gene; ds.
XX CC OS Homo sapiens.
XX CC PN WO200194629-A2.
XX CC PD 13-DEC-2001.
XX CC PF 30-MAY-2001; 2001WO-US010838.
XX CC PR 05-JUN-2000; 2000US-0209473P.
XX CC PR 05-JUN-2000; 2000US-0209531P.
XX CC PR 18-SEP-2000; 2000US-0233133P.
XX CC PR 18-SEP-2000; 2000US-0233617P.
XX CC PR 20-SEP-2000; 2000US-0234009P.
XX CC PR 20-SEP-2000; 2000US-0234034P.
XX CC PR 20-SEP-2000; 2000US-0234052P.
XX CC PR 22-SEP-2000; 2000US-0234509P.
XX CC PR 22-SEP-2000; 2000US-0234567P.
XX CC PR 25-SEP-2000; 2000US-0234923P.
XX CC PR 25-SEP-2000; 2000US-0234924P.
XX CC PR 25-SEP-2000; 2000US-0235077P.
XX CC PR 25-SEP-2000; 2000US-0235082P.
XX CC PR 25-SEP-2000; 2000US-0235134P.
XX CC PR 25-SEP-2000; 2000US-0235280P.
XX CC PR 26-SEP-2000; 2000US-0235637P.
XX CC PR 26-SEP-2000; 2000US-0235638P.
XX CC PR 27-SEP-2000; 2000US-0235711P.
XX CC PR 27-SEP-2000; 2000US-0235720P.
XX CC PR 27-SEP-2000; 2000US-0235840P.
XX CC PR 27-SEP-2000; 2000US-0235863P.
XX CC PR 28-SEP-2000; 2000US-0236028P.
XX CC PR 28-SEP-2000; 2000US-0236032P.
XX CC PR 28-SEP-2000; 2000US-0236033P.
XX CC PR 28-SEP-2000; 2000US-0236034P.
XX CC PR 28-SEP-2000; 2000US-0236109P.
XX CC PR 28-SEP-2000; 2000US-0236111P.
XX CC PR 29-SEP-2000; 2000US-0236842P.
XX CC PR 29-SEP-2000; 2000US-0236891P.
XX CC PR 02-OCT-2000; 2000US-0237172P.
XX CC PR 02-OCT-2000; 2000US-0237173P.
XX CC PR 02-OCT-2000; 2000US-0237278P.
XX CC PR 02-OCT-2000; 2000US-0237294P.
XX CC PR 02-OCT-2000; 2000US-0237295P.
XX CC PR 02-OCT-2000; 2000US-0237316P.
XX CC PR 03-OCT-2000; 2000US-0237425P.
XX CC PR 03-OCT-2000; 2000US-0237598P.
XX CC PR 03-OCT-2000; 2000US-0237604P.
XX CC PR 03-OCT-2000; 2000US-0237606P.
XX CC PR 03-OCT-2000; 2000US-0237608P.
XX CC PR 01-NOV-2000; 2000US-0244867P.
XX CC PR 01-NOV-2000; 2000US-0245084P.
XX CC
XX CC (AVAL-) AVALON PHARM.
XX CC Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX CC Soppet DR, Weaver Z;
XX CC WPI; 2002-188264/24.
XX CC Screening for anti-neoplastic agent involves exposing cells to a chemical
XX CC agent to be tested for anti-neoplastic activity, and determining a change
XX CC in expression of a gene of a signature gene set.
XX CC Claim 1; SEQ ID NO 3243; 44pp; English.

27-SEP-2000; 2000US-0235863P.
28-SEP-2000; 2000US-0236028P.
28-SEP-2000; 2000US-0236032P.
28-SEP-2000; 2000US-0236033P.
28-SEP-2000; 2000US-0236034P.
28-SEP-2000; 2000US-0236109P.
28-SEP-2000; 2000US-0236111P.
29-SEP-2000; 2000US-0236842P.
29-SEP-2000; 2000US-0236891P.
02-OCT-2000; 2000US-0237172P.
02-OCT-2000; 2000US-0237173P.
02-OCT-2000; 2000US-0237278P.
02-OCT-2000; 2000US-0237294P.
02-OCT-2000; 2000US-0237295P.
02-OCT-2000; 2000US-0237316P.
03-OCT-2000; 2000US-0237425P.
03-OCT-2000; 2000US-0237598P.
03-OCT-2000; 2000US-0237604P.
03-OCT-2000; 2000US-0237606P.
03-OCT-2000; 2000US-0237608P.
01-NOV-2000; 2000US-0244867P.
01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX Claim 1; SEQ ID NO 3849; 44pp; English.
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, adenocarcinoma, papillary carcinoma and Wilms
CC tumour
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
Db 313 CCACACCTATTTCATCTC 330
RESULT 18
ABL65915
ID ABL65915 standard; DNA; 562 BP.
XX
AC ABL65915;
XX
DT 15-MAY-2002 (first entry)
XX

DE Lung cancer related gene sequence SEQ ID NO:4252.
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.
OS Homo sapiens.
XX WO200194629-A2.
PN 13-DEC-2001.
XX 30-MAY-2001; 2001WO-US010838.
XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX Claim 1; SEQ ID NO 4252; 44pp; English.
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, adenocarcinoma, papillary carcinoma and Wilms
CC tumour
XX

CC to be tested for anti-neoplastic activity, determining a change in
 CC expression of at least one gene (I) of a signature gene set, where (I)
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
 CC to ABL70110), or is at least 95% identical to (S), where a change in
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
 CC activity and can be used in gene therapy. M1 can be used for screening an
 CC anti-neoplastic agent, and can be used for producing a product which is
 CC the data collected with respect to the anti-neoplastic agent as a result
 CC of M1, and the data is sufficient to convey the chemical structure and/or
 CC properties of the agent. M1 can be used in the treatment of cancer such
 CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
 CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
 CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
 CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' s
 CC tumour
 CC
 SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 6; Length 562;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCACCTATTTCATCTC 18
 Db 313 CCACCTATTTCATCTC 330
 RESULT 19
 ABZ96916
 ID ABZ96916 standard; DNA; 562 BP.
 XX
 AC ABZ96916;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human nucleic acid sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 WPI; 2003-229219/22.
 DR
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 12158; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive, have a
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 10; Length 562;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCACCTATTTCATCTC 18
 Db 313 CCACCTATTTCATCTC 330
 RESULT 20
 ADI31874
 ID ADI31874 standard; cDNA; 562 BP.
 XX
 AC ADI31874;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human cDNA #1200.
 XX
 KW Human; gene; ss; immunological response; immunopathological condition;
 KW Crohn's disease; asthma; ulcerative colitis; hypersensinophilia;
 KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
 KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antitumor;
 KW osteopathic; antiarthritic; antirheumatic; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN US6607879-B1.
 XX
 PD 19-AUG-2003.
 XX
 PF 09-FEB-1998; 98US-00023655.
 XX
 PR 09-FEB-1998; 98US-00023655.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Cocks BG, Stuart SG, Seilhamer JJ;
 XX
 WPI; 2003-895307/82.
 DR
 XX
 PT A composition comprising a plurality of cDNAs, useful for detecting
 PT altered expression of genes in an immunological response or for
 PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
 PT or osteoarthritis.
 XX
 PS Claim 1; SEQ ID NO 1200; 50pp; English.
 XX
 CC The invention relates to a composition comprising a plurality of cDNAs
 CC for detecting the altered expression of genes in an immunological
 CC response. The invention also relates to a method of diagnosing or
 CC monitoring the treatment of an immunopathological condition in a sample,
 CC comprising obtaining nucleic acids from a sample, contacting the nucleic
 CC acids of the sample with an array comprising the plurality of cDNAs under
 CC conditions to form one or more hybridisation complexes, detecting the

CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperesoinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 11; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 313 CCACACCTATTTCATCTC 330

RESULT 21
ABD20765
ID ABD20765 standard; DNA; 562 BP.
AC ABD20765;
XX
XX
XX 29-JUL-2004 (first entry)
XX
XX Human pulmonary and inflammatory target DNA #376.
DE
XX
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285309-A2.
PN
XX
XX 31-OCT-2002.
PD
XX
XX 23-APR-2002; 2002WO-US013143.
PF
XX
XX 24-APR-2001; 2001US-0286036P.
PR
XX
XX (EPIG-) EPIGENESIS PHARM INC.
PA
XX
XX Nyce JW, Li Y, Sandrasegna A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
PI
XX
XX WPI; 2003-093058/08.
DR
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.

PS Claim 15; SEQ ID NO 12158; 763pp; English.
XX
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it

XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 11; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 313 CCACACCTATTTCATCTC 330

RESULT 22
ADS83941
ID ADS83941 standard; cDNA; 562 BP.
XX
XX ADS83941;
AC
XX
XX 11-AUG-2005 (first entry)
DT
XX
XX Human lymph node cDNA #1200.
DE
XX
XX ss; gene; human; immunological response; blood cell; cancer;
KW immunopathological; AIDS; allergy; anaemia; asthma; atherosclerosis;
KW bronchitis; ulcerative colitis; diabetes; multiple sclerosis;
KW osteoporosis; pancreatitis; infection; arthritis; lymph node.
XX
XX Homo sapiens.
OS
XX
XX US2004077003-A1.
PN
XX
XX 22-APR-2004.
PD
XX
XX 14-AUG-2003; 2003US-00641643.
PF
XX
XX 09-FEB-1998; 98US-00023655.
PR
XX
XX (INCY-) INCYTE CORP.
PA
XX
XX Cocks BG, Stuart SG, Seilhamer JJ;
PI
XX

DR WPI; 2004-387937/36.
XX New compositions having a number of first, second and third
PT polynucleotide probes, useful in research and diagnostic applications in
PT cancer and immunological conditions e.g. AIDS, diabetes, osteoporosis and
PT infections.
XX Claim 15; SEQ ID NO 1200; 16pp; English.
XX The invention relates to polynucleotides which are used as probes to
CC detect genes differentially expressed in an immunological response,
CC abundantly expressed in an immunological response and/or coding for a
CC polypeptide known to regulate blood cell biology. The polynucleotides are
CC useful in research and diagnostic applications particularly in cancer and
CC immunopathological conditions, such as AIDS, allergies, anaemia, asthma,
CC atherosclerosis, bronchitis, ulcerative colitis, diabetes, multiple
CC sclerosis, osteoporosis, pancreatitis, infections and arthritis. The
CC present sequence represents a human lymph node cDNA used to detect blood
CC cell and immunological response gene expression. Note: The present
CC sequence does not appear in the printed specification but was obtained in
CC electronic format from the USPTO web site
CC (seqdata.uspto.gov/sequence.html?DocID=20040077003).
XX
SQ Sequence 562 BP; 147 A; 163 C; 125 G; 127 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 13; Length 562;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
DB 313 CCACACCTATTTCATCTC 330
RESULT 23
ID ADO28598
XX ADO28598 standard; cDNA; 585 BP.
AC ADO28598;
DT 12-AUG-2004 (first entry)
DE Human PA21 encoding cDNA SEQ ID NO:27.
XX high-grade dysplasia; HGP; oesophageal adenocarcinoma;
KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
KW phospholipase a2 precursor; PA21; chromosome 12; gene; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS 40..483
FT /*tag= a
FT /product= "phospholipase a2 precursor (PA21)"
FT /transl_except= (pos:172..177,aa:Tyr)
FT /transl_except= (pos:343..348,aa:Ile)
XX
PN WO2004044178-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036260.
XX
XX 13-NOV-2002; 2002US-0425813P.
XX
XX (GETH) GENENTECH INC.
XX Smith V;
XX
XX WPI; 2004-420319/39.
DR P-PSDB; ADO28599.
XX
XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample

PT comprises establishing the level of expression in the test tissue sample
PT of the genes.
XX Claim 1; SEQ ID NO 27; 256pp; English.
XX The present invention describes a method for detecting high-grade
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
CC (1) identifying an oesophageal tissue susceptible to oesophageal
CC adenocarcinoma; (2) determining the predisposition of a mammalian tissue
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;
CC and (3) detecting cancer in a patient. The method can be used in
CC detecting HGD and cancer in cells of a mammalian tissue sample. The
CC methods and compositions of the present invention can be used in treating
CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC encodes human phospholipase a2 precursor (PA21), which is used in the
CC exemplification of the present invention. The human PA21 gene is located
CC on chromosome 12.
XX
SQ Sequence 585 BP; 167 A; 166 C; 125 G; 127 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 12; Length 585;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
DB 312 CCACACCTATTTCATCTC 329
RESULT 24
ID AAC98824
XX AAC98824 standard; cDNA; 630 BP.
AC AAC98824;
XX
XX 09-MAR-2001 (first entry)
XX Human pancreatic cancer antigen nucleotide sequence SEQ ID NO:52.
DE
XX Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection;
KW diagnosis; identification; cytostatic; neuroprotective; nontropic;
KW immunomodulatory; relaxant; contraceptive; gynaecological;
KW antiinflammatory; cardiant; gene therapy; chromosome mapping;
KW linkage analysis; tissue identification; tissue typing; forensic; neural;
KW immune system; muscular; reproductive; gastrointestinal; pulmonary;
KW cardiovascular; renal; proliferative; ss.
XX
OS Homo sapiens.
XX
XX WO2000055320-A1.
XX
XX 21-SEP-2000.
PD
XX
XX 08-MAR-2000; 2000WO-US005989.
PF
XX
XX 12-MAR-1999; 99US-0124270P.
PR
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX Rosen CA, Ruben SM;
PI
XX WPI; 2000-579444/54.
DR P-PSDB; AAB54059.
XX
XX New nucleic acid that is a pancreatic cancer antigen for preventing,
PT treating, or ameliorating a medical condition, particular pancreatic
PT cancer, or for use in assays for diagnosing a pathological condition.
XX
XX Claim 1; Page 532; 1379pp; English.
PS
XX AAC98773 to AAC99231 encode the human pancreatic cancer associated
CC proteins, called pancreatic cancer antigens, given in AAB54008 to
CC AAB54466. The human pancreatic cancer antigens have cytostatic,

CC neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive,
 CC gynaecological, cardiant and antiinflammatory activities, and can be used
 CC in gene therapy. The polynucleotide and proteins can be used for
 CC preventing, treating, or ameliorating a medical condition or in assays
 CC for diagnosing a pathological condition or a susceptibility to one in a
 CC subject. Binding partners to the proteins and the activity of the
 CC proteins can be identified. The pancreatic cancer antigens can be used to
 CC detect, treat or prevent pancreatic disorders, especially cancer.
 CC Agonists and antagonists to the antigens can be screened for. The
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic
 CC acid hybridisation probes that can be used in chromosome mapping, linkage
 CC analysis, tissue identification and/or typing and a variety of forensic
 CC and diagnostic methods. The proteins can be used to generate antibodies
 CC which are used to purify, detect and target the polypeptides, including
 CC both in vivo and in vitro diagnostic and therapeutic methods. The
 CC proteins can be used to treat or prevent neural, immune system, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
 CC sequences used in the exemplification of the present invention
 XX
 SQ Sequence 630 BP; 205 A; 162 C; 136 G; 123 T; 0 U; 4 Other;

Query Match 100.0%; Score 18; DB 3; Length 630;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 302 CCACACCTATTTCATCTC 319

RESULT 25

AAZ41391

ID AAZ41391 standard; cDNA; 644 BP.

XX AAZ41391;

XX 19-JAN-2000 (first entry)

DE Human normal pancreas tissue derived cDNA 6.

XX Human; pancreas; cancer; treatment; anticancer; cytostatic; gene therapy;

KW EST; expressed sequence tag; ss.

XX Homo sapiens.

XX DE19818598-AL.

XX 21-OCT-1999.

XX 19-APR-1998; 98DE-01018598.

XX 19-APR-1998; 98DE-01018598.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

XX WPI; 1999-592039/51.

XX New nucleic acid sequences expressed in normal pancreatic tissues, and
 PT derived polypeptides, for treatment of pancreatic cancer and
 PT identification of therapeutic agents.

XX Claim 3; Page 50; 92pp; German.

XX This invention describes novel cDNA sequences (A) that are highly
 CC expressed in normal human pancreatic tissue and which have anticancer and
 CC cytostatic activity. (A) are used (i) for recombinant expression of
 CC polypeptides (B) and (ii) to isolate complete genes. (B) are used (i) to
 CC identify agents suitable for treatment of pancreatic cancer; (ii)
 CC directly for treating this form of cancer (including expression from gene
 CC therapy vectors) and (iii) for generation of specific antibodies. (A) are

CC identified by assembling ESTs (expressed sequence tags) from a particular
 CC tissue type before comparison of expression patterns. This allows a
 CC significantly longer fragment of the gene to be revealed, so should
 CC reduce the number of failures associated with the fact that ESTs from
 CC different libraries may represent different parts of the same unknown
 CC gene, distorting the estimated frequency of occurrence in a particular
 CC tissue. AAZ41386-Z41423 represent human normal pancreatic tissue derived
 CC cDNA fragments which encode the protein fragments represented in AAY59893
 CC -Y59920

XX Sequence 644 BP; 195 A; 171 C; 145 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 644;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 337 CCACACCTATTTCATCTC 354

RESULT 26

AAH57532

ID AAH57532 standard; cDNA; 654 BP.

XX AAH57532;

XX 10-SEP-2001 (first entry)

DE Human pancreas cell specific cDNA sequence SEQ ID NO:372.

XX Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;
 KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;
 KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
 KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX Homo sapiens.

XX WO200132927-A2.

XX 10-MAY-2001.

XX 02-NOV-2000; 2000WO-US030396.

XX 04-NOV-1999; 99US-0163508P.

XX (INCY-) INCYTE GENOMICS INC.

XX Sornasse T, Seilhamer JJ, Watson GA;

XX WPI; 2001-291057/30.

XX New cell and tissue specific polynucleotides useful for diagnosis,
 PT prognosis or monitoring of treatments for disorders where the gene is
 PT associated with a cancer, immunopathology or neuropathology.

XX Claim 1; Page 288; 327pp; English.

XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
 CC sequences (I). (I) can have cytostatic, immunomodulatory and
 CC neuroprotective activities, and can be used in gene therapy. (I) and
 CC proteins (II) encoded by then are used in high throughput screening
 CC assays to select DNA molecules, RNA molecules, peptide nucleic acids,
 CC mimetics, peptides, proteins, agonists, antagonists, antibodies or their
 CC fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical
 CC agents. Expression of (I) in a sample indicates the differentiation of
 CC embryonic stem cells into a tissue selected from brain, heart, kidney,
 CC liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used
 CC to produce an expression profile that defines a metabolic or
 CC developmental process, treatment, condition, disease or disorder. The
 CC gene profile can be used for diagnosis, prognosis or monitoring of
 CC treatments and for investigating a predisposition to a disorder where the
 CC gene is associated with a cancer, immunopathology or neuropathology

```

XX Sequence 654 BP; 165 A; 193 C; 145 G; 143 T; 0 U; 8 Other;
SQ Query Match 100.0%; Score 18; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 428 CCACACCTATTTCATCTC 445

RESULT 27
AAS76099
ID AAS76099 standard; cDNA; 654 BP.
XX
XX AAS76099;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #11903.
DE Human; Chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYPSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX P-PSDB; ABG11912.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 1; SEQ ID NO 11903; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

Sequence 654 BP; 190 A; 174 C; 170 G; 120 T; 0 U; 0 Other;

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Query Match 100.0%; Score 18; DB 5; Length 654;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 483 CCACACCTATTTCATCTC 500

RESULT 28
ACN42348
ID ACN42348 standard; cDNA; 742 BP.
XX
XX ACN42348;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic polynucleotide SEQ ID NO:1223.
DE ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;
KW dithp.
XX
XX Homo sapiens.
XX
XX WO2004023973-A2.
XX
XX 25-MAR-2004.
XX
XX 12-SEP-2003; 2003WO-US028227.
XX
XX 12-SEP-2002; 2002US-0410259P.
XX
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
XX Mooney EM, Delegeane AM, Panesar IS, Barville SC, Reddy TP;
XX Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
XX Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
XX Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
XX Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
XX Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
XX
XX P-PSDB; ABM83696.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX in diagnosing a condition, disease or disorder associated with human
XX molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX in gene mapping.
XX
XX Claim 1; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorders, endocrine
XX disorders, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dithp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dithp polynucleotide of
XX the invention. Note: The sequence data for this patent is not represented
XX in the printed specification, but was obtained in electronic format
XX directly from WIPO at www.wipo.int/pub/en/sequences/listing.htm
XX
XX Sequence 742 BP; 182 A; 204 C; 191 G; 165 T; 0 U; 0 Other;

```

Query Match 100.0%; Score 18; DB 13; Length 742;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | | | |
DB 488 CCACACCTATTTCATCTC 505

RESULT 29
AAA35101
ID AAA35101 standard; DNA; 3375 BP.
XX AC AAA35101;
XX
XX
DT 28-JUL-2000 (first entry)
DE
DE Human adenosine receptor related polynucleotide SEQ ID NO:2790.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cyostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
XX WO200009525-A2.
PN
XX
XX 24-FEB-2000.
PD
XX
XX 03-AUG-1999; 99WO-US017712.
PF
XX
XX 03-AUG-1998; 98US-0095212P.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX Nyce JW;
PI
XX
XX WPI; 2000-205971/18.
DR
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
PT
XX
XX Disclosure; Page 1056-1057; 1343pp; English.

CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cyostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC

AAA35992) are specifically claimed ONS from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
XX Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 3; Length 3375;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | | | |
DB 3304 CCACACCTATTTCATCTC 3321

RESULT 30
AAF21223
ID AAF21223 standard; DNA; 3375 BP.
XX AC AAF21223;
XX
XX 14-MAR-2001 (first entry)
DT
XX
XX Human low adenosine antisense oligonucleotide related sequence #2790.
DE
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200062736-A2.
PN
XX
XX 26-OCT-2000.
PD
XX
XX 24-MAR-2000; 2000WO-US008020.
PF
XX
XX 06-APR-1999; 99US-0127958P.
PR
XX
XX (UYEC-) UNIV EAST CAROLINA.
PA
XX
XX (NYCE/) NYCE J W.
PI
XX
XX Nyce JW;
PI
XX
XX WPI; 2000-679539/66.
DR
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
PT
XX
XX Disclosure; Page 1135-1136; 1592pp; English.

CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central

CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF1543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 3375;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 3304 CCACACCTATTTCATCTC 3321

RESULT 31
ABZ96917
ID ABZ96917 standard; DNA; 3375 BP.
XX
AC ABZ96917;
DT 17-OCT-2003 (first entry)
XX
DE Human nucleic acid sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US0113135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiqunone.
XX
PS Disclosure; SEQ ID NO 12159; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiqunone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiqunone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 10; Length 3375;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 3304 CCACACCTATTTCATCTC 3321

RESULT 32
ABD20766
ID ABD20766 standard; DNA; 3375 BP.
XX
AC ABD20766;
DT 29-JUL-2004 (first entry)
XX
DE Human pulmonary and inflammatory target DNA #377.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 12159; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impaired respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC thymidines present in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it

XX Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 11; Length 3375;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 3304 CCACACCTATTTCATCTC 3321

RESULT 33

AAA35103
 ID AAA35103 standard; DNA; 6771 BP.

AC AAA35103;

XX 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2792.

XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

XX Homo sapiens.

OS WO200009525-A2.

XX 24-FEB-2000.

PD 03-AUG-1999; 99WO-US017712.

XX 03-AUG-1998; 98US-0095212P.

PA (UYEC-) UNIV EAST CAROLINA.

XX Nyce JW;

XX

DR WPI; 2000-205971/18.

XX New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.

PS Disclosure; Page 1058-1059; 1343pp; English.

XX The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiasthmatic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing

XX Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 3; Length 6771;

Best Local Similarity 100.0%; Pred. No. 18;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 313 CCACACCTATTTCATCTC 330

RESULT 34

AAF21225
 ID AAF21225 standard; DNA; 6771 BP.

XX AAF21225;

XX 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2792.

XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.

XX Homo sapiens.

OS WO2000062736-A2.

XX 26-OCT-2000.

XX

PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX Disclosure; Page 1137-1139; 1592pp; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
XX Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 3; Length 6771;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
DB 313 CCACACCTATTTCATCTC 330

RESULT 35
ABZ96919
ID ABZ96919 standard; DNA; 6771 BP.
XX
AC ABZ96919;
XX
XX 17-OCT-2003 (first entry)
DT Human nucleic acid sequence.
DE
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandraseagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 12161; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive, also
CC immunosuppressive, and cytostatic activity. The composition is useful for treating or
CC use in antisense gene therapy. The composition is useful for treating or
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, for reducing levels of ubiquinone or
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 10; Length 6771;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
DB 313 CCACACCTATTTCATCTC 330

RESULT 36
ABD20768
ID ABD20768 standard; DNA; 6771 BP.
XX
XX ABD20768;
AC
XX 29-JUL-2004 (first entry)
DT Human pulmonary and inflammatory target DNA #379.
DE
XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiasthmatic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
XX
PD 31-OCT-2002.
XX
XX
PF 23-APR-2002; 2002WO-US013143.
XX
XX
PR 24-APR-2001; 2001US-0286036P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
XX
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
XX
PS Claim 15; SEQ ID NO 12161; 763pp; English.
XX

This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, cystic fibrosis, allergic rhinitis, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX

Seq Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 11; Length 6771;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 313 CCACACCTATTTCATCTC 330

RESULT 37
ADI35082
ID ADI35082 standard; DNA; 12174 BP.

XX
AC ADI35082;
XX
DT 22-APR-2004 (first entry)
XX
DE Human PLA2G1B nucleotide sequence.
XX
XX PLA2G1B ; fat deposition; leanness; polymorphism;
KW non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;
KW hypertension; glucose intolerance; dyslipidemia; hypercoagulability;
KW microalbuminuria; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2004002295-A2.
XX
XX 08-JAN-2004.
PD
PF 27-JUN-2003; 2003WO-US020830.
XX
PR 27-JUN-2002; 2002US-0392361P.
XX
PA (SEQU-) SEQUENOM INC.
XX
XX Adam GIR, Langdown ML;
XX
DR WPI; 2004-082843/08.
DR P-PSDB; ADI35083.
XX

Diagnosing a predisposition to fat deposition or leanness, useful for
diagnosing a predisposition to e.g. diabetes or hypertension, comprises
detecting the presence of a polymorphism in the PLA2G1B nucleic acid from
the subject.

Claim 1; SEQ ID NO 1; 91pp; English.

The invention relates to diagnosing a predisposition to fat deposition or
leanness in a subject comprising detecting the presence or absence of a
polymorphic variation associated with fat deposition at a polymorphic
site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a
subject, where the presence of the polymorphic variation indicates a
predisposition to fat deposition in the subject. The polymorphic
variation is a guanine at position 7328 or thymine at position 9182 of
the present sequence. The method is useful for diagnosing a
predisposition to fat deposition or leanness in a subject, and
consequently for diagnosing a predisposition to non-insulin dependent
diabetes mellitus (NIDDM) in a subject and conditions such as
hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia,
hypercoagulability, or microalbuminuria, which can lead to early
prescription of preventive measures. The present sequence represents a
human PLA2G1B nucleotide sequence.

Seq Sequence 12174 BP; 3217 A; 2992 C; 2738 G; 3215 T; 0 U; 12 Other;
Query Match 100.0%; Score 18; DB 12; Length 12174;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 7310 CCACACCTATTTCATCTC 7327

RESULT 38
ADJ09983
ID ADJ09983 standard; DNA; 12174 BP.

XX
AC ADJ09983;
XX
DT 17-JUN-2004 (first entry)

XX Human phospholipase A2 (PLA2G1B) DNA SeqID 1.
XX

KW human; gene; ds; fat reduction; fat deposition; phospholipase A2;
KW PLA2G1B; chromosome 12q24; single nucleotide polymorphism; SNP;
KW appetite suppressant; lipase inhibitor; exercise regimen; obesity;
KW non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder;
KW hypertension; antidiabetic.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(436,c)
FT /tag= a
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(839,a)
FT /tag= b
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(4050,a)
FT /tag= c
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(4689,t)
FT /tag= d
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(6282,a)
FT /tag= e
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(6358,c)
FT /tag= f
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(6653,t)
FT /tag= g
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7256,t)
FT /tag= h
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7300,a)
FT /tag= i
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7301,c)
FT /tag= j
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(7328,g)
FT /tag= k
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(8062,c)
FT /tag= l
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(9182,t)
FT /tag= m
FT /standard_name= "Single nucleotide polymorphisms"
FT variation replace(11649,c)
FT /tag= n
FT /standard_name= "Single nucleotide polymorphisms"
XX
XX WO2004002296-A2.
XX
XX 08-JAN-2004.
XX
XX 27-JUN-2003; 2003WO-US020831.
XX
XX 27-JUN-2002; 2002US-0392362P.
XX
XX (SEQU-) SEQUENOM INC.
XX
XX Adam GIR, Langdown ML, Denissenko MF, Dennis E, Cantor C;
PI Rubin B;
XX
XX WPI; 2004-071944/07.
DR P-PSDB; ADJ09984.
XX
XX Identifying a candidate therapeutic for fat reduction, useful for
PT treating diabetes, by introducing a test molecule to a system comprising
PT PLA2G1B protein or nucleic acid, and determining the presence of
PT interaction between the compounds.
XX

PS Claim 1; SEQ ID NO 1; 116pp; English.
XX
CC This invention relates to a novel candidate therapeutic agent useful for
CC fat reduction and disorders related to fat depositions. Specifically, it
CC refers to polymorphic variations in the phospholipase A2 (PLA2G1B) DNA,
CC which is located on chromosome 12q24 and has been associated with central
CC fat deposition. The present invention describes methods to detect the
CC presence or absence of these single nucleotide polymorphisms of PLA2G1B,
CC in particular G7328A and T9182G, and subsequently provide treatment that
CC reduces fat deposition. This treatment may consist of an appetite
CC suppressant, a lipase inhibitor, a phospholipase inhibitor, an exercise
CC regimen, a dietary regimen, psychological counselling, psychotherapy or a
CC psychotherapeutic. Accordingly, PLA2G1B is a target for reducing fat
CC deposition and it can be used to treat both obesity and non-insulin
CC dependent diabetes mellitus (NIDDM), as well as cardiovascular disorders
CC such as hypertension. As such, it exhibits antidiabetic activity. This
CC polynucleotide sequence is the human PLA2G1B DNA of the invention.
XX
SQ Sequence 12174 BP; 3220 A; 2996 C; 2739 G; 3219 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 12; Length 12174;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
Db 7310 CCACACCTATTTCATCTC 7327
|||||
RESULT 39
ABK47376
ID ABK47376 standard; DNA; 13612 BP.
XX
AC ABK47376;
XX
XX 18-JUN-2002 (first entry)
XX Human Phospholipase A2, groupIB (PLA2G1B) gene.
XX
XX Human; ds; gene; SNP; single nucleotide polymorphism; pancreatitis;
KW pancreatic cancer; Phospholipase A2 groupIB; PLA2G1B; gene therapy;
KW haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation replace(3845,A)
FT /tag= a
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT variation replace(3968,A)
FT /tag= b
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT CDS 4053..9613
FT /tag= c
FT /product= "Pla2G1B"
FT exon 4053..4086
FT /tag= d
FT /number= 1
FT /tag= e
FT /number= 2
FT /tag= f
FT /number= 1
FT /tag= g
FT /number= 2
FT /tag= h
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT
FT

FT exon 6745..6873
FT /*tag= i
FT /number= 3
FT variation replace(6844,A)
FT /*tag= 3
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
FT 6874..9489
FT /*tag= k
FT /number= 3
FT exon 9490..9613
FT /*tag= 1
FT /number= 4
FT variation replace(9531,A)
FT /*tag= m
FT /label= SNP
FT /note= "Single nucleotide polymorphism"
XX WO200212562-A2.
PN XX
PD 14-FEB-2002.
XX
XX 06-AUG-2001; 2001WO-US024663.
XX
XX 04-AUG-2000; 2000US-0223179P.
PR
XX (GENA-) GENAISSANCE PHARM INC.
PA
XX Kazemi A, Kliem SE, Koshy B;
PI WPI; 2002-303982/34.
XX P-PSDB; AAU78667.
DR
XX Novel isolated human Phospholipase A2, Group 1B pancreas polynucleotide,
PT for therapeutic purposes, for studying expression and function of the
PT polynucleotide and for expressing the phospholipase protein.
XX
XX Claim 1; Fig 1; Sipp; English.
PS
XX The invention relates to an isolated human Phospholipase A2, Group 1B
CC (pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a
CC polymorphic variant for a reference sequence for the PLA2G1B gene or its
CC fragment, or a polymorphic variant of a reference sequence for a PLA2G1B
CC cDNA or its fragment. Also included are haplotyping/genotyping the
CC PLA2G1B gene of an individual, predicting the haplotype pair for the
CC PLA2G1B gene of an individual, identifying an association between a trait
CC and at least one haplotype or haplotype pair of the PLA2G1B gene, an
CC isolated genotyping oligonucleotide for detecting a polymorphism in the
CC PLA2G1B gene, a recombinant non-human organism transformed or transfected
CC with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein
CC encoded by the first nucleotide sequence or by the polymorphic variant
CC sequence, an isolated polypeptide comprising a sequence which is a
CC polymorphic variant of a reference sequence for the PLA2G1B protein or
CC its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs
CC targeting PLA2G1B, a computer system for storing and analysing
CC polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B
CC gene. The PLA2G1B variant is useful in studying the expression and
CC function of PLA2G1B, and in expressing PLA2G1B protein for use in
CC screening for candidate drugs to treat diseases related to PLA2G1B
CC activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic
CC purposes. The transgenic organism is useful for studying expression of
CC the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs
CC targeted against PLA2G1B protein, and for testing the efficacy of
CC therapeutic agents and compounds in a biological system. The antibody is
CC useful for studying the effect of the variation on the biological
CC activity of PLA2G1B as well as on the binding affinity of candidate drugs
CC targeting PLA2G1B. The present sequence is the PLA2G1B gene which is
CC located on chromosome 12q23-q24.1
XX
XX Sequence 13612 BP; 3637 A; 3290 C; 3070 G; 3615 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 13612;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACACCTATTCACTC 18
Db 6826 CCACACCTATTCACTC 6843
RESULT 40
ABV95110
ID ABV95110 standard; cDNA; 224 BP.
XX
AC ABV95110;
XX
DT 14-JAN-2003 (first entry)
XX
DE Human pancreatic cancer expressed cDNA SEQ ID NO 518.
XX
KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
KW cytostatic; tumour; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200260317-A2.
XX
PD 08-AUG-2002.
XX
XX 30-JAN-2002; 2002WO-US002781.
PF
XX 30-JAN-2001; 2001US-0265305P.
PR 31-JAN-2001; 2001US-0265682P.
PR 09-FEB-2001; 2001US-0267568P.
PR 21-MAR-2001; 2001US-0278651P.
PR 28-APR-2001; 2001US-0287112P.
PR 16-MAY-2001; 2001US-0291631P.
PR 12-JUL-2001; 2001US-0305484P.
PR 20-AUG-2001; 2001US-0313999P.
PR 27-NOV-2001; 2001US-0333626P.
XX
XX (CORI-) CORIXA CORP.
PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;
XX WPI; 2002-627435/67.
XX
XX New isolated polynucleotide and pancreatic tumor polypeptides, useful for
PT diagnosing, preventing and/or treating cancer, particularly pancreatic
PT cancer.
XX
XX Claim 1; SEQ ID NO 518; 300pp + Sequence Listing; English.
PS
XX The invention relates to an isolated polynucleotide (I) comprising: (a)
CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)
CC complements of (a); (c) sequences consisting of at least 20 contiguous
CC residues of (a); (d) sequences that hybridize to (a), under moderately
CC stringent conditions; (e) sequences having at least 75% or 90% identity
CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-
CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer
CC in a patient and compositions comprising polypeptides, polynucleotides,
CC antibodies, fusion proteins, T cell populations and antigen presenting
CC cells expressing the polypeptide are useful in treating pancreatic cancer
CC and stimulating an immune response. The polynucleotides can be used as
CC probes or primers for nucleic acid hybridisation, in the design and
CC preparation of ribozyme molecules for inhibiting expression of the tumour
CC polypeptides and proteins in the tumour cells, in vaccines and for gene
CC therapy. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 224 BP; 66 A; 63 C; 37 G; 53 T; 0 U; 5 Other;

Query Match 88.9%; Score 16; DB 6; Length 224;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACT 17
DB 5 CCACACCTATTCTATNT 21

RESULT 41
ACN46442
ID ACN46442 standard; cDNA; 611 BP.
XX
AC ACN46442;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton primed seed EST Clone ID: LIB3825-020-Q1-K6-B2, SEQ:1223.
XX
XX Cotton; plant; EST; expressed sequence tag; transgenic plant; seed;
KW variety DP50B; library LIB3825; molecular tag; molecular marker;
KW genetic mapping; molecular mapping; seed germination; plant growth;
KW plant quality; plant yield; plant breeding; tissue printing; ss.
XX
OS Gossypium hirsutum.
XX
XX US2004123340-A1.
XX
XX 24-JUN-2004.
PD
XX
XX 12-DEC-2001; 2001US-00021323.
PF
XX
XX 14-DEC-2000; 2000US-0255619P.
PR
XX
XX (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
XX
XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;
PI WPI; 2004-479808/45.
XX
XX New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
PT tags to map genes.
XX
PS Claim 1; SEQ ID NO 1223; 34pp; English.

CC The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gynoeium
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucleon33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determining whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and carabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a

CC cotton variety DP50B primed seed cDNA library (LIB3825). The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20040123340
XX
SQ Sequence 611 BP; 134 A; 131 C; 145 G; 201 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 13; Length 611;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTCTACTC 18
DB 340 CACACCTATTCTACTC 356

RESULT 42
ADR60118
ID ADR60118 standard; cDNA; 1733 BP.
XX
AC ADR60118;
XX
DT 02-DEC-2004 (first entry)
XX
DE Cotton cDNA sequence, SEQ ID 899.
XX
XX Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
KW drought tolerance; plant disease resistance; galactomannan; lignin;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW homologous recombination; extreme osmotic condition tolerance;
KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
KW stress resistance.
XX
OS Gossypium hirsutum.
XX
XX US2004181830-A1.
XX
XX 16-SEP-2004.
PD
XX
XX 29-JAN-2004; 2004US-00767795.
PF
XX
XX 07-MAY-2001; 2001US-00849529.
PR
XX 12-DEC-2001; 2001US-00021323.
PR
XX (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
XX
XX Kovalic DK, Zhou Y, Cao Y;
PI WPI; 2004-667718/55.
XX
XX New recombinant nucleic acid molecules and polypeptides from Gossypium
PT hirsutum, useful for producing plants with improved biological
PT characteristics (e.g. improved plant cold or drought tolerance).
XX
XX Claim 1; SEQ ID NO 899; 14pp; English.

CC The invention relates to a recombinant polynucleotide comprising any of
CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
CC Also a recombinant polypeptide comprising any of the 58798 amino acid
CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomannan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance

CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The
CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.

XX Sequence 1733 BP; 376 A; 351 C; 389 G; 617 T; 0 U; 0 Other;
SQ Query Match 85.6%; Score 15.4; DB 13; Length 1733;
Best Local Similarity 94.1%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
DB 805 CACACCTATTCATCTC 821
|||||

RESULT 43
ABZ13765/c
ID ABZ13765 standard; DNA; 3093 BP.

AC ABZ13765;
XX
DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1570.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US026685.

XX 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-0264647P.

XX 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and

XX producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 1570; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid with an
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence

CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 3093 BP; 866 A; 592 C; 790 G; 845 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 3093;
Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 17
DB 553 CCACACCTATTCATCTC 537
|||||

RESULT 44
ADZ75114/c
ID ADZ75114 standard; DNA; 3093 BP.

XX ADZ75114;

XX DT 30-JUN-2005 (first entry)

XX Arabidopsis leaf-specific open reading frame, SEQ ID 630.

XX Crop improvement; gene; ds; plant; plant disease; plant fungal disease;
KW drought resistance; herbicide resistance; insect resistance;
KW abiotic stress tolerance; salt tolerance; heat tolerance; cold tolerance;
KW gene expression; food.

XX Arabidopsis thaliana.

XX WO200198480-A2.

XX 27-DEC-2001.

XX 22-JUN-2001; 2001WO-IB001104.

XX 23-JUN-2000; 2000US-0213848P.

XX 23-JUN-2000; 2000US-0214087P.

XX 29-DEC-2000; 2000US-0258692P.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Budworth P, Brown D, Chang H, Zhu T, Han B, Wang X, Cooper B;

XX WPI; 2002-055861/07.

XX Promoters for root-specific, leaf-specific or constitutive regulation of
PT plant gene expression, useful for regulating the expression of selected
PT transgenes (e.g. stress tolerance and defence related genes) in
PT economically important plants.

XX Disclosure; SEQ ID NO 630; 290pp; English.

XX The invention relates to promoters for root-specific, leaf-specific or
CC constitutive regulation of plant gene expression. Also included are an
CC isolated polynucleotide (N1) comprising a plant nucleotide sequence that
CC directs root-specific transcription of an operatively linked nucleic acid
CC segment in a plant cell, where the plant nucleotide sequence is from a
CC gene encoding a polypeptide that is substantially similar to a
CC polypeptide encoded by an Arabidopsis gene comprising a promoter selected
CC from ADZ74492-ADZ74542, ADZ75008-ADZ75016 or ADZ75026-ADZ75034 or a
CC polypeptide encoded by an Rice gene comprising a promoter selected from
CC ADZ75309 and ADZ75327, an isolated polynucleotide (N2) comprising a plant
CC nucleotide sequence that directs constitutive transcription of an
CC operatively linked nucleic acid segment in a plant cell, where the plant
CC nucleotide sequence is from a gene encoding a polypeptide that is
CC substantially similar to a polypeptide encoded by an Arabidopsis gene
CC comprising a promoter selected from ADZ74543-ADZ74830, ADZ74968-ADZ75006,
CC ADZ75007, ADZ75035-ADZ75069, ADZ75310-ADZ75326 and ADZ75328-ADZ75359, an
CC isolated polynucleotide (N3) comprising a plant nucleotide sequence that
CC directs leaf-specific transcription of an operatively linked nucleic acid
CC segment in a plant, where the plant nucleotide sequence is from a gene
CC encoding a polypeptide that is substantially similar to a polypeptide

encoded by an Arabidopsis gene having a promoter selected from one of ADZ15177-ADZ75257, a recombinant vector comprising N1-N3, an expression cassette comprising N1-N3 operatively linked to an open reading frame, a recombinant vector comprising the above expression cassette, a host cell comprising the expression cassette, a plant cell containing the expression cassette, a transformed plant (the genome of which is augmented with the expression cassette), a transformed plant comprising transformed plant cells (where the cells contain the expression cassette), a method (M1) for augmenting a plant genome, a method (M2) to identify a gene having a promoter (the expression of which is altered in root), a method (M3) to identify a gene having a promoter (the expression of which is constitutive in a plant cell), a method (M4) to identify a gene having a promoter (the expression of which is altered in leaves of a plant), and a method to alter the phenotype of a plant cell comprising introducing the expression cassette. For the expression cassette, the open reading frame is from an insect resistance gene, a bacterial disease resistance gene, a fungal disease resistance gene, a viral disease resistance gene, a nematode disease resistance gene, a herbicide resistance gene, a stress resistance gene, a gene affecting grain composition or quality, a nutrient utilization gene, a mycotoxin reduction gene, a male sterility gene, a selectable marker gene, a screenable marker gene, a negative selectable marker, a gene affecting plant agronomic characteristics, or an environment or stress resistance gene. The stress resistance gene confers resistance or tolerance to drought, heat, chilling, freezing, excessive moisture, excessive salt, or excessive oxidative stress. The promoters are useful for regulating the expression of selected transgenes in economically important plants. For example, root-specific promoters may be useful for expressing defense-related genes, including those conferring insecticidal resistance and stress tolerance genes, e.g., salt, cold or drought tolerance, and genes for altering nutrient uptake, and leaf-specific promoters may be useful for producing large quantities of protein, for expressing oils or proteins of interest, and genes for increasing the nutritional value of a plant. Constitutive promoters are useful for expressing a wide variety of genes including those which alter metabolic pathways, confer disease resistance, for protein production, e.g., antibody production, or to improve nutrient uptake. The present sequence is an open reading frame from an Arabidopsis leaf specific promoter gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences

SQ Sequence 3093 BP; 866 A; 592 C; 790 G; 845 T; 0 U; 0 Other;
 Query Match 85.6%; Score 15.4; DB 7; Length 3093;
 Best Local Similarity 94.1%; Pred. No. 4.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACACCTATTCTACT 17
|||
Db 553 CCACACCTATTCTACT 537

RESULT 45
ADE52630/c
ID ADE52630 standard: DNA: 3120 BP.

AC ADE52630;

DT 29-JAN-2004 (first entry)

DE *Caenorhabditis elegans* SOV DNA sequence #1.

KW SQV protein; SQV-1; SQV-2; SQV-4; SQV-5; SQV-6;
 KW glycosaminoglycan biosynthetic activity; connective tissue disease;
 KW Ehlers-Danlos syndrome; progeroid disorder;
 KW aging related cellular damage; ds.

OS Caenorhabditis elegans.

PN WO2003062448-A2.

31-JUL-2003.

XX	17-JAN-2003; 2003WO-US001558.
XX	18-JAN-2002; 2002US-0349630P.
XX	24-JUN-2002; 2002US-0390930P.
XX	(MASI) MASSACHUSETTS INST TECHNOLOGY.
XX	Horvitz HR, Hwang HY;
XX	WPI; 2003-627462/59.
XX	New SQV polypeptides and nucleic acids having a glycosaminoglycan
XX	biosynthetic biological activity, useful for diagnosing and treating a
XX	connective tissue disease, progeroid disorder, or cellular damage related
XX	to aging.
XX	Disclosure; SEQ ID NO 1; 247pp; English.
XX	The invention comprises the amino acid and coding sequences of SQV
XX	proteins (i.e. SQV-1, SQV-2, SQV-4, SQV-5 and SQV-6), having a
XX	glycosaminoglycan biosynthetic biological activity. The SQV DNA and
XX	protein sequences are useful for diagnosing and treating connective
XX	tissue disease, such as: Ehlers-Danlos syndrome, progeroid disorder, or
XX	cellular damage related to aging. The SQV DNA and protein sequences may
XX	also be used to identify compounds that modulate a glycosaminoglycan
XX	biosynthetic biological activity. The present nucleic acid represents an
XX	SQV DNA sequence of the invention.
XX	Sequence 3120 BP; 1004 A; 580 C; 551 G; 985 T; 0 U; 0 Other;
XX	

Query Match	85.6%	Score 15.4;	DB 10;	Length 3120;
Best Local Similarity	94.1%;	Pred. No. 4.1e+02;		
Matches	16;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;

2 CACACCTATTCACTC 18

Db 3067 CACACCTATTCCTACTC 3051

RESULT 46

AAQ46249
ID AAQ46249 standard; DNA; 8528 BP.

AAQ46249;

25-MAR-2003 (revised)

DT 17-MAR-1994 (first entry)

DE Construct EC2L (Contains catR and pyrG coding sequences).

KW *Aspergillus niger*: catR: hydrogen peroxide; ss:

OS Synthetic.

XX	Key	Location/Qualifiers
FH		

FT misc feature

$$\frac{1}{\Gamma T} \frac{d\Gamma T}{dt} = a$$

13

FT 5' UTR 9. .1957

```
ET b  
/*tag= b
```

```

Erf 1058 1270
Erf /function=

```

ET CDS
1958. .4370
/*rad= C

```
FT
/label= catR coding region.
```

FT 3'UTR 4371. .4432

FT / *tag= d

FT	misc_feature	4433.	.4440
----	--------------	-------	-------

```
FT =
/*tag= e
```

[illegible]

polyA_site

```
FT /label= q1aA polyadenylation and termination signals
```

```
FT CDS 6094..8510
FT     /*tag= g
FT misc_feature 8511..8528
FT     /*tag= h
FT     /*label= Linker sequence.
XX PN WO9318166-A2.
XX PD 16-SEP-1993.
XX PF 04-MAR-1993; 93WO-US002020..
XX PR 04-MAR-1992; 92US-00845989.
XX PR 04-MAR-1992; 92US-00846181.
XX PA (GENV ) GENENCOB INT INC.
XX PI Berka RM, Fowler T, Rey MW;
XX WI WIPI; 1993-303480/38.
XX PR Aspergillus niger catR gene sequence - from which catR promoter has been
XX PT deleted and Aspergillus glucoamylase promoter gene has been inserted.
XX PS Disclosure; Fig 3; 43pp; English.
XX CC The Aspergillus niger catR gene was identified and isolated. The native
XX CC promoter of the gene was removed and replaced with the Aspergillus
XX CC glucoamylase promoter gene. This modification allows increased expression
XX CC of the catR gene without the need to supply hydrogen peroxide to induce
XX CC expression. Cells into which this construct is inserted preferably have
XX CC the glucose oxidase gene (goxA) deleted. This deletion minimises the
XX CC generation of gluconate waste material and the use of waste treatment
XX CC processes. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 8528 BP; 1951 A; 2321 C; 2209 G; 2047 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 2; Length 8528;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
Db 5916 CCACACCTATTTCCTACT 5932

RESULT 47
ABL33718/c
ID ABL33718 standard; DNA; 17934 BP.
AC ABL33718;
XX
XX 26-MAR-2002 (first entry)
XX
XX Human immune system associated gene SEQ ID NO: 1691.
XX
XX Human; immune system disease; cytosine methylation; antiasthmatic;
XX antiarteriosclerotic; antianaemic; cytosstatic; nootropic;
XX neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
XX antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
XX antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
XX acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
XX neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
XX ds.
XX
XX Homo sapiens.
XX
XX WO200200928-A2.
XX
XX 03-JAN-2002.
XX
XX 02-JUL-2001; 2001WO-EP007537.

XX 30-JUN-2000; 2000DE-01032529.
XX PR 01-SEP-2000; 2000DE-01043826.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX WI WIPI; 2002-130909/17.
XX
XX Nucleic acid comprising fragment of chemically modified gene, useful for
XX PT diagnosis and treatment of diseases associated with abnormal cytosine
XX PT methylation.
XX
XX Claim 1; SEQ ID NO 1691; 32pp + Sequence Listing; German.
XX
XX The present invention provides a number of human immune system associated
XX CC genes which are modified by the methylation of cytosines. The sequences
XX CC can be used in the diagnosis and treatment of immune system disorders,
XX CC including eye diseases such as retinopathy, neovascular glaucoma and
XX CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX CC diseases. The present sequence is a gene of the invention
XX
XX SQ Sequence 17934 BP; 4443 A; 283 C; 4663 G; 8545 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 17934;
Best Local Similarity 94.1%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
Db 14397 CACACCTATACATCTC 14381

RESULT 48
ACN44150_0
WP Sequence split into 5 fragments LOCUS ACN44150 Accession ACN44150
WP Fragment Name Begin End
WP ACN44150_0 1 110000
WP ACN44150_1 100001 210000
WP ACN44150_2 200001 310000
WP ACN44150_3 300001 410000
WP ACN44150_4 400001 439892
WP ID ACN44150 standard; DNA; 439892 BP.
XX
XX ACN44150;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human genomic sequence hCG272728.
XX
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX
XX Homo sapiens.
XX
XX WO2003073826-A2.
XX
XX 12-SEP-2003.
XX
XX 28-FEB-2003; 2003WO-US006235.
XX
XX 01-MAR-2002; 2002US-00087192.
XX
XX (SAGR-) SAGRES DISCOVERY.
XX
XX Morris DW;
XX
XX WIPI; 2003-328604/31.
XX
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
XX PT comprises a nucleotide sequence.
```

XX
PS Claim 1; SEQ ID NO 454; Opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which
CC are associated with carcinomas. The sequences are useful for: (i) for
CC screening drug candidates; (ii) for screening of bioactive agent capable
CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
CC a bioactive agent capable of modulating the activity of CAP; (iv) for
CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) as a biochip;
CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for
CC determining Carcinoma Associated (CA) gene copy number. In addition, the
CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
CC carcinoma including lymphoma. The present sequence is one such CA coding
CC sequence. Note: This patent is an equivalent to basic patent
CC US2002182586A1, for which no sequence data was published
XX
SQ Sequence 439892 BP; 100791A; 104435C; 106090G; 116168T; 0U; 124080Other;

Query Match 85.6%; Score 15.4; DB 11; Length 110000;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
DB 54190 CACACCTTTTCATCTC 54206

RESULT 49
ADP44620/C
ID ADP44620 standard; DNA; 118777 BP.
XX
AC ADP44620;
XX
XX 26-AUG-2004 (first entry)
XX
DE Murine alpha-synuclein (SNCA) DNA - SEQ ID 10.
XX
KW neurodegenerative disorder; CNS; Parkinson's disease; Alzheimer's;
KW Huntington's; spinocerebellar ataxia type 1;
KW spinocerebellar ataxia type 3; SCA; Machado-Joseph disease;
KW dentatorubral-pallidoluysian atrophy; DRPLA; alpha-synuclein; SNCA; ds;
KW murine; house mouse.
XX
OS Mus musculus.
XX
XX WO2004047872-A2.
XX
PD 10-JUN-2004.
XX
PF 26-NOV-2003; 2003WO-US037650.
XX
PR 26-NOV-2002; 2002US-0429387P.
PR 03-FEB-2003; 2003US-0444614P.
XX
XX (MEDT) MEDTRONIC INC.
PA
PI Kaemmerer WF;
XX
XX WPI; 2004-441106/41.
XX
PT New medical system comprising an intracranial access device, a mapping
PT means, a small interfering RNA or vector encoding the RNA, and a delivery
PT means, useful for treating a neurodegenerative disorder.
XX
PS Claim 23; SEQ ID NO 10; 228pp; English.
XX
CC The invention relates to a novel medical system for treating a
CC neurodegenerative disorder comprising an intracranial access device, a
CC mapping means for locating a predetermined location in the brain, a
CC deliverable amount of a small interfering RNA (siRNA), or vector encoding
CC the siRNA, and a delivery means. The system of the invention has

CC applications related to the CNS and may be useful for treating a
CC neurodegenerative disorder, such as Parkinson's disease, Alzheimer's
CC disease, Huntington's disease, spinocerebellar ataxia (SCA) types 1 and 3
CC (Machado-Joseph disease) or dentatorubral-pallidoluysian atrophy (DRPLA).
CC The current sequence is that of the murine alpha-synuclein (SNCA) DNA
CC (SEQ ID 10) of the invention.
XX
SQ Sequence 118777 BP; 35967 A; 22351 C; 22620 G; 37839 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 12; Length 118777;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 17
DB 77795 CCACACATATTTCATCTC 77779

RESULT 50
ABQ28339
ID ABQ28339 standard; DNA; 544 BP.
XX
AC ABQ28339;
XX
DT 12-JUL-2002 (first entry)
XX
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 14930.
XX
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX
OS Homo sapiens.
XX
XX WO200218632-A2.
XX
PD 07-MAR-2002.
XX
PF 01-SEP-2001; 2001WO-EP010074.
XX
PR 01-SEP-2000; 2000DE-01043826.
PR 05-SEP-2000; 2000DE-01044543.
XX
XX (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX
XX WPI; 2002-371829/40.
XX
PT Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX
PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
CC This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used:
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ13410-

CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX Sequence 544 BP; 247 A; 145 C; 42 G; 110 T; 0 U; 0 Other;
SQ Query Match 83.3%; Score 15; DB 6; Length 544;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
DB 13 CACCTATTTCATCTC 27

RESULT 51
ABQ28338/c
ID ABQ28338 standard; DNA; 544 BP.
XX AC ABQ28338;
XX 12-JUL-2002 (first entry)
XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 14929.
DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
XX OS Homo sapiens.
XX WO200218632-A2.
XX PD 07-MAR-2002.
XX 01-SEP-2001; 2001WO-BF010074.
XX 01-SEP-2000; 2000DE-01043826.
XX 05-SEP-2000; 2000DE-01044543.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful for
PT diagnosis and prognosis, comprises selective hybridization of amplicons
PT from chemically treated DNA.
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one member,
CC of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC degree of hybridisation to both classes is determined from the label on
CC the amplicon. From the ratio of labels hybridised to the two classes of
CC oligomers, the degree of methylation is calculated. The method is used;
CC (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC and of a wide range of diseases, e.g. cancer, disorders of the central
CC nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC particularly by detecting mutations or single nucleotide polymorphisms
CC (SNP's); and (ii) for differentiation of cell or tissue types and for
CC investigating cell differentiation. The method allows the methylation
CC status of many C residues to be determined simultaneously. ABQ1410-
CC ABQ54121 represent genomic DNA sequences used to illustrate the method
CC for determining the degree of cytosine methylation described in the
CC disclosure of the invention

XX Sequence 544 BP; 110 A; 42 C; 145 G; 247 T; 0 U; 0 Other;
SQ Query Match 83.3%; Score 15; DB 6; Length 544;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
DB 532 CACCTATTTCATCTC 518

RESULT 52
ADQ63331
ID ADQ63331 standard; cDNA; 3951 BP.
XX AC ADQ63331;
XX 07-OCT-2004 (first entry)
XX Novel human cDNA sequence #492.
XX ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;
KW cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW cancer.
XX OS Homo sapiens.
XX EP1440981-A2.
XX 28-JUL-2004.
XX 21-JAN-2004; 2004EP-00001196.
XX 21-JAN-2003; 2003JP-00102206.
XX 09-MAY-2003; 2003JP-00131392.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Nagai K, Irie R;
XX WPI; 2004-535376/52.
XX P-PSDB; ADQ65519.
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX Claim 1; SEQ ID NO 492; 2449pp; English.
XX The invention relates to 2495 novel polynucleotides (I) and their encoded
CC polypeptides, sequences hybridizing to these nucleotides, sequences
CC encoding partial polypeptides and sequences having 70% or 90% identity to
CC the nucleotide and protein sequences. The nucleotides and polypeptides
CC are useful as diagnostic markers or therapeutic target for the diseases
CC or morbid states. They are also useful for treating osteoporosis,
CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,
CC dementia and various cancers. This sequence corresponds to a nucleotide
CC sequence of the invention.
XX Sequence 3951 BP; 992 A; 1043 C; 1111 G; 805 T; 0 U; 0 Other;
SQ Query Match 83.3%; Score 15; DB 12; Length 3951;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACTATTTCATA 15
DB 3820 CCACACTATTTCATA 3834

RESULT 53

```
AAA69665
ID AAA69665 standard; cDNA; 362 BP.
AC
XX AAA69665;
AC
XX
DT
XX
DE 08-NOV-2000 (first entry)
XX
XX Pinus radiata methyl sterol oxidase cDNA SEQ ID NO:139.
DE
XX Eucalyptus grandis; Pinus radiata; modification; isoprenoid; plant;
XX metabolism; isoprenoid biosynthetic pathway; terpenoid; steroid;
XX genome mapping; physical mapping; positional cloning; forestry;
XX agriculture; medicine; fermentation; plant development; pest resistance;
XX pinene; myrcene; Monterey pine; ss.
XX
OS Pinus radiata.
XX
PN WO200036081-A2.
XX
XX 22-JUN-2000.
XX
XX 16-DEC-1999; 99WO-NZ000219.
XX
XX 17-DEC-1998; 98US-00215504.
XX
XX 29-JUL-1999; 99US-0146441P.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX
XX Havukkala IJ;
XX
XX WPI; 2000-431575/37.
XX P-PSDB; AAB18065.
XX
XX New plant polynucleotides encoding polypeptides involved in the
XX production and modification of isoprenoids, useful in forestry and
XX agriculture for manipulation of isoprenoid metabolism.
XX
XX Claim 1; Page 95; 164pp; English.
XX
XX The present invention describes plant polynucleotides encoding
XX polypeptides involved in the production and modification of isoprenoids,
XX such as terpenoid and steroid compounds. The polynucleotides are used in
XX genome mapping, in physical mapping and in positional cloning of genes.
XX The polynucleotides and polypeptides are useful in forestry and
XX agriculture for manipulation of isoprenoid metabolism, in medicine for
XX therapeutic effects, including direct application in diseased organisms
XX or indirect application by transgenic organisms and in fermentation and
XX chemical processing industries involving isoprenoids. In plant
XX applications, manipulating isoprenoid pathways or isoprenoid composition
XX may, for example, affect plant development, pest resistance, and the
XX value of extractives (e.g. pinene and myrcene). The ubiquitous and varied
XX roles of isoprenoids make the polynucleotides attractive targets for
XX biotechnical applications in a variety of fields. AAA69527 to AAA69690
XX and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus radiata
XX polynucleotides and proteins used in the exemplification of the present
XX invention
XX
XX Sequence 362 BP; 101 A; 69 C; 86 G; 106 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 3; Length 362;
Best Local Similarity 88.9%; Pred. No. 7.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 5 CCTCACCTATTTCACATC 22

RESULT 54
AB208767/c
ID AB208767 standard; cDNA; 466 BP.
XX
```

```
AC
XX ABZ08767;
DT 09-JAN-2003 (first entry)
XX
XX Human leukocyte derived cDNA SEQ ID NO 8758.
XX
XX Human; leukocyte; gene expression profiling; allograft rejection;
XX atherosclerosis; congestive heart failure; systemic lupus erythematosus;
XX rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200257414-A2.
XX
XX 25-JUL-2002.
XX
XX 22-OCT-2001; 2001WO-US047856.
XX
XX 20-OCT-2000; 2000US-0241994P.
XX
XX 08-JUN-2001; 2001US-0296764P.
XX
XX (BIOC-) BIOCARDIA INC.
XX
XX Wohlgemuth J, Fry K, Marcuk G, Altman P, Prentice J, Phillips J;
XX Ly N, Woodward R, Quettermous T, Johnson F;
XX
XX WPI; 2002-636525/68.
XX
XX New system for leukocyte expression profiling, diagnosing a disease, or
XX monitoring (the rate of) progression of a disease, e.g. atherosclerosis
XX or congestive heart failure, comprises diagnostic oligonucleotides.
XX
XX Claim 26; Page 2011; Opp; English.
XX
XX The invention relates to a system for detecting gene expression, which
XX comprises one or two isolated DNA molecules that detect expression of a
XX gene, where the gene corresponds to any of 8143 oligonucleotides
XX (ABZ00010-ABZ08132) each having 50 base pairs (bp). The system is useful
XX for leukocyte expression profiling. It is particularly useful for
XX diagnosing a disease, monitoring (rate of) progression of a disease,
XX predicting therapeutic outcome, determining prognosis for a patient,
XX predicting disease complications in an individual or monitoring response
XX to treatment in an individual. The diseases include cardiac allograft
XX rejection, kidney allograft rejection, liver allograft rejection,
XX atherosclerosis, congestive heart failure, systemic lupus erythematosus,
XX rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The
XX present sequence is that of a human leukocyte expressed cDNA of the
XX invention
XX
XX Sequence 466 BP; 135 A; 74 C; 131 G; 110 T; 0 U; 16 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 466;
Best Local Similarity 88.9%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 298 CCACTCCTATTCATCTC 281

RESULT 55
ACC62584/c
ID ACC62584 standard; cDNA; 506 BP.
XX
XX ACC62584;
XX
XX 27-JUN-2003 (first entry)
XX
XX Rice endosperm EST #3.
XX rice; endosperm; expressed sequence tag; biochip; EST; ss.
XX
```

OS Oryza sativa.
 XX
 PN CN1366079-A.
 XX
 XX
 PD 28-AUG-2002.
 XX
 PF 31-OCT-2001; 2001CN-00137670.
 XX
 PR 31-OCT-2001; 2001CN-00137670.
 XX
 PA (UYZH-) UNIV ZHEJIANG.
 XX
 PI Dong H, Li D;
 XX
 DR WPI; 2003-269237/27.
 XX
 PT New rice endosperm specific expression sequence label for use in a
 PT biochip and for DNA sequencing to configure a rice endosperm cDNA
 PT library.
 XX
 PS Claim 1; Page 11-12; 30pp; Chinese.
 XX
 CC The invention relates to a novel rice endosperm specific expressed
 CC sequence tag (EST) and its constituted biochip. The cDNA sequence has one
 CC of 50 sequences. The EST technique is used for DNA sequencing to
 CC configure a rice endosperm cDNA library. The obtained expression sequence
 CC label goes through removing redundant sequences, indexing Internet
 CC database, sorting and collecting non-redundant sequences to obtain 50 new
 CC expression sequence labels. The biochip is prepared from them by the
 CC microarray technique and has broad-spectrum application. The sequences
 CC shown in ACC62582-ACC62631 represent the EST's of the invention
 XX
 SQ Sequence 506 BP; 119 A; 122 C; 124 G; 141 T; 0 U; 0 Other;
 Query Match 82.2%; Score 14.8; DB 8; Length 506;
 Best Local Similarity 88.9%; Pred. No. 7.4e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CCACACCTTATTCATCTC 18
 DB 255 CAACACCAATTCATCTC 238
 RESULT 56
 ACH91848
 ID ACH91848 standard; DNA; 584 BP.
 XX
 AC ACH91848;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #25043.
 XX
 KW Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 PN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR WPI; 2004-119264/12.

XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 1; SEQ ID NO 25043; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704
 XX
 SQ Sequence 584 BP; 145 A; 166 C; 66 G; 204 T; 0 U; 3 Other;
 Query Match 82.2%; Score 14.8; DB 12; Length 584;
 Best Local Similarity 88.9%; Pred. No. 7.5e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CCACACCTTATTCATCTC 18
 DB 364 CCACATTATTCCTACTC 381
 RESULT 57
 ABQ20739
 ID ABQ20739 standard; DNA; 591 BP.
 XX
 AC ABQ20739;
 XX
 DT 12-JUL-2002 (first entry)
 XX
 DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 7330.
 XX
 KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200218632-A2.

```
XX PD 07-MAR-2002.
XX PF 01-SEP-2001; 2001WO-EP010074.
XX PR 01-SEP-2000; 2000DE-01043826.
XX PR 05-SEP-2000; 2000DE-01044543.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX CC This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's); and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention
XX SQ Sequence 591 BP; 230 A; 175 C; 52 G; 134 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 591;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db | ||||| ||||| |||
26 CAACACCTATTTCATATC 9

RESULT 59
ABQ26403
ID ABQ26403 standard; DNA; 601 BP.
XX
XX AC ABQ26403;
XX
XX DT 12-JUL-2002 (first entry)
XX
XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12994.
XX
XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200218632-A2.
XX
XX PD 07-MAR-2002.
XX
XX PF 01-SEP-2001; 2001WO-EP010074.
XX PR 01-SEP-2000; 2000DE-01043826.
XX PR 05-SEP-2000; 2000DE-01044543.
XX PA (EPiG-) EPIGENOMICS AG.
XX PI Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX PT Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX PS Claim 12; 56pp + Sequence Listing; 56pp; German.
XX CC This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's); and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention
XX SQ Sequence 591 BP; 230 A; 175 C; 52 G; 134 T; 0 U; 0 Other;

Query Match 82.2%; Score 14.8; DB 6; Length 591;
Best Local Similarity 88.9%; Pred. No. 7.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db | ||||| ||||| |||
566 CAACACCTATTTCATATC 583

RESULT 58
ABQ20738/c
ID ABQ20738 standard; DNA; 591 BP.
XX
XX AC ABQ20738;
XX
XX DT 12-JUL-2002 (first entry)
XX
XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 7329.
XX
XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200218632-A2.
XX
XX PD 07-MAR-2002.
XX
XX PF 01-SEP-2001; 2001WO-EP010074.
XX PR 01-SEP-2000; 2000DE-01043826.
XX PR 05-SEP-2000; 2000DE-01044543.
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PR 05-SEP-2000; 2000DE-01044543.
XX (EPIG-) EPIGENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's); and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention
XX
XX Sequence 601 BP; 183 A; 266 C; 70 G; 82 T; 0 U; 0 Other;
XX
XX Query Match 82.2%; Score 14.8; DB 6; Length 601;
XX Best Local Similarity 88.9%; Pred. No. 7.5e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CCACACCTATTTCATCTC 18
XX ||||| ||||| ||||| |||||
XX Db 164 CCACCCCTACTCATCTC 181
XX
XX RESULT 60
XX ABQ26402/c
XX ID ABQ26402 standard; DNA; 601 BP.
XX
XX AC ABQ26402;
XX
XX DT 12-JUL-2002 (first entry)
XX
XX DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12993.
XX
XX KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
XX drug; side effect; cancer; central nervous system; cardiovascular;
XX gastrointestinal; respiratory system; single nucleotide polymorphism;
XX SNP; cell differentiation; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200218632-A2.
XX
XX PD 07-MAR-2002.
XX
XX PF 01-SEP-2001; 2001WO-EP010074.
XX
XX PR 01-SEP-2000; 2000DE-01043826.
XX PR 05-SEP-2000; 2000DE-01044543.
XX
XX PA (EPIG-) EPIGENOMICS AG.
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XX Olek A, Piepenbrock C, Berlin K, Guetig D;
XX WPI; 2002-371829/40.
XX
XX Determining the degree of cytosine methylation in genomic DNA, useful for
XX diagnosis and prognosis, comprises selective hybridization of amplicons
XX from chemically treated DNA.
XX
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX
XX This invention describes a novel method for determining the degree of
XX methylation of a particular cytosine in a motif 5'-CpG-3', present in a
XX genomic sample of DNA. The sample is treated chemically to convert
XX cytosine (C) but not methylated C, to uracil, then part of the genomic
XX DNA that contains the target C is amplified to form a labeled amplicon.
XX The amplicon is hybridised to two classes, each with at least one member,
XX of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
XX degree of hybridisation to both classes is determined from the label on
XX the amplicon. From the ratio of labels hybridised to the two classes of
XX oligomers, the degree of methylation is calculated. The method is used:
XX (i) for diagnosis and/or prognosis of side effects of therapeutic drugs
XX and of a wide range of diseases, e.g. cancer, disorders of the central
XX nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
XX particularly by detecting mutations or single nucleotide polymorphisms
XX (SNP's); and (ii) for differentiation of cell or tissue types and for
XX investigating cell differentiation. The method allows the methylation
XX status of many C residues to be determined simultaneously. ABQ13410-
XX ABQ54121 represent genomic DNA sequences used to illustrate the method
XX for determining the degree of cytosine methylation described in the
XX disclosure of the invention
XX
XX Sequence 601 BP; 82 A; 70 C; 266 G; 183 T; 0 U; 0 Other;
XX
XX Query Match 82.2%; Score 14.8; DB 6; Length 601;
XX Best Local Similarity 88.9%; Pred. No. 7.5e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 1 CCACACCTATTTCATCTC 18
XX ||||| ||||| ||||| |||||
XX Db 438 CCACCCCTACTCATCTC 421
XX
XX Search completed: May 10, 2006, 04:14:04
XX Job time : 682 secs
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 18:53:06 ; Search time 3760 Seconds
(without alignments)
223.981 Million cell updates/sec

Title: US-10-608-296-38
Perfect score: 18
Sequence: 1 ccacaccattaccactc 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_hrc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	100.0	263	1	AW873835 hg51e08.x
C 2	18	100.0	267	1	AA921407 ak56h08.s
C 3	18	100.0	270	1	AA921386 ak56f06.s
C 4	18	100.0	287	1	AA366418 EST77396
C 5	18	100.0	289	1	AA844966 ak57e12.s
C 6	18	100.0	309	11	DQ047208 Homo sapi
C 7	18	100.0	330	1	AA983889 op63d03.s
C 8	18	100.0	349	3	BI791451 id98b09.x
C 9	18	100.0	352	2	BGI92232 RST11340
10	18	100.0	356	6	CA867922 ir83a11.y
11	18	100.0	369	5	BU786585 in56g05.y
12	18	100.0	380	5	BX113838 BX113838
C 13	18	100.0	405	6	CA943648 ir83a11.x
C 14	18	100.0	405	6	CA943649 ir83a12.x
15	18	100.0	409	3	BI712863 id98b09.y
16	18	100.0	416	6	CA867923 ir83a12.y
17	18	100.0	423	5	BU949507 in68e07.y
C 18	18	100.0	425	1	AW139696 UI-H-B11-
C 19	18	100.0	426	3	BQ271823 ik15a01.y
C 20	18	100.0	442	3	BQ100865 lj24n05.x
21	18	100.0	443	5	BU071934 im52b08.y
22	18	100.0	444	3	BQ126651 il17e08.y

BU949152 in66f07.x
AA835575 ak68h10.s
BU949187 in67b10.x
BU075990 im52h05.x
AA845006 ak61f09.s
BU949393 in66f07.y
BM504818 ig90h06.x
BU071991 im52h05.y
AA921338 ak56a06.s
BM505143 ig90h06.y
BG142111 ia49b01.y
AA835294 ak66b10.s
CK902774 in68e07.x
AI985509 ws08d11.x
AA844755 ak59b12.s
BU949263 in68e07.x
BO631720 il21c12.y
BU949263 in68e07.x
BU952425 io74d05.x
AM583679 ia03a06.y
BU954926 in67b10.y
AA835293 ak66b09.s
BO101169 ij24h05.y
AA835315 ak66e08.s
BU950878 io74d05.y
AA844827 ak61a06.s
BM264109 ig31a01.y
CK902775 in68e07.y
AI925956 wh12g03.x
BP323152 BP323152
BC013384 Homo sapi
BP322008 BP322008
BP323927 BP323927
BP324031 BP324031
BP324615 BP324615
BP324960 BP324960
BP323989 BP323989
BP324302 BP324302
BP325524 BP325524
BP323356 BP323356
BP322177 BP322177
BP322424 BP322424
BP322827 BP322827
BP322937 BP322937
BP325167 BP325167
AW951287 EST363357
BS969699 601679662
BS969737 601679687
BS969664 601679602
BB147765 BB147765
AK037040 Mus muscu
DQ047209 Pan trogl
CA736765 wp1le.pk0
CF190679 k8p22j2.f
AV214968 RST14966
BG185996 AV214966
T29344 EST77254 Hu
BZ835788 CH240_236
AA835121 ak63e02.s
BQ171759 WHE1659-1
CF705448 CCAFR13TO
AA536183 nf96c06.s
CF691710 CCAGK20TF
CB230127 AGENCOURT
AO725293 HS_5404_A
CF721282 CCAQ13TO
BG907012 TaLR11505
CF718422 CCA1657TF


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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1411935"
/sex="female"
/dev_stages="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pTT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI, Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15'
TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pTT73 vector.
Library constructed by Bob Barstead. "

ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCACTC 18
|||||
Db 253 CCACACCTATTCACTC 236

RESULT 3
AA921386/c
LOCUS
DEFINITION
ak56f06.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1411907 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN); mRNA sequence.
ACCESSION
AA921386
VERSION
AA921386.1 GI:3068165
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 270)
AUTHORS
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m3 fwd. ET from Amersham.

FEATURES
source
1..270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1411907"
/sex="female"
/dev_stages="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pTT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI, Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15'
TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTT

```

```

3']; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pTT73 vector.
Library constructed by Bob Barstead. "

ORIGIN
Query Match 100.0%; Score 18; DB 1; Length 270;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCACTC 18
|||||
Db 262 CCACACCTATTCACTC 245

RESULT 4
AA366418
LOCUS
DEFINITION
AA366418 Pancreas tumor III Homo sapiens cDNA 5' end similar to
phospholipase A2 (GB:M21054), mRNA sequence.
ACCESSION
AA366418
VERSION
AA366418.1 GI:2018768
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 287)
AUTHORS
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Coston,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillion,P.J., Rannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Praser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
7566098
Other ESTs: THC165995
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
FEATURES
source
1..287
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (inhost):171116"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="Pancreas tumor III"
/note="Organ: pancreas; Vector: pbluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

```

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Query Match      100.0%; Score 18; DB 1; Length 287;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
Db 261 CCACACCTATTTCATCTC 278

RESULT 5
AA844966/c
LOCUS
DEFINITION
ak57el2.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412014 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
AA844966
VERSION
AA844966.1 GI:2931417
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 289)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amer sham.
FEATURES
Location/Qualifiers
source
1..289
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412014"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pTT3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5].
TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
3'; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGGACCTTGG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pTT3 vector.
Library constructed by Bob Barstead."
ORIGIN
Query Match      100.0%; Score 18; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
Db 200 CCACACCTATTTCATCTC 183

RESULT 6
DQ047208
LOCUS
DEFINITION
Homo sapiens PLA2G1B gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
DQ047208
VERSION
DQ047208.1 GI:66900407
KEYWORDS
GSS.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 309)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(er) PLOS Biol. 3 (6), E170 (2005)
15869325
2 (bases 1 to 309)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
Location/Qualifiers
source
1..309
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
<1..>309
/gene="PLA2G1B"
/locus_tag="HC15100"
ORIGIN
Query Match      100.0%; Score 18; DB 11; Length 309;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
Db 82 CCACACCTATTTCATCTC 99

RESULT 7
AA983889/c
LOCUS
DEFINITION
op3id03.s1 Soares NFL T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1581509 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
AA983889
VERSION
AA983889.1 GI:3162414
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 330)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2522 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amer sham.

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FEATURES
source

Location/Qualifiers
1. .330
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1581509"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 250 CCACACCTATTTCATCTC 233

RESULT 8

BI791451/c
LOCUS BI791451 349 bp mRNA linear EST 11-MAR-2002
DEFINITION id98b09.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5085640 3' mRNA similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION BI791451

VERSION BI791451.1 GI:15819176

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 349)

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Other ESTs: id98b09.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

TITLE

JOURNAL

COMMENT

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.
Location/Qualifiers
1. .349
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"

FEATURES
source

Query Match 100.0%; Score 18; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

/clone="IMAGE:5085640"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1: Not1; Site 2: Xho1; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' Xho1 site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 255 CCACACCTATTTCATCTC 238

RESULT 9

BI912232
LOCUS BI912232 352 bp mRNA linear EST 21-APR-2001
DEFINITION RST11340 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.

ACCESSION BI912232

VERSION BI912232.1 GI:13713919

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 352)

AUTHORS

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Booser,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL

PUBMED

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scaine@atersys.com
High quality sequence stop: 352.
Location/Qualifiers
1. .352

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 352;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

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Db      88 CCACACCTATTTCATCTC 105
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ir83all.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6608758 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION      CA867922
VERSION        CA867922
KEYWORDS       CA867922.1 GI:27319471
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 356)
AUTHORS        Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 357
Seq primer: -40UP from Gibco.
FEATURES
Location/Qualifiers
1..356
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608758"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
ORIGIN
Query Match      100.0%; Score 18; DB 6; Length 356;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
|||||
Db      95 CCACACCTATTTCATCTC 112
|||||
CA867922      356 bp      mRNA      linear      EST 07-FEB-2003
ir83all.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6126153 5'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION      CA867922
VERSION        CA867922
KEYWORDS       CA867922.1 GI:23833402
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 369)
AUTHORS        Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
High quality sequence stop: 257.
FEATURES
Location/Qualifiers
1..369
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6126153"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
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Db      201 CCACACCTATTTCATCTC 218
|||||
CA867922      380 bp      mRNA      linear      EST 07-FEB-2003
ir83all.y1 HR85 islet Homo sapiens cDNA clone IMAGE:1461104, mRNA sequence.
ACCESSION      CA867922
VERSION        CA867922
KEYWORDS       CA867922.1 GI:27879441
SOURCE         Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS 1 (bases 1 to 380)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,B., Peters,M.,
Radelet,U., Schneider,D. and Korn,B.
Human Unigeneset - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998E093695.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

This clone is available royalty-free from RZPD;
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGAAACAGCTATGAC.

FEATURES
source
1..380
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998E093695 ; IMAGE:1461104"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

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TITLE JOURNAL
COMMENT

FEATURES
source
1..405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608758"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 249 CCACACCTATTCTACTC 232

RESULT 14
CA943649/c
LOCUS
DEFINITION ir83a12.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6608760 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION CA943649
VERSION CA943649.1 GI:27432129
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 405)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other_ESTs: ir83a12.y1
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TITLE JOURNAL
COMMENT

FEATURES
source
1..405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608758"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."
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ORIGIN
Query Match 100.0%; Score 18; DB 5; Length 380;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 116 CCACACCTATTCTACTC 133

RESULT 13
CA943648/c
LOCUS
DEFINITION ir83a11.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6608758 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION CA943648
VERSION CA943648.1 GI:27432128
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 405)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
```

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -4ORP from Gibco.
Location/Qualifiers
1. .405

FEATURES

source
1. .405
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608760"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"

/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||
Db 249 CCACACCTATTCATCTC 232

RESULT 15

BI712863 409 bp mRNA linear EST 11-MAR-2002
LOCUS
ID98b09.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5085640 5'
DEFINITION
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA
sequence.

ACCESSION

BI712863 GI:15688558

VERSION

EST.

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 409)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Trace considered overall poor quality
Seq primer: -4ORP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .409

FEATURES

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1. .409
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5085640"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"

/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 409;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCTC 18
|||||
Db 241 CCACACCTATTCATCTC 258

RESULT 16

CA867923 416 bp mRNA linear EST 20-DEC-2002
LOCUS
ir93a12.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6608760 5'
DEFINITION
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA
sequence.

ACCESSION

CA867923 GI:27319472

VERSION

EST.

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE

1 (bases 1 to 416)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Putative full length read

vector to vector length is

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Seq primer: -40UP from Gibco.
Location/Qualifiers
1. 416
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6608760"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 416;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACTTATTCATCTC 18
|||||
Db 155 CCACACTTATTCATCTC 172

RESULT 17
BU949507 423 bp mRNA linear EST 21-OCT-2002
LOCUS in68e07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127213 5'
DEFINITION similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION BU949507
VERSION BU949507.1 GI:24200858
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marrs,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: in68e07.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 470
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 423
/organism="Homo sapiens"
/mol_type="mRNA"

FEATURES
source
/db_xref="taxon:9606"
/clone="IMAGE:2717813"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Sub3"
/notes="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NCI CGAP Sub3 library is a subtracted library derived from
the NCI CGAP Sub1 library, which is a subtracted library
derived from B1. B1 constitutes a mixture of 21
normalized or subtracted NCI CGAP libraries:
NCI CGAP Co4, NCI CGAP Pr22, NCI CGAP Pr28, NCI CGAP Co10,
NCI CGAP Co16, NCI CGAP Kid5, NCI CGAP Kid12,
NCI CGAP Kid3, NCI CGAP Kid11, NCI CGAP Lym2,
NCI CGAP Br2, NCI CGAP Co8, NCI CGAP CLL1, NCI CGAP Lei2,
NCI CGAP Brn23, NCI CGAP Lu5, NCI CGAP Lu24,

```

NCI CGAP Lul9, NCI CGAP GC4, NCI CGAP GC6,
 NCI CGAP Brn25. These 21 libraries were pooled and a
 single-stranded DNA preparation of the resulting mixture
 was used as a tracer in a subtractive hybridization with
 a driver whose composition is detailed below:
 NCI CGAP Kid3 pool 1 LLM 3334-3337, 3682-3683,
 3798-3803 (IMAGE CloneIDs 1322376-1323911,
 1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1
 LLM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs
 1323912-1325831, 1471368-1472903, 1492104-1493255);
 NCI CGAP LUS pool 1 LLM 3575-3582, 3851-3854 (IMAGE
 CloneIDs 1414920-1417991, 1520904-1522439); NCI CGAP GC4
 pool 1 LLM 3164-3167, 3716-3720, 3733-3735 (IMAGE
 CloneIDs 1257096-1258631, 1469064-1470983, LLM 2457-2459,
 1475592-1476743); NCI CGAP Pr22 pool 1
 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759,
 1101192-1101959, 1217928-1220615); NCI CGAP Col10 pool 1
 LLM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255,
 114584-1145351). Subtraction was performed as previously
 described [Bonaldo, Lennon & Soares (1996): Normalization
 and Subtraction: Two Approaches To Facilitate Gene
 Discovery. Genome Research 6, 791-806.
 TAG TISSUE=lung
 TAG_LIB=NCI CGAP_Lus
 TAG_SEQ=CAAC"

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
 Db 265 CCACACCTATTTCATCTC 248

RESULT 19

BQ271823
 LOCUS
 DEFINITION
 BQ271823.1 HR85 islet Homo sapiens cDNA clone IMAGE:5781000 5',
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ271823 426 bp mRNA linear EST 15-JUL-2003
 ik15a01.y1 HR85 islet Homo sapiens cDNA clone IMAGE:5781000 5',
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
 sequence.
 BQ271823
 EST.
 Homo sapiens
 Homo sapiens (human)

REFERENCE

AUTHORS
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

TITLE

JOURNAL
 COMMENT
 Other ESTs: ik15a01.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Putative full length read

vector to vector length is 465
 Seq primer: -40RP from Gibco
 High quality sequence stop: 403.
 Location/Qualifiers
 1. 426

FEATURES

source
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clones="IMAGE:5781000"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 426;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
 Db 201 CCACACCTATTTCATCTC 218

RESULT 20

BQ100865/c
 LOCUS
 DEFINITION
 BQ100865.1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:6135800 3', similar to SW:PA21_HUMAN P04054
 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BQ100865 442 bp mRNA linear EST 29-APR-2002
 ij24h05.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:6135800 3', similar to SW:PA21_HUMAN P04054
 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
 BQ100865.1 GI:20133849
 EST.
 Homo sapiens (human)

REFERENCE

AUTHORS
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

TITLE

JOURNAL
 COMMENT
 Other ESTs: ij24h05.y1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through LNL; please contact the IMAGE
 consortium (info@image.llnl.gov) for further information
 Trace considered overall poor quality

Seq primer: -40UP from Gibco
 High quality sequence stop: 1.
 Location/Qualifiers
 1. 442


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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6135900"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/notes="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dr priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

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ORIGIN

```

Query Match      100.0%; Score 18; DB 3; Length 442;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCACACCTTATTCATCTC 18
|||||
Db 167 CCACACCTTATTCATCTC 150

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RESULT 21

```

BU071934
LOCUS          443 bp mRNA linear EST 27-AUG-2002
DEFINITION    im52b08.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6038726 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
ACCESSION     BU071934.1 GI:22513123
VERSION       BU071934
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

```

```

REFERENCE
AUTHORS      Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
              Endocrine Pancreas Consortium
              Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
              Endocrine Pancreas Consortium
              Harvard University, Howard Hughes Medical Institute
              Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

```

```

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 463
Seq primer: -40RP from Gibco
High quality sequence stop: 404.

```

FEATURES

```

source
1..443
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6038726"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/notes="Organ: Pancreas; Vector: pBluescript SK(-); Site 1: Not 1; Site 2: XhoI; cDNA made by oligo-dr priming. ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
Query Match      100.0%; Score 18; DB 5; Length 443;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

ORIGIN

```

QY 1 CCACACCTTATTCATCTC 18
|||||
Db 202 CCACACCTTATTCATCTC 219

```

RESULT 22

```

BU126651
LOCUS          444 bp mRNA linear EST 19-APR-2002
DEFINITION    i117e08.y1 Melton Amplified Mouse E16 5 Pancreas 3 M16S1 A Mus musculus cDNA clone IMAGE:5942102 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
ACCESSION     BU126651
VERSION       BU126651.1 GI:20200562
KEYWORDS      EST.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus

```

```

REFERENCE
AUTHORS      Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
              Endocrine Pancreas Consortium
              Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
              Endocrine Pancreas Consortium
              Harvard University, Howard Hughes Medical Institute
              Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu

```

```

Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center This clone is
available royalty-free through LiNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Putative full length read
vector to vector length is 526
Seq primer: -40RP from Gibco.

```

```

FEATURES
source
1..444
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5942102"

```

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/sex="Both"
/tissue_type="pancreas"
/dev_stage="Embryonic day E16.5"
/lab_host="DH10B"
/clone_lib="Melton Amplified Mouse E16 5 Pancreas 3 M16S1
A"
/note="Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1;
Library constructed using SuperScript Plasmid Library kit
(life technologies). cDNA made by oligo-dT priming.
Size-selected by column fractionation; average insert size
0.97 kb. Amplified once on solid support. cDNA Library
Preparation: Guolin Chen."

ORIGIN

Query Match      100.0%; Score 18; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 CCACACCTATTCATC 18
     ||| ||||| ||||| |||||
Db    267 CCACACCTATTCATC 284

RESULT 23
BU949152/c
LOCUS
DEFINITION
BU949152          448 bp mRNA linear EST 21-OCT-2002
in66f07.x1 HR85 islet Homo sapiens CDNA clone IMAGE:6127237 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
BU949152          GI:24200503
BU949152          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS           Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Paper,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R.,
Williams,T., Jackson,Y. and Bowers,Y.
JOURNAL            Endocrine Pancreas Consortium
COMMENT            Unpublished (2000)
Other_Etrs: in66f07.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoueeim.wustl.edu)
Seq primer: -40UP from Gibco.
Location/Qualifiers
FEATURES
source
1..448
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:612723"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: XhoI; cDNA made by oligo-dr priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning."

ORIGIN

Query Match      100.0%; Score 18; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1 CCACACCTATTCATC 18
     ||| ||||| ||||| |||||
Db    248 CCACACCTATTCATC 231

RESULT 24
AA835575/c
LOCUS
DEFINITION
AA835575          449 bp mRNA linear EST 23-FEB-1998
ak68hi0.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1413091 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
AA835575          GI:2909303
AA835575          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS           Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
FEATURES
source
1..449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1413091"
/sex="female"
/dev_stage="adult, 34 years"
/lab_host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5',
TGTTACGAATCTGAAGTGGGAGCGCCGCTTTTTTTTTTTTTTTTTTTT
3'] ; double-stranded cDNA was ligated to Eco RI adaptors
[AAATCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT73 vector.
Library constructed by Bob Barstead."

```

```

QY      1 CCACACCTATTCTACTC 18
      |||||||
Db      242 CCACACCTATTCTACTC 225

RESULT 25
BU949187/c
LOCUS
DEFINITION
BU949187      449 bp      mRNA      linear      EST 21-OCT-2002
in67b10.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6127074 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION
BU949187      1 GI:24200538
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 449)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..449
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6127074"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 449;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      |||||||
Db      248 CCACACCTATTCTACTC 231

RESULT 26
BU075990/c
LOCUS
DEFINITION
BU075990      455 bp      mRNA      linear      EST 27-AUG-2002
in67b10.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6127074 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.
ACCESSION
BU075990      1 GI:22517179
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
1 (bases 1 to 455)
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Teagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..455
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6039008"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match      100.0%; Score 18; DB 5; Length 455;
Best Local Similarity 100.0%; Pred.No.1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTCTACTC 18
      |||||||
Db      249 CCACACCTATTCTACTC 232

RESULT 27
AA845006/c
LOCUS
DEFINITION
AA845006      459 bp      mRNA      linear      EST 04-MAR-1998
ak61f09.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412393 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION
AA845006      1 GI:2931457
VERSION
EST.
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, P., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE
JOURNAL
COMMENT
 WashU-NCI Human EST Project
 Contact: Wilton RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 377.

FEATURES
 source
 1..459
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1412393"
 /sex="female"
 /dev_stage="adult, 34 years"
 /lab_host="DH10B"
 /clone_lib="Barstead pancreas HPLRBI"
 /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
 TGTTCGATCGATCGAATGGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors [AATCGGATCTTGG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector.
 Library constructed by Bob Barstead."

ORIGIN
 Query Match 100.0%; Score 18; DB 1; Length 459;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
Db 263 CCACACCTATTTCATCTC 246

RESULT 28
BU949393
LOCUS
DEFINITION
 BU949393 459 bp mRNA linear EST 21-OCT-2002
 in66f07.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127237 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
 1 (bases 1 to 459)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

TITLE
JOURNAL
 Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 putative full length read
 vector to vector length is 523
 Seq primer: -40RP from Gibco.

FEATURES
 source
 1..459
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6127237"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN
 Query Match 100.0%; Score 18; DB 5; Length 459;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
Db 262 CCACACCTATTTCATCTC 279

RESULT 29
BM504818/c
LOCUS
DEFINITION
 BM504818 465 bp mRNA linear EST 14-FEB-2002
 ig90h06.x1 HR85 islet Homo sapiens cDNA 3' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
 1 (bases 1 to 465)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

TITLE
JOURNAL
COMMENT
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 375.
 Location/Qualifiers
 1..465
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

FEATURES

source

Seq primer: -40RP from Gibco.
 Location/Qualifiers
 1..466
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6039008"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 466;
 Best Local Similarity 100.0%; Pred. NO. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 CCACACTTATTCATCTC 18
 |||||
 Db 281 CCACACTTATTCATCTC 298

RESULT 30
 BU071991
 LOCUS
 DEFINITION
 CCACACTTATTCATCTC 236

BU071991 466 bp mRNA linear EST 27-AUG-2002
 im52h05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6039008 5'
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
 sequence.
 BU071991
 BU071991.1 GI:22513180
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 466)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, F., Martin, J., Blistein, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R.,
 Williams, T., Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other_Ests: im52h05.x1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Putative full length read
 vector to vector length is 541

RESULT 31
 AA921338/c
 LOCUS
 DEFINITION
 ak56a06.81 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
 IMAGE:1411858 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
 (HUMAN);, mRNA sequence.

AA921338 474 bp mRNA linear EST 20-APR-1998
 ak56a06.81 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
 IMAGE:1411858 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
 (HUMAN);, mRNA sequence.
 AA921338
 AA921338.1 GI:3068117
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.
 1 (bases 1 to 474)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..474
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1411858"
 /sex="female"
 /dev_stage="adult, 34 years"
 /lab_host="DH10B"
 /clone_lib="Barstead pancreas HPLRB1"
 /note="Organ: pancreas; Vector: pT73D-Pac (Pharmacia)

REFERENCE
 AUTHORS

TITLE
 JOURNAL
 COMMENT

REFERENCE
 AUTHORS
 1 (bases 1 to 474)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.
 Location/Qualifiers
 1..474
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1411858"
 /sex="female"
 /dev_stage="adult, 34 years"
 /lab_host="DH10B"
 /clone_lib="Barstead pancreas HPLRB1"
 /note="Organ: pancreas; Vector: pT73D-Pac (Pharmacia)

with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15,
TGTTCAGAACTCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[AATTCGATCTTGG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
DB 242 CCACACCTATTTCATCTC 225

RESULT 32

BM505143
LOCUS
DEFINITION
P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA linear EST 14-FEB-2002
BM505143
BM505143.1 GI:18668167
EST.
Homo sapiens (human)
SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE

1 (bases 1 to 479)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other ESTs: ig90h06.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Putative full length read
vector to vector length is 545
Seq primer: -40RP from gibco.

FEATURES source

1. 479
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Purified pancreatic islet"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box #127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:

314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
DB 279 CCACACCTATTTCATCTC 296

RESULT 33

BM505143
LOCUS
DEFINITION
P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA linear EST 13-MAR-2002
BM505143
BM505143.1 GI:12645506
EST.
Homo sapiens (human)
SOURCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo

REFERENCE

1 (bases 1 to 495)
Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
Wyllie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
Bowers,Y.
WashU-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stop: 458.

FEATURES source

1. 495
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5641656"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="TOP10"
/clone_lib="Melton Human Islets HIZ1"
/note="Organ: Pancreas; Vector: pZeo-2; Site 1: Not I;
Site 2: Xho I; Library constructed using SuperScript
Plasmid Library kit (Life Technologies). cDNA made by
oligo-dT priming. Xho I site destroyed during cloning.
Size-selected by column fractionation; average insert
size 1.59 kb. Primary library, unamplified."

ORIGIN

Query Match 100.0%; Score 18; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 53.
Location/Qualifiers

1. .501
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1412159"
/sex="female"
/dev stage="adult, 34 years"
/lab host="DH10B"
/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACGAATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (AATTCGATCCTTG), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 268 CCACACCTATTTCATCTC 251

RESULT 38
BQ631720 517 bp mRNA linear EST 02-JUL-2002
LOCUS il21c12.Y1 HR85 islet Homo sapiens cDNA clone IMAGE:6030718 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
BQ631720
BQ631720.1 GI:21683238
EST.
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 517)
AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishevili,R., Williams,T., Jackson,Y. and Bowers,Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@um.wustl.edu)
Pucative full length read
vector to vector length is 520
Seq primer: -40Rp from Gibco
High quality sequence stop: 461.

1 (bases 1 to 497)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 386.
Location/Qualifiers

1. .497
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2496597"
/lab host="DH10B"
/clone_lib="NCI CGAP Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid1 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 497;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||

Db 253 CCACACCTATTTCATCTC 236

RESULT 37
AA844755/c 501 bp mRNA linear EST 04-MAR-1998
LOCUS ak59b12.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412159 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.
AA844755
AA844755.1 GI:2931206
EST.
Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 501)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE Wash-NCI human EST Project
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

FEATURES
source

Location/Qualifiers
1. .517
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6030718"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCACTC 18
|||||
Db 261 CCACACCTATTCACTC 278

RESULT 39

BU949263/c
LOCUS
DEFINITION BU949263 520 bp mRNA linear EST 21-OCT-2002
in69e07.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6127213 3'
similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
sequence.

ACCESSION

BU949263

VERSION

BU949263.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 520)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 464.

Location/Qualifiers

1. .520

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6127213"

/tissue_type="Purified pancreatic islet"

FEATURES
source

Location/Qualifiers
1. .520
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6132129"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning.

/lab_host="DH10B"

/clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTCACTC 18
|||||
Db 248 CCACACCTATTCACTC 231

RESULT 40

BU952425/c

LOCUS

DEFINITION BU952425 520 bp mRNA linear EST 21-OCT-2002

io74d05.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6132129 3'

similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA

sequence.

BU952425

BU952425.1

GI:24204177

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.
1 (bases 1 to 520)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: io74d05.y1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 361.

Location/Qualifiers

1. .520

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6132129"

/tissue_type="Purified pancreatic islet"

/lab_host="DH10B"

/clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning.

```

Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match      100.0%; Score 18; DB 5; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACTTATTCATCTC 18
    |||||
Db 245 CCACACTTATTCATCTC 228

RESULT 41
AW583679          522 bp mRNA linear EST 13-MAR-2002
LOCUS             ia03a06.y1 Human Pancreatic Islets Homo sapiens cDNA clone
DEFINITION        IMAGE:5637202.5' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
                  (HUMAN); mRNA sequence.
ACCESSION         AW583679.1 GI:7260653
VERSION           AW583679
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE         1 (bases 1 to 522)
AUTHORS           Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
                  Wylie,T., Martin,J., Blistain,A., Schmitt,J., Theising,B.,
                  Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
                  McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
                  Bowers,Y.
                  WashU-Harvard Pancreas EST Project
                  Unpublished (2000)
                  Other_ESTs: ia03a06.x3
                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                  Endocrine Pancreas Consortium
                  Harvard University, Howard Hughes Medical Institute
                  Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                  MA 02138
                  Tel: 617-495-1812
                  Fax: 617-495-8557
                  Email: dmelton@biohp.harvard.edu
                  Libraries were constructed by Dr. Douglas Melton
                  DNA sequencing by: Washington University Genome Sequencing Center
                  For information on obtaining a clone please contact: Juliana Brown
                  (brown@fas.harvard.edu)
                  This sequence now available from the IMAGE consortium, for clone
                  orders contact: info@image.llnl.gov
                  Seq primer: -40RP from Gibco
                  High quality sequence stop: 397.
FEATURES          source
                  1..522
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:5637202"
                   /tissue_type="Islets of Langerhans"
                   /dev_stage="Adult"
                   /lab_host="DH10B"
                   /clone_lib="Human Pancreatic Islets"
                   /notes="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
                   Site 2: Sal 1; Library constructed using SuperScript
                   Plasmid Library kit (Life Technologies). cDNA made by
                   oligo-dT priming. Size-selected by column fractionation;
                   unamplified."

ORIGIN

Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match      100.0%; Score 18; DB 5; Length 520;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACTTATTCATCTC 18
    |||||
Db 282 CCACACTTATTCATCTC 299

RESULT 42
BU949426          523 bp mRNA linear EST 21-OCT-2002
LOCUS             in67b10.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6127074.5'
DEFINITION        similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA
                  sequence.
ACCESSION         BU949426
VERSION           BU949426.1 GI:24200777
KEYWORDS          EST.
SOURCE            Homo sapiens (human)
ORGANISM          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE         1 (bases 1 to 523)
AUTHORS           Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
                  Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
                  Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
                  Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
                  Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
                  Williams,T., Jackson,Y. and Bowers,Y.
                  Endocrine Pancreas Consortium
                  Unpublished (2000)
                  Other_ESTs: in67b10.x1
                  Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                  Endocrine Pancreas Consortium
                  Harvard University, Howard Hughes Medical Institute
                  Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                  MA 02138
                  Tel: 617-495-1812
                  Fax: 617-495-8557
                  Email: dmelton@biohp.harvard.edu
                  Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
                  Washington University Genome Sequencing Center For information on
                  obtaining a clone please contact: Dr. Hiroshi Inoue
                  (hinoue@im.wustl.edu)
                  Putative full length read
                  vector to vector length is 524
                  Seq primer: -40RP from Gibco
                  High quality sequence stop: 467.
FEATURES          source
                  1..523
                   /organism="Homo sapiens"
                   /mol_type="mRNA"
                   /db_xref="taxon:9606"
                   /clone="IMAGE:6127074"
                   /tissue_type="Purified pancreatic islet"
                   /lab_host="DH10B"
                   /clone_lib="HR85 islet"
                   /notes="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
                   Not1; Site 2: XhoI; cDNA made by oligo-dT priming.
                   Size-selected on agarose gel. Average insert size ~1kb. 5'
                   XhoI site was destroyed after directional cloning.
                   Amplified once. Contact information: Hiroshi Inoue, MD,
                   Metabolism Div. (Alan Permutt Lab), Washington University
                   School of Medicine, Box 8127, 660 South Euclid Ave., St.
                   Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                   314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match      100.0%; Score 18; DB 5; Length 523;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```


Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: il17e08.y1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center This clone is
 available royalty-free through LLNL; please contact the IMAGE
 consortium (info@image.llnl.gov) for further information
 Seq primer: -40UP from Gibco
 High quality sequence stop: 443.

FEATURES
 source
 1..526
 Location/Qualifiers
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:5942102"
 /sex="Both"
 /tissue_type="pancreas"
 /dev_stage="Embryonic day E16.5"
 /lab_host="DH10B"
 /clone_lib="Melton Amplified Mouse E16 5 Pancreas 3 M16S1
 A"
 /note="Vector: pSPORT1; Site 1: Not 1; Site 2: Sal 1;
 Library constructed using SuperScript Plasmid Library kit
 (Life Technologies). cDNA made by oligo-dr priming.
 Size-selected by column fractionation; average insert size
 0.97 kb. Amplified once on solid support. cDNA library
 Preparation: Guolin Chen."

ORIGIN
 Query Match 100.0%; Score 18; DB 3; Length 526;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACTTATTCATCTC 18
 |||||
 Db 248 CCACACTTATTCATCTC 231

RESULT 46
 BQ271518/c
 LOCUS
 DEFINITION
 BQ271518 526 bp mRNA linear EST 15-JUL-2003
 ik15a01.x1 HR85 islet Homo sapiens cDNA clone IMAGE:5781000 3'
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
 sequence.

ACCESSION
 BQ271518
 VERSION
 BQ271518.1 GI:20496584
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 (bases 1 to 526)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute

TITLE
 JOURNAL
 COMMENT

Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: il17e08.y1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 410.

FEATURES
 source
 1..526
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5781000"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
 Not1; Site_2: Xho1; cDNA made by oligo-dr priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN
 Query Match 100.0%; Score 18; DB 3; Length 526;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACTTATTCATCTC 18
 |||||
 Db 251 CCACACTTATTCATCTC 234

RESULT 47
 BU951064
 LOCUS
 DEFINITION
 BU951064 526 bp mRNA linear EST 21-OCT-2002
 io75d05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6132152 5'
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA
 sequence.

ACCESSION
 BU951064
 VERSION
 BU951064.1 GI:24202816
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE
 1 (bases 1 to 526)
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
 Williams, T., Jackson, Y. and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 484.

FEATURES

source
Location/Qualifiers
1..526
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6132152"
/issue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_lib="HR85 islet"

Note: "Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110. E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 526;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 300 CCACACCTATTTCATCTC 317

RESULT 48

AA835293/c

LOCUS
DEFINITION
AA835293 ak66b09.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
IMAGE:1412825 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
(HUMAN); mRNA sequence.

ACCESSION
AA835293

VERSION
AA835293.1

KEYWORDS
GT:2909021

SOURCE
EST.

ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 529)

Author: Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: esc@watson.wustl.edu

This clone is available royalty-free through LiNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 478.

Location/Qualifiers

1..529

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1412825"

/sex="female"

/dev_stage="adult, 34 years"

/lab_host="DH10B"

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6135800"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 529;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 252 CCACACCTATTTCATCTC 235

RESULT 49

BQ101169

LOCUS

DEFINITION

BQ101169 529 bp mRNA linear EST 29-APR-2002
ij24h05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6135800 5' similar to SW:PA21_HUMAN P04054
PHOSPHOLIPASE A2 PRECURSOR ; mRNA sequence.

ACCESSION
BQ101169

VERSION
BQ101169.1

KEYWORDS
GI:20134153

SOURCE
EST.

ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Crniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 529)

Author: Melton, D., Brown, J., Kenty, G., Pàmutt, A., Lee, C., Kaestner, K.,

Lenishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blistain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other ESTs: ij24h05.xl

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohpc.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center This clone is

available royalty-free through LiNL; please contact the IMAGE

consortium (info@image.llnl.gov) for further information

Putative full length read

vector to vector length is 572

Seq primer: -40RP from Gibco

High quality sequence stop: 475.

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6135800"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;

/clone_lib="Barstead pancreas HPLRB1"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: NotI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
15'

TGTTACGAATCTGAAGTCGGAGCGCCGCTTTTTTTTTTTTTTTTTTTTTT
3'); double-stranded cDNA was ligated to Eco RI adaptors
[AATTCCGATCCTTG], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pT7T3 vector.
Library constructed by Bob Barstead."

Site 2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 280 CCACACCTATTTCATCTC 297

RESULT 50

AA835315/c

LOCUS ak66e08.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone
 DEFINITION IMAGE:1412870 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
 (HUMAN); mRNA sequence.

ACCESSION AA835315.1

VERSION GI:2909043

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 532)

Authors Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,

Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,

Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,

Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

WashU-NCI human EST Project

Unpublished (1997)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: setowatson.wustl.edu

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 458.

FEATURES

source

1..532

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1412870"

/sex="female"

/dev_stage="adult, 34 years"

/lab_host="DH10B"

/clone_lib="Barstead pancreas HPLRB1"

/notes="Organ: pancreas; Vector: pT73D-Pac (Pharmacia)

with a modified polylinker; Site 1: EcoRI; Site 2: NotI;

1st strand cDNA was primed with a Not I - oligo(dT) primer

[5'

TGTTAGATCTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors

(AATTCGATCCCTTG), digested with Not I and cloned into the

Not I and Eco RI sites of the modified pT7T3 vector.

Library constructed by Bob Barstead."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 532;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

Db 254 CCACACCTATTTCATCTC 237

RESULT 51

BU950978

LOCUS BU950978

DEFINITION io74d05.y1 HR85 islet Homo sapiens cDNA clone IMAGE:6132129 5'
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA
 sequence.

ACCESSION BU950978

VERSION BU950978.1

KEYWORDS GI:24202730

SOURCE EST.

ORGANISM Homo sapiens

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 537)

Authors Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,

Lemishka, I., Searce, M., Prestelli, J., Gradwohl, G., Clifton, S.,

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bliscain, A.,

Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,

Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareighvili, R.,

Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Putative full length read

vector to vector length is 572

Seq primer: -40RP from Gibco

High quality sequence stop: 480.

FEATURES

source

1..537

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6132129"

/tissue_type="Purified pancreatic islet"

/lab_host="DH10B"

/clone_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:

NotI; Site 2: XhoI; cDNA made by oligo-dT priming.

Size-selected on agarose gel. Average insert size ~1kb. 5'

XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,

Metabolism Div. (Alan Permutt Lab), Washington University

School of Medicine, Box 8127, 660 South Euclid Ave., St.

Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:

314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 18; DB 5; Length 537;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
 Db 313 CCACACCTATTTCATCTC 330

RESULT 52
 AA844927/c

LOCUS
 DEFINITION
 ak61a06.s1 Barstead pancreas HP1RB1 Homo sapiens cDNA clone
 IMAGE:1412338 3' similar to gb:M21054 PHOSPHOLIPASE A2 PRECURSOR
 (HUMAN);, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AA844927
 AA844927.1 GI:2931378
 EST.
 Homo sapiens (human)
 Homo sapiens

REFERENCE
 AUTHORS
 Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
 Krieman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
 Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
 Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
 WashU-NCI human EST Project
 Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 423.

FEATURES
 Location/Qualifiers
 1..539
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1412338"
 /sex="female"
 /dev_stage="adult, 34 years"
 /lab_host="DH10B"
 /clone_lib="Barstead pancreas HP1RB1"
 /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
 with a modified polylinker; Site 1: EcoRI; Site 2: NotI;
 1st strand cDNA was primed with a Not I - oligo(dT) primer
 [5'
 TGTTCAGGATCTGAAGTGGAGCGCGCCCTTTTCTTTTCTTTTCTTTTCTTTT
 3']; double-stranded cDNA was ligated to Eco RI adaptors
 [AATTTCGGATCTTGG], digested with Not I and cloned into the
 Not I and Eco RI sites of the modified pT7T3 vector.
 Library constructed by Bob Barstead."

ORIGIN
 Query Match 100.0%; Score 18; DB 1; Length 539;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
 Db 260 CCACACCTATTTCATCTC 243

RESULT 53
 BQ632018/c

LOCUS
 DEFINITION
 BQ632018
 1121c12.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6030718 3'
 similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA

sequence.
 BQ632018
 BQ632018.1 GI:21683536
 EST.
 Homo sapiens (human)
 Homo sapiens

REFERENCE
 AUTHORS
 1 (bases 1 to 544)
 Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wyllie,T., Martin,J., Blisfain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishevili,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Other ESTs: 1121c12.y1
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 455.

FEATURES
 Location/Qualifiers
 1..544
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6030718"
 /tissue_type="Purified pancreatic islet"
 /lab_host="DH10B"
 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size-selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN
 Query Match 100.0%; Score 18; DB 5; Length 544;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
 |||||
 Db 249 CCACACCTATTTCATCTC 232

RESULT 54
 BM264109

LOCUS
 DEFINITION
 BM264109
 ig31a01.y1 HR85 islet Homo sapiens cDNA 5' similar to SW:PA21_HUMAN
 P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM264109
 BM264109.1 GI:17927149
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 552) Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu This read is a 5' RESEQUENCE of a previously sequenced pancreas clone
TITLE JOURNAL COMMENT	WaehU-Harvard Pancreas EST Project Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu This read is a 5' RESEQUENCE of a previously sequenced pancreas clone Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR MOUSE-PANCREAS VERIFICATION Possible reversed clone: similarity on wrong strand Seq primer: -400P from Gibco. Location/Qualifiers 1. .553 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6127213" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. -1kb. 5' Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
FEATURES source	1. .553 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6127213" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. -1kb. 5' Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
ORIGIN	Query Match 100.0%; Score 18; DB 7; Length 552; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CCACACCTATTTCATCTC 18 Db 268 CCACACCTATTTCATCTC 251
RESULT 56 CK902775/c LOCUS	A1925956 562 bp mRNA linear EST 07-MAR-2000 wh12903.x1 NCI CGAP Kid11 Homo sapiens cDNA clone IMAGE:2380564 3' similar to gb:M21051 PHOSPHOLIPASE A2 PRECURSOR (HUMAN);, mRNA sequence.
DEFINITION	ACCESSION A1925956 VERSION A1925956.1 GI:5661920 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 562) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

REFERENCE AUTHORS	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 552) Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 473. Location/Qualifiers 1. .552 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
TITLE JOURNAL COMMENT	WaehU-Harvard Pancreas EST Project Unpublished (2000) Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu This read is a 5' RESEQUENCE of a previously sequenced pancreas clone Good hit to opposite strand read. . .wrong orientation BUT PASSED FOR MOUSE-PANCREAS VERIFICATION Possible reversed clone: similarity on wrong strand Seq primer: -400P from Gibco. Location/Qualifiers 1. .553 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6127213" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. -1kb. 5' Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
FEATURES source	1. .552 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6127213" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. -1kb. 5' Size-selected on agarose gel. Average insert size -1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
ORIGIN	Query Match 100.0%; Score 18; DB 3; Length 552; Best Local Similarity 100.0%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 CCACACCTATTTCATCTC 18 Db 291 CCACACCTATTTCATCTC 308
RESULT 55 CK902775/c LOCUS	CK902775 553 bp mRNA linear EST 11-MAR-2004 in68e07.y5 HR85 islet Homo sapiens cDNA clone IMAGE:6127213 5' similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ;, mRNA sequence.
DEFINITION	ACCESSION CK902775 VERSION CK902775.1 GI:45364306 KEYWORDS EST. SOURCE Homo sapiens (human) ORGANISM Homo sapiens
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 553) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 672 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 462.

FEATURES

source

1. .562
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2380564"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Kid11"
 /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
 Plasmid DNA from the normalized library NCI CGAP Kid3 was
 prepared, and ss circles were made in vitro. Following HAP
 purification, this DNA was used as tracer in a subtractive
 hybridization reaction. The driver was PCR-amplified cDNAs
 from a pool of 5,000 clones made from the same library
 (cloneIDs 1322376-1323911, 1456007-1456775, and
 1500552-1502855). Subtraction by Bento Soares and M.
 Fatina Bonaldo."

ORIGIN

Query Match 100.0%; Score 18; DB 1; Length 562;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 248 CCACACCTATTTCATCTC 231
 |||||

RESULT 57

BP323152 572 bp mRNA linear EST 17-SEP-2004
 LOCUS BP323152 Sugano cDNA library, pancreas Homo sapiens cDNA clone
 DEFINITION PNC03992, mRNA sequence.

ACCESSION BP323152

VERSION BP323152.1 GI:52252127

KEYWORDS

EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 572)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,

Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous

block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

15342556

Contact: Yutaka Suzuki

Department of Virology

Institute of Medical Science, University of Tokyo

4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: yusuzuki@ims.u-tokyo.ac.jp.

Location/Qualifiers

1. .572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PNC03992"

/tissue_type="pancreas"

/clone_lib="Sugano cDNA library, pancreas"

ORIGIN

Query Match 100.0%; Score 18; DB 3; Length 572;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

DB 302 CCACACCTATTTCATCTC 319

|||||

RESULT 58

LOCUS BC013384

DEFINITION

Homo sapiens, phospholipase A2, group IB (pancreas), clone

IMAGE:3950037, mRNA.

ACCESSION BC013384

VERSION BC013384.1 GI:15426542

KEYWORDS

HTC.

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 577)

Direct Submission

Straussberg,R.

TITLE

Submitted (31-AUG-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

Contact: MGC help desk

Email: cgapbs@mail.nih.gov

Tissue Procurement: CLONTECH

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

http://www.systemsbio.org

contact: amadan@systemsbiology.org

Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia

Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAL Plate: 31 Row: h Column: 11

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 4505846

This clone has the following problem: frame shifted.

Location/Qualifiers

1. .577

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="GeneID:5319"

/db_xref="taxon:9606"

/clone="IMAGE:3950037"

/tissue_type="Pancreas"

/clone_lib="NIH MGC_78"

/lab_host="DH10B"

/note="vector: pDNR-LIB"

Query Match 100.0%; Score 18; DB 4; Length 577;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18

|||||

DB 306 CCACACCTATTTCATCTC 323

|||||

RESULT 59

LOCUS BP322008

DEFINITION

BP322008 Sugano cDNA library, pancreas Homo sapiens cDNA clone

PNC01231, mRNA sequence.

ACCESSION BP322008

VERSION BP322008.1 GI:52250983

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 579)	
AUTHORS	Suzuki.Y., Yamashita.R., Shiota,M., Sakakibara.Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.	
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)	
PUBMED	15342556	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.	
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Best Local Similarity	100.0%;	Pred. No. 1.9e+02;
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Db	304 CCACACCTATTTCATCTC 321	
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DEFINITION	BP323927 Sugano cDNA library, pancreas Homo sapiens cDNA clone	
ACCESSION	PNC05643, mRNA sequence.	
VERSION	BP323927	
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SOURCE	EST.	
ORGANISM	Homo sapiens (human)	
	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 580)	
AUTHORS	Suzuki.Y., Yamashita.R., Shiota,M., Sakakibara.Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.	
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)	
PUBMED	15342556	
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.	
FEATURES	Location/Qualifiers	
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	/tissue type="pancreas"	
	/clone_lib="Sugano cDNA library, pancreas"	
ORIGIN		
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Best Local Similarity	100.0%;	Pred. No. 1.9e+02;
Matches	18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
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Db 302 CCACACCTATTTCATCTC 319

Search completed: May 10, 2006, 20:28:54
Job time : 3772 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 02:36:42 ; Search time 188 Seconds
(without alignments)
170.192 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18

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Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1303057 seqs, 889780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	IDB	Description
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147 13.8 76.7 117807 3 US-09-949-016-15525 Sequence 15525, A
c 148 13.8 76.7 130563 3 US-09-949-016-12273 Sequence 12273, A
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ALIGNMENTS

RESULT 1
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; Sequence 1200, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO

; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: gl90012
; US-09-023-655-1200

Query Match 100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
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RESULT 2
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; Sequence 140490, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140490
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-140490

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Best Local Similarity 94.1%; Pred. No. 1e+02; Indels 0; Gaps 0;
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Db 307 CCACACCTATTGATCTACT 323
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RESULT 3
US-07-846-181-6
; Sequence 6, Application US/07846181
; Patent No. 5360732
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/846,181
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC204-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-846-181-6
Query Match 85.6%; Score 15.4; DB 2; Length 8533;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTGATCTACT 17
Db 5921 CCACACCTATTGATCTACT 5937
|||||
RESULT 4
US-07-845-989-6
; Sequence 6, Application US/07845989
; Patent No. 5360901
; GENERAL INFORMATION:
; APPLICANT: BERKA, RANDY M
; APPLICANT: FOWLER, TIMOTHY
; APPLICANT: REY, MICHAEL W
; TITLE OF INVENTION: PRODUCTION OF ASPERGILLUS NIGER
; TITLE OF INVENTION: CATALASE-R
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENENCOR INTERNATIONAL, INC.
; STREET: 180 KIMBALL WAY
; CITY: SOUTH SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/845,989
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC208-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-845-989-6
Query Match 85.6%; Score 15.4; DB 2; Length 8533;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTGATCTACT 17
Db 5921 CCACACCTATTGATCTACT 5937
|||||

ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/845,989
; FILING DATE: 19920304
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HORN MS, MARGARET A
; REGISTRATION NUMBER: 33401
; REFERENCE/DOCKET NUMBER: GC208-US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-742-7536
; TELEFAX: 415-742-7217
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8533 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-845-989-6
Query Match 85.6%; Score 15.4; DB 2; Length 8533;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTGATCTACT 17
Db 5921 CCACACCTATTGATCTACT 5937
|||||
RESULT 5
US-09-949-002-660/C
; Sequence 660, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 660
; LENGTH: 30172
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(30172)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-660
Query Match 85.6%; Score 15.4; DB 3; Length 30172;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACACCTATTGATCTACT 17
Db 28366 CCACACCTATTGATCTACT 28350
|||||
RESULT 6
US-09-949-016-15721
; Sequence 15721, Application US/09949016

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15721
; LENGTH: 49487
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(49487)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15721

Query Match 85.6%; Score 15.4; DB 3; Length 49487;
Best Local Similarity 94.1%; Pred. No. 1.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
|||||
DB 22985 CCACACCTATTTCATCT 23001

RESULT 7
US-10-131-827-8758/c
; Sequence 8758, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE
; CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8758
; LENGTH: 466
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(466)
; OTHER INFORMATION: n = A, C, T or G
US-10-131-827-8758

Query Match 82.2%; Score 14.8; DB 3; Length 466;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 18
|||||
DB 298 CCACCTCCTATCCATCT 281

RESULT 8
US-09-270-767-29684
; Sequence 29684, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29684
; LENGTH: 482
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-29684

Query Match 82.2%; Score 14.8; DB 3; Length 482;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 18
|||||
DB 210 CCACATCTTTCATCTC 227

RESULT 9
US-09-949-016-132353
; Sequence 132353, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132353
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-132353

Query Match 82.2%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 18
|||||
DB 423 CCACACCTATTTCACAC 440

RESULT 10
US-09-949-016-140957
; Sequence 140957, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140957
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-140957

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 601;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
Db 141 CCACACCTTTCATCTC 158

RESULT 11
US-09-328-352-46
; Sequence 46, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Berton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 46
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-46

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 834;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
Db 468 CCAGACATATTCATCTC 485

RESULT 12
US-09-270-767-13670
; Sequence 13670, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13670
; LENGTH: 1298
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-13670

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 1298;
```

```
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
Db 1026 CCACATCTTTCATCTC 1043

RESULT 13
US-10-104-047-1028
; Sequence 1028, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1028
; LENGTH: 3237
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-1028

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3237;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
Db 1669 CCACCTTTCACACAC 1686

RESULT 14
US-09-575-081B-7
; Sequence 7, Application US/09575081B
; Patent No. 6692934
; GENERAL INFORMATION:
; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
; TITLE OF INVENTION: NOVEL ORGANIC ANION TRANSPORT PROTEINS
; FILE REFERENCE: DB23
; CURRENT APPLICATION NUMBER: US/09/575,081B
; CURRENT FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 60/135,081
; PRIOR FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 3692
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (713)..(713)
; OTHER INFORMATION: y = c or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2397)..(2397)
; OTHER INFORMATION: k = g or t
US-09-575-081B-7

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 3692;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
Db 1449 CCACCTTTCATCTC 1466
```

```
RESULT 15
; Sequence 260, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yundong
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt FL_genes Version 2.0
; SEQ ID NO 260_
; LENGTH: 3725
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (718)..(2778)
US-09-799-451-260

Query Match      82.2%; Score 14.8; DB 3; Length 3725;
Best Local Similarity 88.9%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTATTTCATCTC 18
DB      1550 CCACCTATTTCATCTC 1567

RESULT 16
US-09-949-016-15540/c
; Sequence 1540, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15540
; LENGTH: 14673
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15540

Query Match      82.2%; Score 14.8; DB 3; Length 14673;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTATTTCATCTC 18
DB      1622 CCACCTTTTCACACTC 1605

RESULT 17
US-09-949-016-15491
; Sequence 15491, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15491
; LENGTH: 86877
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15491

Query Match      82.2%; Score 14.8; DB 3; Length 86877;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACCTATTTCATCTC 18
DB      29326 CTACACATATTTCATCTC 29343

RESULT 18
US-09-949-016-15492
; Sequence 15492, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15492
; LENGTH: 86877
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15492

Query Match      82.2%; Score 14.8; DB 3; Length 86877;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


QY 1 CCACACCTTATTCATCTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 29326 CTACACATATTCATCTC 29343

RESULT 19
US-09-949-016-15729
; Sequence 15729, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15729
; LENGTH: 148783
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(148783)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15729

Query Match 82.2%; Score 14.8; DB 3; Length 148783;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 140850 CCACACCTTATTCATCTC 140867

RESULT 20
US-09-949-016-15830/c
; Sequence 15830, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15830
; LENGTH: 192506
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15830

Query Match 82.2%; Score 14.8; DB 3; Length 192506;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18

Db 129567 CCACACCTTATTCACAC 129550
| | | | | | | | | | | | | | | | | | | | | |

RESULT 21
US-09-949-016-13358/c
; Sequence 13358, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13358
; LENGTH: 260247
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13358

Query Match 82.2%; Score 14.8; DB 3; Length 260247;
Best Local Similarity 88.9%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 74550 CCACACCTTATTCGTACAC 74533

RESULT 22
US-09-949-016-17371
; Sequence 17371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17371
; LENGTH: 373182
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(373182)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17371

Query Match 82.2%; Score 14.8; DB 3; Length 373182;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
| | | | | | | | | | | | | | | | | | | | | |

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Db      274013 CCACACCTCTTCAGACTC 274030

RESULT 23
US-09-949-016-12062
; Sequence 12062, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12062
; LENGTH: 373694
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(373694)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12062

Query Match      82.2%; Score 14.8; DB 3; Length 373694;
Best Local Similarity 88.9%; Pred. No. 3.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      274068 CCACACCTCTTCAGACTC 274085

RESULT 24
US-09-949-016-15473
; Sequence 15473, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15473
; LENGTH: 450395
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(450395)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15473

Query Match      82.2%; Score 14.8; DB 3; Length 450395;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db      274013 CCACACCTCTTCAGACTC 274030

RESULT 25
US-09-949-016-49992
; Sequence 49992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49992
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-49992

Query Match      80.0%; Score 14.4; DB 3; Length 601;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      95949 CCACACCTATTTCACAC 95966

US-09-949-016-49993
; Sequence 49993, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49993
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-49993

Query Match      80.0%; Score 14.4; DB 3; Length 601;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 16
      |||||
Db      461 CCACACCTATTTCATCC 476

RESULT 26
US-09-949-016-49993
; Sequence 49993, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49993
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-49993

Query Match      80.0%; Score 14.4; DB 3; Length 601;
Best Local Similarity 93.8%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 16
      |||||
Db      354 CCACACCTATTTCATCC 369
```

```
RESULT 27
US-09-543-681A-3390
; Sequence 3390, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3390
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3390

Query Match      80.0%; Score 14.4; DB 3; Length 1728;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CACACCTATTCATC 17
Db      1152 CACACCTATTCATCCT 1167

RESULT 28
US-10-104-047-150/c
; Sequence 150, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. 6943241el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 150
; LENGTH: 3154
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-150

Query Match      80.0%; Score 14.4; DB 3; Length 3154;
Best Local Similarity 93.8%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCACACCTATTCATC 16
Db      2863 CCACACATATTCATC 2848

RESULT 29
US-09-762-311-1
; Sequence 1, Application US/09762311
; Patent No. 6825004
; GENERAL INFORMATION:
; APPLICANT: BLUMENFELD, Marta
; APPLICANT: BOUGELERET, Lydie
; APPLICANT: CHUMAKOV, Ilya
; TITLE OF INVENTION: Nucleic Acids Encoding Human TBC-1 Protein And Polymorphic Markers
; FILE REFERENCE: Theroef.
; PRIOR FILING DATE: 2001-06-21
; CURRENT APPLICATION NUMBER: US/09/762,311
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/095,653
```

```
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 17590
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: 1..2000
; OTHER INFORMATION: 5' regulatory region
; NAME/KEY: exon
; LOCATION: 2001..2077
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 12292..12373
; OTHER INFORMATION: exon 1b
; NAME/KEY: exon
; LOCATION: 12740..13249
; OTHER INFORMATION: exon 2
; NAME/KEY: allele
; LOCATION: 9494
; OTHER INFORMATION: 99-430-352 : polymorphic base A or G
; NAME/KEY: primer bind
; LOCATION: 9391..9408
; OTHER INFORMATION: 99-430.rp
; NAME/KEY: primer bind
; LOCATION: 9828..9845
; OTHER INFORMATION: 99-430.pu complement
; NAME/KEY: primer bind
; LOCATION: 9475..9493
; OTHER INFORMATION: 99-430-352.mis
; NAME/KEY: primer bind
; LOCATION: 9495..9513
; OTHER INFORMATION: 99-430-352.mis complement
; NAME/KEY: primer bind
; LOCATION: 9482..9506
; OTHER INFORMATION: 99-430-352.probe
; NAME/KEY: misc feature
; LOCATION: 3953..4056,4167,4739,6217,6245,6860,9998..9999,10006,10012,10104
; LOCATION: 10477,10822,10825,11095,11256,11273,11857..11858,11895..11896
; LOCATION: 14057,15912..15913,16217..16218,16329..16330,17504
; OTHER INFORMATION: n=a, g, c or t
US-09-762-311-1
```

```
Query Match Similarity 80.0%; Score 14.4; DB 3; Length 17590;
Best Local Similarity 93.8%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      3 ACACCTATTCATC 18
Db      8958 ACACCTATTCATC 8973
```

```
RESULT 30
US-09-949-016-13200
; Sequence 13200, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
```

; SEQ ID NO 13200
; LENGTH: 28494
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13200

Query Match 80.0%; Score 14.4; DB 3; Length 28494;
Best Local Similarity 93.8%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATAC 16
| | | | | | | | | | | | | | | | | | | | | |
Db 5232 CCACACCTATTTCATCC 5247

RESULT 31
US-09-949-016-17285/c
; Sequence 17285, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17285
; LENGTH: 33353
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17285

Query Match 80.0%; Score 14.4; DB 3; Length 33353;
Best Local Similarity 93.8%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATAC 16
| | | | | | | | | | | | | | | | | | | | | |
Db 4322 CCACACCTTTTCATAC 4307

RESULT 32
US-09-780-049-18/c
; Sequence 18, Application US/09780049
; Patent No. 6465250
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT
; EXPRESSION
; FILE REFERENCE: RTS-0134
; CURRENT APPLICATION NUMBER: US/09/780,049
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 18
; LENGTH: 40000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-780-049-18

Query Match 80.0%; Score 14.4; DB 3; Length 40000;
Best Local Similarity 93.8%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATAC 16
| | | | | | | | | | | | | | | | | | | | | |
Db 3791 CCACACCTTTTCATAC 3776

RESULT 33
US-09-949-016-17192/c
; Sequence 17192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17192
; LENGTH: 107937
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) -- (107937)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17192

Query Match 80.0%; Score 14.4; DB 3; Length 107937;
Best Local Similarity 93.8%; Pred. No. 5.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | | | | | | | |
Db 59479 AGACCTATTTCATCTC 59464

RESULT 34
US-09-949-016-15393/c
; Sequence 15393, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15393
; LENGTH: 194790
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15393

Query Match 80.0%; Score 14.4; DB 3; Length 194790;
Best Local Similarity 93.8%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATAC 16

```
Db 139221 CCACACCTATTTCATTC 139206
|||||
RESULT 35
US-09-949-016-13840/c
; Sequence 13840, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13840
; LENGTH: 276687
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(276687)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13840
Query Match 80.0%; Score 14.4; DB 3; Length 276687;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATTC 16
|||||
Db 181287 CCACACCTATTTCATTC 181272

RESULT 36
US-09-790-988-1/c
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEKI
; APPLICANT: HATTORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
Query Match 80.0%; Score 14.4; DB 3; Length 640681;
Best Local Similarity 93.8%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACACCTATTTCATTC 18
|||||
Db 10623 ACACCTATTTCATTC 10608
```

```
RESULT 37
US-09-304-232-737
; Sequence 737, Application US/09304232
; Patent No. 6525185
; GENERAL INFORMATION:
; APPLICANT: Fan, Jian Bing
; APPLICANT: Chakravarti, Aravinda
; APPLICANT: Halushka, Marc Kenneth
; APPLICANT: Case Western Reserve University School of Medicine
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Polymorphisms Associated With
; FILE REFERENCE: 018547-034210US
; CURRENT APPLICATION NUMBER: US/09/304,232
; CURRENT FILING DATE: 1999-05-03
; EARLIER APPLICATION NUMBER: US 60/084,641
; NUMBER OF SEQ ID NOS: 909
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 737
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PLA2AEX3 131
US-09-304-232-737
Query Match 77.8%; Score 14; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ACCTATTTCATTC 18
|||||
Db 1 ACCTATTTCATTC 14

RESULT 38
US-09-513-999C-34796
; Sequence 34796, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34796
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 47
; OTHER INFORMATION: w=a or t
; NAME/KEY: misc_feature
; LOCATION: 63
; OTHER INFORMATION: v=a or c or g
; NAME/KEY: misc_feature
; LOCATION: 130
; OTHER INFORMATION: d=a or g or t
US-09-513-999C-34796
Query Match 77.8%; Score 14; DB 3; Length 162;
```

Best Local Similarity 83.3%; Pred. No. 4.9e+02;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
| | | | | | | | | | | | | | | | | | | | | |
DB 51 CAACACCAATTCVTCATCTC 68

RESULT 39
US-09-949-016-168810/c
; Sequence 168810, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 168810
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-168810

Query Match 77.8%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCAT 14
| | | | | | | | | | | | | | | | | | | | | |
DB 400 CCACACCTATTTCAT 387

RESULT 40
US-09-533-559-293
; Sequence 293, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849, 200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(636)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-293

Query Match 77.8%; Score 14; DB 3; Length 636;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATA 15
| | | | | | | | | | | | | | | | | | | | | |
DB 454 CACACCTATTTCATA 467

RESULT 41
US-09-328-352-321
; Sequence 321, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 321
; LENGTH: 1020
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-321

Query Match 77.8%; Score 14; DB 3; Length 1020;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATACT 17
| | | | | | | | | | | | | | | | | | | | | |
DB 569 CACCTATTTCATACT 582

RESULT 42
US-09-949-016-17511/c
; Sequence 17511, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17511
; LENGTH: 44676
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17511

Query Match 77.8%; Score 14; DB 3; Length 44676;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATACT 17
| | | | | | | | | | | | | | | | | | | | | |
DB 18115 CACCTATTTCATACT 18102

RESULT 43
US-09-949-016-16502
; Sequence 16502, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16502
; LENGTH: 157032
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...((157032))
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16502

Query Match 77.8%; Score 14; DB 3; Length 157032;
Best Local Similarity 100.0%; Pred. No. 9.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1 CCACACCTTATTCAT 14
|||||

Db 91068 CCACACCTTATTCAT 91081

RESULT 44
US-09-363-939A-153/c
; Sequence 153, Application US/09363939A
; Patent No. 6346611
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX87
; CURRENT APPLICATION NUMBER: US/09/363,939A
; CURRENT FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 65
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(65)
; OTHER INFORMATION: All pyrimidines are 2'F.

US-09-363-939A-153

Query Match 76.7%; Score 13.8; DB 3; Length 65;
Best Local Similarity 88.2%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTTATTCATCTC 18
|||||

Db 45 CACAGCTATACATCTC 29

RESULT 45
US-09-791-301-153/c
; Sequence 153, Application US/09791301
; Patent No. 6713616
; GENERAL INFORMATION:
; APPLICANT: Pagratis, Nikos
; APPLICANT: Lochrie, Michael
; APPLICANT: Gold, Larry
; TITLE OF INVENTION: High Affinity TGFbeta Nucleic Acid Ligands and
; FILE OF INVENTION: Inhibitors
; FILE REFERENCE: NEX 87/C
; CURRENT APPLICATION NUMBER: US/09/791,301
; CURRENT FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 09/046,247
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: 08/458,424
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: 07/714,131
; PRIOR FILING DATE: 1991-06-10
; PRIOR APPLICATION NUMBER: 07/931,473
; PRIOR FILING DATE: 1992-08-17
; PRIOR APPLICATION NUMBER: 07/964,624
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: 08/117,991
; PRIOR FILING DATE: 1993-09-08
; PRIOR APPLICATION NUMBER: 07/536,428
; PRIOR FILING DATE: 1990-06-11
; PRIOR APPLICATION NUMBER: 09/363,939
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 153
; LENGTH: 65
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified base
; LOCATION: (1)..(65)
; OTHER INFORMATION: All pyrimidines are 2'F.

US-09-791-301-153
Query Match 76.7%; Score 13.8; DB 3; Length 65;
Best Local Similarity 88.2%; Pred. No. 5.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTTATTCATCTC 18
|||||

Db 45 CACAGCTATACATCTC 29

RESULT 46
US-09-270-767-30909/c
; Sequence 30909, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30909
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-30909

Query Match 76.7%; Score 13.8; DB 3; Length 273;
Best Local Similarity 88.2%; Pred. No. 6.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCT 17
Db 81 CCACACCTATTCATATT 65

RESULT 47

US-09-621-976-15284
; Sequence 15284, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 15284
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-15284

Query Match 76.7%; Score 13.8; DB 3; Length 295;
Best Local Similarity 88.2%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCT 17
Db 27 CCACAGCTATTCAGACT 43

RESULT 48

US-10-131-827-8755/c
; Sequence 8755, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8755
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8755

Query Match 76.7%; Score 13.8; DB 3; Length 496;

Best Local Similarity 88.2%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACACCTATTTCATCTC 18
Db 262 CACTCCTATCCATCTC 246

RESULT 49

US-10-131-827-8885
; Sequence 8885, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8885
; LENGTH: 524
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(524)
; OTHER INFORMATION: n =A, C, T or G
US-10-131-827-8885

Query Match 76.7%; Score 13.8; DB 3; Length 524;
Best Local Similarity 88.2%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CACACCTATTTCATCTC 18
Db 462 CACTCCTATCCATCTC 478

RESULT 50

US-09-949-016-21757
; Sequence 21757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21757
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21757

Query Match 76.7%; Score 13.8; DB 3; Length 601;


```
Best Local Similarity 88.2%; Pred. No. 7.1e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 2 CACACCTATTCACTC 18
Db 21 CAGACCTATTCAAACTC 37

RESULT 51
US-09-949-016-21758
; Sequence 21758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21758
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21758

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCACTC 18
Db 112 CAGACCTATTCAAACTC 128

RESULT 52
US-09-949-016-21759
; Sequence 21759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21759
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21759

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCACTC 18
Db 112 CAGACCTATTCAAACTC 128

RESULT 53
US-09-949-016-23388/c
; Sequence 23388, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23388
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-23388

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATC 17
Db 234 CCACACCTATGCACAC 218

RESULT 54
US-09-949-016-36971/c
; Sequence 36971, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36971
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36971

Query Match 76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATC 18
Db 184 CACACCTATTTCATC 168

RESULT 55
US-09-949-016-67685/c
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; Sequence 67685, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67685
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67685

Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
Db 41 CACACCTGTCCTACTC 25

RESULT 56
US-09-949-016-67686/c
; Sequence 67686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67686
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-67686

Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
Db 297 CACACCTGTCCTACTC 281

RESULT 57
US-09-949-016-86494/c
; Sequence 86494, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86494
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-86494

Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
Db 306 CACACCTATACATAC 290

RESULT 59
US-09-949-016-144569
; Sequence 144569, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105324
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105324/c
; Sequence 105324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105324
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105324

Query Match          76.7%; Score 13.8; DB 3; Length 601;
Best Local Similarity 88.2%; Pred. No. 7.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
Db 306 CACACCTATACATAC 290

RESULT 59
US-09-949-016-144569
; Sequence 144569, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105324
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105324/c
; Sequence 105324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105324
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-105324
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; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14569
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ;
 US-09-949-016-144569

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 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 417 CCACACCTAATCATATT 433

RESULT 60
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 ; Sequence 153387, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 153387
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ;
 US-09-949-016-153387

Query Match 76.7%; Score 13.8; DB 3; Length 601;
 Best Local Similarity 88.2%; Pred. No. 7.1e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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 Db 128 CACACCTTTCTCTACTC 144

Search completed: May 10, 2006, 04:17:17
 Job time : 197 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 19:12:50 ; Search time 425 Seconds
(without alignments)
350.232 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18

Sequence: 1 ccacaccattcattc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	18	100.0	224	US-10-060-036-3604
6	18	100.0	224	US-10-060-036-3941
7	18	100.0	224	US-10-060-036-4030
8	18	100.0	427	US-10-425-115-153893
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20	18	100.0	644	US-10-330-051A-6
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22	18	100.0	12174	US-10-607-806-1
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27	16.4	91.1	251199	8	US-10-482-029-205	Sequence 205, App
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29	15.4	85.6	321	7	US-10-424-599-127447	Sequence 127447, A
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73	14.8	82.2	568	4	US-09-925-065A-523201	Sequence 523201,
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77	14.8	82.2	585	5	US-10-027-632-208289	Sequence 208289,
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ALIGNMENTS

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; Sequence 38, Application US/10607806
; Publication No. US20050014158A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel Reid
; APPLICANT: Langdown, Maria L.
; APPLICANT: Denissenko, Mikhaili F.
; APPLICANT: Dennis, Edward
; APPLICANT: Cantor, Charles
; APPLICANT: Rubin, Byron
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR REDUCING FAT
; TITLE OF INVENTION: DEPOSITION AND TREATING ASSOCIATED CONDITIONS
; FILE REFERENCE: 524592003200

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Sequence 236534, A
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Sequence 870153, A
Sequence 873079, A
Sequence 873080, A
Sequence 852313, A
Sequence 260204, A
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Sequence 919332, A
Sequence 118115, A
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Sequence 693989, A
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Sequence 249, App
Sequence 117894, A
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Sequence 9631, Ap
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Sequence 1551, Ap
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RESULT 2
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; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugliu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3000
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3000

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Best Local Similarity 100.0%; Pred. No. 30;
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Db 5 CCACACCTATTTCATCTC 22
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; Sequence 3110, Application US/100600036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugliu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3110
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3110

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 5 CCACACCTATTTCATCTC 22

RESULT 4
US-10-060-036-3600
; Sequence 3600, Application US/100600036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3600
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3600

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Best Local Similarity 100.0%; Pred. No. 30;
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; Sequence 3604, Application US/100600036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3604
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3604

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 CCACACCTATTTCATCTC 22

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US-10-060-036-3941
; Sequence 3941, Application US/100600036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-3941

Query Match      100.0%; Score 18; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 5 CCACACCTATTTCATCTC 22

RESULT 7
US-10-060-036-4030
; Sequence 4030, Application US/100600036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4030
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-4030

Query Match      100.0%; Score 18; DB 5; Length 224;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 5 CCACACCTATTTCATCTC 22
```



```

; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 822
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-822

Query Match      100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTTATTCATCTC 18
      |||
Db      313 CCACACCTTATTCATCTC 330

RESULT 12
US-09-954-456-1225, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 822
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-822

Query Match      100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTTATTCATCTC 18
      |||
Db      313 CCACACCTTATTCATCTC 330

RESULT 13
US-10-641-643-1200, Application US/10641643
; Sequence 1200, Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
;              Susan G. Stuart
;              Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: gl90012
; SEQUENCE DESCRIPTION: SEQ ID NO: 1200 :
US-10-641-643-1200

Query Match      100.0%; Score 18; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTTATTCATCTC 18
      |||

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```

; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1225
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1225

Query Match      100.0%; Score 18; DB 3; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTTATTCATCTC 18
      |||
Db      313 CCACACCTTATTCATCTC 330

RESULT 13
US-10-641-643-1200, Application US/10641643
; Sequence 1200, Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
;              Susan G. Stuart
;              Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1200:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: gl90012
; SEQUENCE DESCRIPTION: SEQ ID NO: 1200 :
US-10-641-643-1200

Query Match      100.0%; Score 18; DB 7; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTTATTCATCTC 18
      |||

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```
Db      313 CCACACCTATTTCATCTC 330

RESULT 14
US-10-607-806-3
; Sequence 3, Application US/10607806
; Publication No. US20050014158A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel Reid
; APPLICANT: Langdown, Maria L.
; APPLICANT: Denisessenko, Mikhail F.
; APPLICANT: Dennis, Edward
; APPLICANT: Cantor, Charles
; APPLICANT: Rubin, Byron
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR REDUCING FAT
; TITLE OF INVENTION: DEPOSITION AND TREATING ASSOCIATED CONDITIONS
; FILE REFERENCE: 524592003200
; CURRENT APPLICATION NUMBER: US/10/607,806
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,362
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-806-3

Query Match      100.0%; Score 18; DB 8; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      313 CCACACCTATTTCATCTC 330

RESULT 15
US-10-607-806-3
; Sequence 3243, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3243
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-607-806-3

Query Match      100.0%; Score 18; DB 8; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      313 CCACACCTATTTCATCTC 330

RESULT 16
US-10-843-641A-3849
; Sequence 3849, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3849
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-3849

Query Match      100.0%; Score 18; DB 9; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      313 CCACACCTATTTCATCTC 330

RESULT 17
US-10-843-641A-4252
; Sequence 4252, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
```

```

; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4252
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-4252

Query Match 100.0%; Score 18; DB 9; Length 562;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 313 CCACACCTATTTCATCTC 330

RESULT 18
US-10-712-124-27
; Sequence 27, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
; APPLICANT: SMITH, VICTORIA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
; FILE REFERENCE: P2000R1
; CURRENT APPLICATION NUMBER: US/10/712,124
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/425,813
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 27
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-712-124-27

Query Match 100.0%; Score 18; DB 7; Length 585;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 312 CCACACCTATTTCATCTC 329

RESULT 19
US-09-925-297-52
; Sequence 52, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; APPLICANT: Rosen et al.
```

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; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 52
; LENGTH: 630
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (556)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (628)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-297-52

Query Match 100.0%; Score 18; DB 3; Length 630;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 302 CCACACCTATTTCATCTC 319

RESULT 20
US-10-330-051A-6
; Sequence 6, Application US/10330051A
; Publication No. US20040002471A1
; GENERAL INFORMATION:
; APPLICANT: Specht, Thomas
; APPLICANT: Hinzmann, Bernd
; APPLICANT: Schmitt, Armin
; APPLICANT: Pilarsky, Christian
; APPLICANT: Dahl, Edgar
; APPLICANT: Rosenthal, Andre
; TITLE OF INVENTION: Human Nucleic Acid Sequences Which Are Overexpressed In No. US2004
; FILE REFERENCE: ALBRE-2D1
; CURRENT APPLICATION NUMBER: US/10/330,051A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/647,801
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 6
; LENGTH: 644
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-330-051A-6

Query Match 100.0%; Score 18; DB 6; Length 644;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
DB 337 CCACACCTATTTCATCTC 354

RESULT 21
US-10-450-763-11903
; Sequence 11903, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
```

```
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 11903
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(711)
; OTHER INFORMATION: 87% homologous to Homo sapiens syntaxin 8, accession number
; OTHER INFORMATION: AF036715, Smith-Waterman Score=1008.
US-10-450-763-11903
```

```
Query Match 100.0%; Score 18; DB 9; Length 654;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 CCACACCTATTTCATCTC 18
Db 483 CCACACCTATTTCATCTC 500
|||||
```

```
RESULT 22
US-10-607-806-1
; Sequence 1, Application US/10607806
; Publication No. US20050014158A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel Reid
; APPLICANT: Langdown, Maria L.
; APPLICANT: Denissenko, Mikhail F.
; APPLICANT: Dennis, Edward
; APPLICANT: Cantor, Charles
; APPLICANT: Rubin, Byron
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR REDUCING FAT
; FILE REFERENCE: 524592003200
; CURRENT APPLICATION NUMBER: US/10/607,806
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,362
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12174
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 436
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4050)...(4050)
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 4689
; OTHER INFORMATION: w = A or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6282
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: 6358
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7256
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7300
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7301)...(7301)
; OTHER INFORMATION: m = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7328)...(7328)
; OTHER INFORMATION: r = A or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8062)...(8062)
; OTHER INFORMATION: y = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9182)...(9182)
; OTHER INFORMATION: k = G or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11649)...(11649)
; OTHER INFORMATION: m = A or C
US-10-607-806-1
```

```
Query Match 100.0%; Score 18; DB 8; Length 12174;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CCACACCTATTTCATCTC 18
Db 7310 CCACACCTATTTCATCTC 7327
|||||
```

```
RESULT 23
US-09-925-065A-935053
; Sequence 935053, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935053
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935053
```

```
Query Match 91.1%; Score 16.4; DB 4; Length 586;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      320 CCACACCTATTTCATACAC 337

RESULT 24
US-09-925-065A-935054
; Sequence 935054, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935054
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935054

Query Match      91.1%; Score 16.4; DB 4; Length 586;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      320 CCACACCTATTTCATACAC 337

RESULT 25
US-09-925-065A-952779
; Sequence 952779, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 952779
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-952779

Query Match      91.1%; Score 16.4; DB 4; Length 586;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      320 CCACACCTATTTCATACAC 337

RESULT 26
US-09-925-065A-919397/c
; Sequence 919397, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 919397
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-919397

Query Match      91.1%; Score 16.4; DB 4; Length 770;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      158 CCACACCTATTTCATACAC 141

RESULT 27
US-10-482-029-205
; Sequence 205, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 205
; LENGTH: 251199
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-029-205

Query Match      91.1%; Score 16.4; DB 8; Length 251199;
Best Local Similarity 94.4%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
      |||||
Db      159523 CCACACCTATTTCATACAC 159540
```

RESULT 28
US-10-060-036-518
; Sequence 518, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 518
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 20, 53, 56, 58, 59
; OTHER INFORMATION: n = A, T, C or G
US-10-060-036-518

Query Match 88.9%; Score 16; DB 5; Length 224;
Best Local Similarity 94.1%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
|||||
DB 5 CCACACCTATTTCATCT 21

RESULT 29
US-10-424-599-127447
; Sequence 127447, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 127447
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_8608C.1
US-10-424-599-127447

Query Match 85.6%; Score 15.4; DB 7; Length 321;
Best Local Similarity 94.1%; Pred. No. 7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCACACCTATTTCATCT 18
|||||
DB 152 CCACACCTATTTCCTACT 168

RESULT 30
US-10-425-115-33674
; Sequence 33674, Application US/10425115

; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 33674
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_130716C.1
US-10-425-115-33674

Query Match 85.6%; Score 15.4; DB 8; Length 533;
Best Local Similarity 94.1%; Pred. No. 7.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
DB 136 CACACCTATTCATCTC 152

RESULT 31
US-09-925-065A-459786/c
; Sequence 459786, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459786
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-459786

Query Match 85.6%; Score 15.4; DB 4; Length 567;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
|||||
DB 66 CACACCTATTCATCTC 50

RESULT 32
US-09-925-065A-366085
; Sequence 366085, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.

;
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366085
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366085

Query Match 85.6%; Score 15.4; DB 4; Length 603;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCATCT 17
Db 197 CCACACCTATTCATCT 213

RESULT 33
US-10-021-323-1223
; Sequence 1223, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Deikman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 1223
; LENGTH: 611
; TYPE: DNA
; ORGANISM: Gossypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3825-020-Q1-K6-B2
US-10-021-323-1223

Query Match 85.6%; Score 15.4; DB 7; Length 611;
Best Local Similarity 94.1%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
Db 340 CACACCTATTCATCTC 356

RESULT 34
US-10-027-632-122849
; Sequence 122849, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

;
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122849
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122849

Query Match 85.6%; Score 15.4; DB 5; Length 1202;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18
Db 468 CACACCTATTCATCTC 484

RESULT 35
US-10-027-632-122850
; Sequence 122850, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122850
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-122850

Query Match 85.6%; Score 15.4; DB 5; Length 1202;
Best Local Similarity 94.1%; Pred. No. 7.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTCATCTC 18

Query Match 85.6%; Score 15.4; DB 3; Length 3093;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACT 17
Db 553 CCACACCTATTGTACT 537

RESULT 40
US-09-938-842A-1570/c
; Sequence 1570, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1570
; LENGTH: 3093
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1570

Query Match 85.6%; Score 15.4; DB 3; Length 3093;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACT 17
Db 553 CCACACCTATTGTACT 537

RESULT 41
US-10-347-470A-1/c
; Sequence 1, Application US/10347470A
; Publication No. US2004002054A1
; GENERAL INFORMATION:
; APPLICANT: Horvitz, H. Robert
; APPLICANT: Hwang, Ho Yon
; TITLE OF INVENTION: SQV NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 01997/542003
; CURRENT APPLICATION NUMBER: US/10/347,470A
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 60/349,630
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/390,930
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3120
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-10-347-470A-1

Query Match 85.6%; Score 15.4; DB 6; Length 3120;
Best Local Similarity 94.1%; Pred. No. 8.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCACACCTATTCTACT 18

Db 3067 CACACCTATTCTACT 3051
|||||

RESULT 42
US-10-311-455-1691/c
; Sequence 1691, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining
; FILE REFERENCE: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1691
; LENGTH: 17934
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1691

Query Match 85.6%; Score 15.4; DB 6; Length 17934;
Best Local Similarity 94.1%; Pred. No. 1e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTCTACT 18
Db 14397 CACACCTATACATCTC 14381
|||||

RESULT 43
US-10-721-693-10/c
; Sequence 10, Application US/10721693
; Publication No. US20040162255A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: siRNA
; FILE REFERENCE: P11089.00
; CURRENT APPLICATION NUMBER: US/10/721,693
; CURRENT FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 118777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(118777)
; OTHER INFORMATION: LOCUS AF163865
; OTHER INFORMATION: OD 24-JAN-2001
; OTHER INFORMATION: DEFINITION Mus musculus alpha-synuclein (Snca) gene, complete cd
; OTHER INFORMATION: s.
; OTHER INFORMATION: ACCESSION AF163865
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF163865
; DATABASE ENTRY DATE: 2001-01-24
; RELEVANT RESIDUES: (1)..(118777)
US-10-721-693-10

```
Query Match      85.6%; Score 15.4; DB 7; Length 118777;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACT 17
Db 77795 CCACACATATTTCATACT 77779

RESULT 44
US-10-852-997-10/c
; Sequence 10, Application US/10852997
; Publication No. US20040220132A1
; GENERAL INFORMATION:
; APPLICANT: Medtronic, Inc.
; APPLICANT: Kaemmerer, William F.
; TITLE OF INVENTION: Treatment of Neurodegenerative Disease Through Intracranial Delivery
; FILE REFERENCE: P11089.02
; CURRENT APPLICATION NUMBER: US/10/852,997
; CURRENT FILING DATE: 2004-05-25
; PRIOR APPLICATION NUMBER: 10/721,693
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 118777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(118777)
; OTHER INFORMATION: LOCUS AF163865 118777 bp DNA linear R
; OTHER INFORMATION: OD 24-JAN-2001
; OTHER INFORMATION: DEFINITION Mus musculus alpha-synuclein (Snca) gene, complete cds
; OTHER INFORMATION: 8
; OTHER INFORMATION: ACCESSION AF163865
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AF163865
; DATABASE ENTRY DATE: 2001-01-24
; RELEVANT RESIDUES: (1)..(118777)
US-10-852-997-10

Query Match      85.6%; Score 15.4; DB 8; Length 118777;
Best Local Similarity 94.1%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACT 17
Db 77795 CCACACATATTTCATACT 77779

RESULT 45
US-10-087-192-454
; Sequence 454, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhardt, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 454
; LENGTH: 439892
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(439892)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-454

Query Match      85.6%; Score 15.4; DB 5; Length 439892;
Best Local Similarity 94.1%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
Db 54190 CACACCTTTTCATACTC 54206

RESULT 46
US-10-242-535A-27057/c
; Sequence 27057, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27057
; LENGTH: 136
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-27057

Query Match      83.3%; Score 15; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATACTC 18
Db 63 CACCTATTTCATACTC 49

RESULT 47
US-10-085-783A-27057/c
; Sequence 27057, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27057
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; LENGTH: 136
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-27057

Query Match      83.3%; Score 15; DB 7; Length 136;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
   |||||
DB 63 CACCTATTTCATCTC 49

RESULT 48
US-10-425-115-78961/c
; Sequence 78961, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 78961
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172037C.1
US-10-425-115-78961

Query Match      83.3%; Score 15; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
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DB 100 CCACACCTATTTCATA 86

RESULT 49
US-09-925-065A-817638/c
; Sequence 817638, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817638
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Cpg-island No: 14929
US-10-363-345A-14929/c
; Sequence 14929, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14929
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 14929
US-10-363-345A-14929
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US-09-925-065A-817638

Query Match      83.3%; Score 15; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
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DB 258 CCACACCTATTTCATA 244

RESULT 50
US-09-925-065A-817639/c
; Sequence 817639, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817639
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817639

Query Match      83.3%; Score 15; DB 4; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
   |||||
DB 258 CCACACCTATTTCATA 244

RESULT 51
US-10-363-345A-14929/c
; Sequence 14929, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; APPLICANT: Christian Piepenbrock
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14929
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: Cpg-island No: 14929
US-10-363-345A-14929

Query Match      83.3%; Score 15; DB 8; Length 544;
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Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
Db 532 CACCTATTTCATCTC 518

RESULT 52
US-10-363-345A-14930
; Sequence 14930, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14930
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14930
US-10-363-345A-14930

Query Match 83.3%; Score 15; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
Db 13 CACCTATTTCATCTC 27

RESULT 53
US-10-363-483A-14929/c
; Sequence 14929, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14929
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14929
US-10-363-483A-14929

Query Match 83.3%; Score 15; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CACCTATTTCATCTC 18
Db 532 CACCTATTTCATCTC 518

RESULT 54
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US-10-363-483A-14930
; Sequence 14930, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 14930
; LENGTH: 544
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 14930
US-10-363-483A-14930
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Query Match 83.3%; Score 15; DB 9; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 4 CACCTATTTCATCTC 18
Db 13 CACCTATTTCATCTC 27
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RESULT 55
US-10-424-599-127043
; Sequence 127043, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 127043
; LENGTH: 203
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(203)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_85726C.1
US-10-424-599-127043
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Query Match 82.2%; Score 14.8; DB 7; Length 203;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CCACACTTATTCATCTC 18
Db 93 CCACACTTATTCATCTC 110
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RESULT 56
US-10-425-115-104465
; Sequence 104465, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
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; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369336
; SEQ ID NO 104465
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(241)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_26775C.1
US-10-425-115-104465

Query Match 82.2%; Score 14.8; DB 8; Length 241;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 5 CCACACCTACTCTACTC 22

RESULT 57
US-10-424-599-72836
; Sequence 72836, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 72836
; LENGTH: 323
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(323)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36786C.1
US-10-424-599-72836

Query Match 82.2%; Score 14.8; DB 7; Length 323;
Best Local Similarity 88.9%; Pred. No. 1.4e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 102 CCACACCTATTCTACTC 119

RESULT 58
US-09-925-065A-614775
; Sequence 614775, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614775
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614775

Query Match 82.2%; Score 14.8; DB 4; Length 392;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 133 CCACACCTATTCTACTC 150

RESULT 59
US-09-925-065A-614776
; Sequence 614776, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614776
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614776

Query Match 82.2%; Score 14.8; DB 4; Length 392;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTCTACTC 18
|||||
Db 133 CCACACCTATTCTACTC 150

RESULT 60
US-09-925-065A-614778
; Sequence 614778, Application US/09925065A
; Publication No. US20050228172A9

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614778
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614778

Query Match 82.2%; Score 14.8; DB 4; Length 392;
Best Local Similarity 88.9%; Pred. No. 1.5e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 133 CCACACCTATTTCACAC 150
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Search completed: May 10, 2006, 19:48:29
Job time : 428 secs

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2006, 19:26:26 ; Search time 681 Seconds
(without alignments)
107.802 Million cell updates/sec

Title: US-10-608-296-38

Perfect score: 18

Sequence: 1 ccacaccattcattacc 18

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 9312410 seqs, 2039259788 residues

Total number of hits satisfying chosen parameters: 18624820

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 150 summaries

Database :

Published Applications NA New:*
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19: /SIDSS/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	16.4	91.1	586	7	US-09-925-065A-935054
3	16.4	91.1	586	7	US-09-925-065A-952779
C 4	16.4	91.1	770	7	US-09-925-065A-919397
5	16.4	91.1	156344	17	US-11-121-086-81
6	16	88.9	25	17	US-11-121-849-134677
C 7	15.4	85.6	566	12	US-10-301-480-517106
C 8	15.4	85.6	566	12	US-10-301-480-1130515
C 9	15.4	85.6	567	7	US-09-925-065A-459786
10	15.4	85.6	589	12	US-10-301-480-436566
11	15.4	85.6	589	12	US-10-301-480-1049975
12	15.4	85.6	603	7	US-09-925-065A-366085
C 13	15.4	85.6	990	12	US-10-301-480-556079
C 14	15.4	85.6	990	12	US-10-301-480-1169488

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c 113 14.8 82.2 2462 7 US-09-925-065A-678157
c 114 14.8 82.2 3237 18 US-11-072-512-1028
c 115 14.8 82.2 20945 10 US-10-995-561-13463
c 116 14.8 82.2 23082 10 US-10-995-561-13457
c 117 14.8 82.2 29360 11 US-10-330-773-165
c 118 14.8 82.2 70549 11 US-10-330-773-413
c 119 14.8 82.2 98862 17 US-11-121-086-76
c 120 14.8 82.2 172756 18 US-11-114-798-48
c 121 14.8 82.2 175100 17 US-11-121-086-21
c 122 14.8 82.2 197241 18 US-11-114-798-47
c 123 14.8 82.2 199868 11 US-10-330-773-808
c 124 14.8 82.2 380749 10 US-10-995-561-13216
c 125 14.6 81.1 446 7 US-09-824-755A-3
c 126 14.6 81.1 456 7 US-09-925-065A-730125
c 127 14.4 80.0 379 7 US-09-925-065A-808879
c 128 14.4 80.0 392 7 US-09-925-065A-599197
c 129 14.4 80.0 490 7 US-09-925-065A-614774
c 130 14.4 80.0 490 7 US-09-925-065A-649037
c 131 14.4 80.0 490 7 US-09-925-065A-649038
c 132 14.4 80.0 497 7 US-09-925-065A-439259
c 133 14.4 80.0 509 7 US-09-925-065A-439259
c 134 14.4 80.0 522 7 US-09-925-065A-459014
c 135 14.4 80.0 527 12 US-09-925-065A-316303
c 136 14.4 80.0 527 12 US-10-301-480-391279
c 137 14.4 80.0 527 12 US-10-301-480-1004688
c 138 14.4 80.0 529 12 US-10-301-480-431996
c 139 14.4 80.0 529 12 US-10-301-480-1045405
c 140 14.4 80.0 532 12 US-10-301-480-1045406
c 141 14.4 80.0 532 12 US-10-301-480-1113828
c 142 14.4 80.0 534 12 US-10-301-480-337583
c 143 14.4 80.0 534 12 US-10-301-480-950992
c 144 14.4 80.0 536 11 US-10-301-480-19086
c 145 14.4 80.0 536 11 US-10-301-480-19087
c 146 14.4 80.0 536 12 US-10-301-480-632495
c 147 14.4 80.0 536 12 US-10-301-480-632496
c 148 14.4 80.0 537 11 US-10-301-480-19084
c 149 14.4 80.0 537 12 US-10-301-480-632493
c 150 14.4 80.0 539 7 US-09-925-065A-360917
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ALIGNMENTS

RESULT 1

US-09-925-065A-935053

; Sequence 935053, Application US/09925065A

; Publication No. US20040181048A1

; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935053
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935053
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Query Match 91.1%; Score 16.4; DB 7; Length 586;

Best Local Similarity 94.4%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCACACCTTATTCATCTC 18
Db 320 CCACACCTTATTCATCAC 337
|||||
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RESULT 2

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US-09-925-065A-935054
; Sequence 935054, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935054
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935054
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Query Match 91.1%; Score 16.4; DB 7; Length 586;

Best Local Similarity 94.4%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCACACCTTATTCATCTC 18
Db 320 CCACACCTTATTCATCAC 337
|||||
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RESULT 3

US-09-925-065A-952779

; Sequence 952779, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 952779
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-952779

Query Match 91.1%; Score 16.4; DB 7; Length 586;
Best Local Similarity 94.4%; Pred. No. 42;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
| | | | | | | | | | | | | | | | | |
DB 320 CCACACCTTTCATCTC 337

RESULT 4
US-09-925-065A-919397/c
; Sequence 919397, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 919397
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-919397

Query Match 91.1%; Score 16.4; DB 7; Length 770;
Best Local Similarity 94.4%; Pred. No. 45;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
| | | | | | | | | | | | | | | | | |
DB 158 CCACACCTTTCATCTC 141

RESULT 5
US-11-121-086-81
; Sequence 81, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 156544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-81

Query Match 91.1%; Score 16.4; DB 17; Length 156544;
Best Local Similarity 94.4%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
| | | | | | | | | | | | | | | | | |
DB 92675 CCACACCTTTCATCTC 92692

RESULT 6
US-11-121-849-134677
; Sequence 134677, Application US/11121849
; Publication No. US20050272080A1
; GENERAL INFORMATION:
; APPLICANT: John Palma
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded S
; FILE REFERENCE: 3684.1
; CURRENT APPLICATION NUMBER: US/11/121,849
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 60/567,949
; PRIOR FILING DATE: 2004-05-03
; NUMBER OF SEQ ID NOS: 673904
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134677
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-121-849-134677

Query Match 98.9%; Score 16; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ACACCTTTCATCTC 18
| | | | | | | | | | | | | | | | | |
DB 1 ACACCTTTCATCTC 16

RESULT 7
US-10-301-480-517106/c
; Sequence 517106, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598

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; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517106
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-517106

Query Match      85.6%; Score 15.4; DB 12; Length 566;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
Db 65 CACACCCATTTCATCTC 49

RESULT 8
US-10-301-480-1130515/c
; Sequence 1130515, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1130515
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1130515

Query Match      85.6%; Score 15.4; DB 12; Length 566;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
Db 65 CACACCCATTTCATCTC 49

RESULT 9
US-09-925-065A-459786/c
; Sequence 459786, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 459786
; LENGTH: 567
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-459786

Query Match      85.6%; Score 15.4; DB 7; Length 567;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATCTC 18
Db 66 CACACCCATTTCATCTC 50

RESULT 10
US-10-301-480-436566
; Sequence 436566, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 436566
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-436566

Query Match      85.6%; Score 15.4; DB 12; Length 589;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCT 17
Db 183 CCACACCTATTCATCT 199

RESULT 11
US-10-301-480-1049975
; Sequence 1049975, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1049975
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1049975

Query Match      85.6%; Score 15.4; DB 12; Length 589;
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Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACT 17
Db 183 CCACACCTATTCATACT 199

RESULT 12
US-09-925-065A-366085
; Sequence 366085, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366085
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-366085

Query Match 85.6%; Score 15.4; DB 7; Length 603;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACT 17
Db 197 CCACACCTATTCATACT 213

RESULT 13
US-10-301-480-556079/c
; Sequence 556079, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 556079
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-556079

Query Match 85.6%; Score 15.4; DB 12; Length 990;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
Db 560 CACACCTATTCATACTC 576

RESULT 14
US-10-301-480-1169488/c
; Sequence 1169488, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1169488
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1169488

Query Match 85.6%; Score 15.4; DB 12; Length 990;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
Db 977 CACACCTGTTCATACTC 961

RESULT 15
US-10-750-185-59851
; Sequence 59851, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59851
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Bovine 19866881032028
US-10-750-185-59851

Query Match 85.6%; Score 15.4; DB 10; Length 1201;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACACCTATTTCATACTC 18
Db 560 CACACCTATTCATACTC 576

RESULT 16
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US-10-750-623-59851
; Sequence 59851, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59851
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Bovine 19866881032028
US-10-750-623-59851

Query Match      85.6%; Score 15.4; DB 10; Length 1201;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCTC 18
Db      560 CACACCCATTCATCTC 576
      ||||| ||||| ||||| |||||

RESULT 17
US-11-124-367A-5020
; Sequence 5020, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5020
; LENGTH: 3416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2379-2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388,
; LOCATION: 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398,
; LOCATION: 18551, 18552, 18553, 18554, 18555, 18556, 18557, 18558,
; LOCATION: 18559, 18560, 18561, 18562, 18563, 18564, 18565, 18566
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18567, 18568, 18569, 18570, 18571, 18572, 18573, 18574, 18575,
; LOCATION: 18576, 18577, 18578, 18579, 18580, 18581, 18582, 18583,
; LOCATION: 18584, 18585, 18586, 18587, 18588, 18589, 18590, 18591,
; LOCATION: 18592, 18593, 18594, 18595, 18596, 18597, 18598, 18599
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18600, 18601, 18602, 18603, 18604, 18605, 18606, 18607, 18608,
; LOCATION: 18609, 18610, 18611, 18612, 18613, 18614, 18615, 18616,
; LOCATION: 18617, 18618, 18619, 18620, 18621, 18622, 18623, 18624,
; LOCATION: 18625, 18626, 18627, 18628, 18629, 18630, 18631, 18632
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18633, 18634, 18635, 18636, 18637, 18638, 18639, 18640, 18641,
; LOCATION: 18642, 18643, 18644, 18645, 18646, 18647, 18648, 18649,
; LOCATION: 18650, 18651, 18652, 18653, 18654, 18655, 18656, 18657,
; LOCATION: 18658, 18659, 18660, 18661, 18662, 18663, 18664, 18665
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18666, 18667, 18668, 18669, 18670, 18671, 18672, 18673, 18674,
; LOCATION: 18675, 18676, 18677, 18678, 18679, 18680, 18681, 18682,
; LOCATION: 18683, 18684, 18685, 18686, 18687, 18688, 18689, 18690,
; LOCATION: 18691, 18692, 18693, 18694, 18695, 18696, 18697, 18698
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18699, 18700, 18701, 18702, 18703, 18704, 18705, 18706, 18707,
; LOCATION: 18708, 18709, 18710, 18711, 18712, 18713, 18714, 18715,
; LOCATION: 18716, 18717, 18718, 18719, 18720, 18721, 18722, 18723,
; LOCATION: 18724, 18725, 18726, 18727, 18728, 18729, 18730, 18731
; OTHER INFORMATION: n = A,T,C or G
US-11-124-367A-5020

Query Match      85.6%; Score 15.4; DB 17; Length 34116;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCTC 18
Db      21744 CACACCCATTCATCTC 21760
      ||||| ||||| ||||| |||||

RESULT 18
US-11-101-244-376219
; Sequence 376219, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 376219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-376219

Query Match      83.3%; Score 15; DB 15; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATA 15
Db      5 CCACACCUAUUCAUA 19
      ||||| ||||| ||||| |||||
```

```
US-10-750-623-59851
; Sequence 59851, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59851
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Bovine 19866881032028
US-10-750-623-59851

Query Match      85.6%; Score 15.4; DB 10; Length 1201;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCTC 18
Db      560 CACACCCATTCATCTC 576
      ||||| ||||| ||||| |||||

RESULT 17
US-11-124-367A-5020
; Sequence 5020, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5020
; LENGTH: 3416
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 2379-2380, 2381, 2382, 2383, 2384, 2385, 2386, 2387, 2388,
; LOCATION: 2389, 2390, 2391, 2392, 2393, 2394, 2395, 2396, 2397, 2398,
; LOCATION: 18551, 18552, 18553, 18554, 18555, 18556, 18557, 18558,
; LOCATION: 18559, 18560, 18561, 18562, 18563, 18564, 18565, 18566
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18567, 18568, 18569, 18570, 18571, 18572, 18573, 18574, 18575,
; LOCATION: 18576, 18577, 18578, 18579, 18580, 18581, 18582, 18583,
; LOCATION: 18584, 18585, 18586, 18587, 18588, 18589, 18590, 18591,
; LOCATION: 18592, 18593, 18594, 18595, 18596, 18597, 18598, 18599
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18600, 18601, 18602, 18603, 18604, 18605, 18606, 18607, 18608,
; LOCATION: 18609, 18610, 18611, 18612, 18613, 18614, 18615, 18616,
; LOCATION: 18617, 18618, 18619, 18620, 18621, 18622, 18623, 18624,
; LOCATION: 18625, 18626, 18627, 18628, 18629, 18630, 18631, 18632
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18633, 18634, 18635, 18636, 18637, 18638, 18639, 18640, 18641,
; LOCATION: 18642, 18643, 18644, 18645, 18646, 18647, 18648, 18649,
; LOCATION: 18650, 18651, 18652, 18653, 18654, 18655, 18656, 18657,
; LOCATION: 18658, 18659, 18660, 18661, 18662, 18663, 18664, 18665
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18666, 18667, 18668, 18669, 18670, 18671, 18672, 18673, 18674,
; LOCATION: 18675, 18676, 18677, 18678, 18679, 18680, 18681, 18682,
; LOCATION: 18683, 18684, 18685, 18686, 18687, 18688, 18689, 18690,
; LOCATION: 18691, 18692, 18693, 18694, 18695, 18696, 18697, 18698
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 18699, 18700, 18701, 18702, 18703, 18704, 18705, 18706, 18707,
; LOCATION: 18708, 18709, 18710, 18711, 18712, 18713, 18714, 18715,
; LOCATION: 18716, 18717, 18718, 18719, 18720, 18721, 18722, 18723,
; LOCATION: 18724, 18725, 18726, 18727, 18728, 18729, 18730, 18731
; OTHER INFORMATION: n = A,T,C or G
US-11-124-367A-5020

Query Match      85.6%; Score 15.4; DB 17; Length 34116;
Best Local Similarity 94.1%; Pred. No. 3.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACACCTATTTCATCTC 18
Db      21744 CACACCCATTCATCTC 21760
      ||||| ||||| ||||| |||||

RESULT 18
US-11-101-244-376219
; Sequence 376219, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 376219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-376219

Query Match      83.3%; Score 15; DB 15; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATA 15
Db      5 CCACACCUAUUCAUA 19
      ||||| ||||| ||||| |||||
```

```
RESULT 19
US-11-083-784-376219
; Sequence 376219, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 376219
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-376219

Query Match      83.3%; Score 15; DB 16; Length 19;
Best Local Similarity 73.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
Db 5 CCACACCUAUUCAUA 19

RESULT 20
US-09-925-065A-817638/c
; Sequence 817638, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817638
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817638

Query Match      83.3%; Score 15; DB 15; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
Db 5 CCACACCUAUUCAUA 19

RESULT 21
US-09-925-065A-817639/c
; Sequence 817639, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817639
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817639

Query Match      83.3%; Score 15; DB 7; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
Db 258 CCACACCTATTTCATA 244

RESULT 22
US-10-995-561-74454
; Sequence 74454, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74454
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-74454

Query Match      82.2%; Score 14.8; DB 10; Length 201;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACTC 18
Db 156 CCACACCTATTTCATAC 173

RESULT 23
US-10-995-561-75240
```

```
Db 258 CCACACCTATTTCATA 244

RESULT 21
US-09-925-065A-817639/c
; Sequence 817639, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817639
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-817639

Query Match      83.3%; Score 15; DB 7; Length 478;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATA 15
Db 258 CCACACCTATTTCATA 244

RESULT 22
US-10-995-561-74454
; Sequence 74454, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74454
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-74454

Query Match      82.2%; Score 14.8; DB 10; Length 201;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATACTC 18
Db 156 CCACACCTATTTCATAC 173

RESULT 23
US-10-995-561-75240
```

```
; Sequence 75240, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75240
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-75240

Query Match      82.2%; Score 14.8; DB 10; Length 201;
Best Local Similarity 88.9%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATCTC 18
Db      156 CCACACCTATCCATACAC 173

RESULT 24
US-09-925-065A-614775
; Sequence 614775, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614775
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614775

Query Match      82.2%; Score 14.8; DB 7; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATCTC 18
Db      133 CCACACCTATTTCACAC 150

RESULT 25
US-09-925-065A-614776
; Sequence 614776, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614776
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614776

Query Match      82.2%; Score 14.8; DB 7; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATCTC 18
Db      133 CCACACCTATTTCACAC 150

RESULT 26
US-09-925-065A-614778
; Sequence 614778, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614778
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614778

Query Match      82.2%; Score 14.8; DB 7; Length 392;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCACACCTATTTCATCTC 18
Db      133 CCACACCTATTTCACAC 150

RESULT 27
US-10-301-480-461153
; Sequence 461153, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 461153
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-461153

Query Match      82.2%; Score 14.8; DB 12; Length 470;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
DB 143 CCACACCTTTCACAGTC 160

RESULT 28
US-10-301-480-1074562
; Sequence 1074562, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1074562
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1074562

Query Match      82.2%; Score 14.8; DB 12; Length 470;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
DB 143 CCACACCTTTCACAGTC 160

RESULT 29
US-09-925-065A-393035
; Sequence 393035, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
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; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393035
; LENGTH: 477
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-393035

Query Match      82.2%; Score 14.8; DB 7; Length 477;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
DB 143 CCACACCTTTCACAGTC 160

RESULT 30
US-10-301-480-326616/c
; Sequence 326616, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 326616
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-326616

Query Match      82.2%; Score 14.8; DB 12; Length 484;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTTCATCTC 18
DB 79 CCACACCTTTCACAC 62

RESULT 31
US-10-301-480-940025/c
; Sequence 940025, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 940025
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-940025

Query Match      82.2%; Score 14.8; DB 12; Length 484;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
   ||||| ||||| |||||
Db 79 CCACACCTATTTCACAC 62

RESULT 32
US-09-925-065A-246390/c
; Sequence 246390, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246390
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-246390

Query Match      82.2%; Score 14.8; DB 7; Length 489;
Best Local Similarity 88.9%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
   ||||| ||||| |||||
Db 84 CCACACCTATTTCACAC 67

RESULT 33
US-11-128-061-1580
; Sequence 1580, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
```

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; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1580
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-1580

Query Match      82.2%; Score 14.8; DB 17; Length 503;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
   ||||| ||||| |||||
Db 73 CCACACCTAGTCATACAC 90

RESULT 34
US-11-128-061-5222
; Sequence 5222, Application US/11128061
; Publication No. US20060003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5222
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Cricetulus griseus
US-11-128-061-5222

Query Match      82.2%; Score 14.8; DB 17; Length 503;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACACCTATTTCATCTC 18
   ||||| ||||| |||||
Db 73 CCACACCTAGTCATACAC 90

RESULT 35
US-11-128-049-1580
; Sequence 1580, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; MAKING AND USING SAME
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
```


; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1580
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-049-1580

Query Match 82.2%; Score 14.8; DB 17; Length 503;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
|||||
DB 73 CCACACCTAGTCATACAC 90

RESULT 36

US-11-128-049-5222
; Sequence 5222, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:

; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5222
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-049-5222

Query Match 82.2%; Score 14.8; DB 17; Length 503;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
|||||
DB 73 CCACACCTAGTCATACAC 90

RESULT 37

US-10-301-480-370251
; Sequence 370251, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370251

; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-370251

Query Match 82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
|||||
DB 409 CCACACCTATTCACACAC 426

RESULT 38

US-10-301-480-370252
; Sequence 370252, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370252
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-370252

Query Match 82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
|||||
DB 409 CCACACCTATTCACACAC 426

RESULT 39

US-10-301-480-983660
; Sequence 983660, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 983660
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-983660

Query Match 82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 409 CCACACCTATTTCACAC 426

RESULT 40
US-10-301-480-983661
; Sequence 983661, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 983661
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-983661

Query Match 82.2%; Score 14.8; DB 12; Length 533;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 409 CCACACCTATTTCACAC 426

RESULT 41
US-09-925-065A-293390
; Sequence 293390, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293390
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-293390

Query Match 82.2%; Score 14.8; DB 7; Length 535;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 411 CCACACCTATTTCACAC 428

RESULT 42
US-09-925-065A-293391
; Sequence 293391, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 293391
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-293391

Query Match 82.2%; Score 14.8; DB 7; Length 535;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 411 CCACACCTATTTCACAC 428

RESULT 43
US-09-925-065A-523202/c
; Sequence 523202, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523202
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523202

Query Match 82.2%; Score 14.8; DB 7; Length 538;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 492 CCACACCTGTTTCACATC 475

RESULT 44

US-09-925-065A-523203/c
; Sequence 523203, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523203
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523203

Query Match 82.2%; Score 14.8; DB 7; Length 538;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 492 CCACACCTGTTTCACATC 475

RESULT 45

US-09-925-065A-143110/c
; Sequence 143110, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143110
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-143110

Query Match 82.2%; Score 14.8; DB 7; Length 565;

Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCACACCTATTTCATCTC 18
|||||
Db 125 CCACACCTATTTCGTACAC 108

RESULT 46

US-09-925-065A-143111/c
; Sequence 143111, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143111
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-143111

Query Match 82.2%; Score 14.8; DB 7; Length 565;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
|||||
Db 125 CCACACCTATTTCGTACAC 108

RESULT 47

US-10-301-480-59147/c
; Sequence 59147, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59147
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-59147

Query Match 82.2%; Score 14.8; DB 11; Length 566;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 211 CCACACCTATTTCACAC 194

RESULT 48

US-10-301-480-672556/c
; Sequence 672556, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 672556
; LENGTH: 566
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-672556

Query Match 82.2%; Score 14.8; DB 12; Length 566;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 211 CCACACCTATTTCACAC 194

RESULT 49

US-09-925-065A-523201/c
; Sequence 523201, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523201
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523201

Query Match 82.3%; Score 14.8; DB 7; Length 568;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 493 CCACACCTGTTTCACACTC 476

RESULT 50

US-09-925-065A-523204/c
; Sequence 523204, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 523204
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-523204

Query Match 82.2%; Score 14.8; DB 7; Length 568;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 493 CCACACCTGTTTCACACTC 476

RESULT 51

US-10-301-480-237818/c
; Sequence 237818, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237818
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-237818

Query Match 82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
Db 125 CCACACCTATTTCGTACAC 108

RESULT 52

```
US-10-301-480-237819/c
; Sequence 237819, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 237819
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-237819

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
Db 125 CCACACCTTATTCGTACAC 108

RESULT 53
US-10-301-480-851227/c
; Sequence 851227, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 851227
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-851227

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
Db 125 CCACACCTTATTCGTACAC 108

RESULT 54
US-10-301-480-851228/c
; Sequence 851228, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 851228
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-851228

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
Db 125 CCACACCTTATTCGTACAC 108

RESULT 55
US-09-925-065A-630983/c
; Sequence 630983, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630983
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-630983

Query Match      82.2%; Score 14.8; DB 7; Length 584;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
Db 309 CCATTCTTATTCATCTC 292

RESULT 56
US-09-925-065A-305234/c
; Sequence 305234, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
```

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US-10-301-480-237819/c
; Sequence 237819, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 851228
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-851228

Query Match      82.2%; Score 14.8; DB 12; Length 570;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
Db 125 CCACACCTTATTCGTACAC 108

RESULT 55
US-09-925-065A-630983/c
; Sequence 630983, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630983
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-630983

Query Match      82.2%; Score 14.8; DB 7; Length 584;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTTATTCATCTC 18
Db 309 CCATTCTTATTCATCTC 292

RESULT 56
US-09-925-065A-305234/c
; Sequence 305234, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 305234
; LENGTH: 589
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-305234

Query Match      82.2%; Score 14.8; DB 7; Length 589;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
Db      292 CCACACCTATTTCACAC 275

RESULT 57
US-10-301-480-381253/c
; Sequence 381253, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 381253
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-381253

Query Match      82.2%; Score 14.8; DB 12; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
Db      292 CCACACCTATTTCACAC 275

RESULT 58
US-10-301-480-994662/c
; Sequence 994662, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
```

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 994662
; LENGTH: 599
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-994662

Query Match      82.2%; Score 14.8; DB 12; Length 599;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
Db      292 CCACACCTATTTCACAC 275

RESULT 59
US-09-925-065A-614773
; Sequence 614773, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 614773
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614773

Query Match      82.2%; Score 14.8; DB 7; Length 606;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCACACCTATTTCATCTC 18
Db      367 CCACACCTATTTCACAC 384

RESULT 60
US-09-925-065A-614777
; Sequence 614777, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
```

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 614777
; LENGTH: 606
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-614777

Query Match 82.2%; Score 14.8; DB 7; Length 606;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACACCTATTTCATCTC 18
||| ||||| |||
Db 367 CCACACCTATTTCACAC 384

Search completed: May 10, 2006, 20:40:19
Job time : 685 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 12, 2006, 06:55:35 ; Search time 16293 Seconds
(without alignments)
17447.622 Million cell updates/sec

Title: SEQ1-4500-9500-7328G

Perfect score: 4997.8

Sequence: 1 ctggcatctcagttctttt.....tttagaccagcctggaaca 5001

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_cm.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4997.8	100.0	8368	8	AY438977 Homo sapi
2	4997.8	100.0	122302	8	AC003982 Homo sapi
3	4986	99.8	13612	6	AX377239 Sequence
4	4961.8	99.3	220384	14	AC078926 Homo sapi
5	2690.8	53.8	3375	8	HUMPLA2A1
6	2226.2	44.5	189729	14	AC073930 Homo sapi
7	558.6	11.2	99370	8	AC005057 Homo sapi
8	547.8	11.0	162240	14	AC145756 Pan trogl
9	534.4	10.7	161716	8	AC087434 Pan trogl
10	524.2	10.5	121272	14	AC004956 Homo sapi
11	513.6	10.3	183798	14	AC145523 Papio ham
12	499.8	10.0	158595	8	AC010614 Homo sapi
13	499.8	10.0	189534	14	AL354656 Homo sapi
14	496.6	9.9	57320	8	AY886519 Homo sapi
15	496.6	9.9	133391	8	HSDJ315G1
16	481.8	9.6	147330	8	AC008753 Homo sapi
17	481.6	9.6	189056	14	AC017052 Homo sapi
18	473.8	9.5	43242	8	AC145647 Homo sapi

19	473	9.5	171585	14	AC148301	AC148301 Pan trogl
20	472.4	9.5	201197	14	HS424712	Z82207 Homo sapien
21	465	9.3	45858	8	AC006123	AC006123 Homo sapi
22	463.4	9.3	110000	14	AC004085_2	Continuation (3 of
23	463.4	9.3	114842	8	AC002996	AC002996 Homo sapi
24	462.6	9.3	178887	14	AC068981	AC068981 Homo sapi
25	462.6	9.3	190162	8	AC009244	AC009244 Homo sapi
26	462	9.2	222759	14	AC073177	AC073177 Homo sapi
27	461.4	9.2	134957	8	HSJ930L11	AL049759 Human DNA
28	461	9.2	207441	14	AC140719	AL040719 Homo sapi
29	460.6	9.2	123192	14	AP000589	AP000589 Homo sapi
30	460.4	9.2	150266	8	AC022408	AC022408 Homo sapi
31	460.2	9.2	60153	8	AC025574	AC025574 Homo sapi
32	459.4	9.2	167996	8	AC021753	AC021753 Homo sapi
33	457.4	9.2	4119	14	AC138418	AC138418 Homo sapi
34	457.4	9.2	137693	8	AC003689	AC003689 Homo sapi
35	456.2	9.1	201460	8	AP003721	AP003721 Homo sapi
36	452.4	9.1	123851	8	AC113410	AC113410 Homo sapi
37	452.2	9.0	179087	14	AC069489	AC069489 Homo sapi
38	451.4	9.0	112646	8	AC010240	AC010240 Homo sapi
39	451.2	9.0	195986	14	AC115933	AC115933 Papio anu
40	451	9.0	164394	8	AC008706	AC008706 Homo sapi
41	449.2	9.0	134210	8	AC005052	AC005052 Homo sapi
42	447.8	9.0	131943	8	AC005484	AC005484 Homo sapi
43	447.8	9.0	136119	8	HS1028D15	AL121886 Human DNA
44	447.8	9.0	186197	14	AL627384	AL627384 Homo sapi
45	446.2	8.9	13001	8	AC087314	AC087314 Homo sapi
46	446.2	8.9	163681	8	AL136992	AL136992 Human DNA
47	445.8	8.9	82171	8	AC036164	AC036164 Homo sapi
48	445.6	8.9	98697	8	AC004854	AC004854 Homo sapi
49	445	8.9	117336	8	AC093171	AC093171 Homo sapi
50	445	8.9	191986	14	AC159023	AC159023 Pan trogl
51	444.4	8.9	126990	8	HS73M23	AL031230 Human DNA
52	442.6	8.9	91927	8	AC004771	AC004771 Homo sapi
53	442.4	8.9	140666	8	AC120114	AC120114 Homo sapi
54	442.4	8.9	157481	8	AC093512	AC093512 Homo sapi
55	442	8.8	208726	8	AP006287	AP006287 Homo sapi
56	441.8	8.8	199045	14	AC149081	AC149081 Pan trogl
57	441.8	8.8	200430	8	AC011500	AC011500 Homo sapi
58	441	8.8	202544	8	AC104447	AC104447 Homo sapi
59	440.4	8.8	163704	14	AC141415	AC141415 Pan trogl
60	439.4	8.8	180076	14	AC022177	AC022177 Homo sapi
61	439.2	8.8	190185	8	AC026464	AC026464 Homo sapi
62	439.2	8.8	196220	8	AC026474	AC026474 Homo sapi
63	439	8.8	125638	8	AC004706	AC004706 Homo sapi
64	438.8	8.8	186959	8	AY191612	AY191612 Pan trogl
65	438.8	8.8	201227	14	AC160565	AC160565 Pan trogl
66	437.8	8.8	185574	14	AC161822	AC161822 Pan trogl
67	437	8.7	185909	8	AL590434	AL590434 Human DNA
68	436.2	8.7	195646	8	AC093709	AC093709 Pan trogl
69	435.8	8.7	203790	8	AC010422	AC010422 Homo sapi
70	435.6	8.7	182547	8	AP001201	AP001201 Homo sapi
71	435	8.7	119043	8	AC139451	AC139451 Homo sapi
72	435	8.7	163542	14	AC129071	AC129071 Pan trogl
73	435	8.7	166941	14	AC008049	AC008049 Homo sapi
74	434.8	8.7	96995	8	AC008149	AC008149 Homo sapi
75	434.8	8.7	147364	8	AC110598	AC110598 Homo sapi
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77	434.2	8.7	152659	8	AL591503	AL591503 Human DNA
78	434	8.7	40634	8	AC005305	AC005305 Homo sapi
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88	432.6	8.7	156933	8	AC020750	AC020750 Homo sapi
89	432.2	8.6	81117	8	AC016898	AC016898 Homo sapi
90	432.2	8.6	192961	8	AP002770	AP002770 Homo sapi
91	432	8.6	153392	8	AL133548	AL133548 Human DNA

92	432	8.6	171779	14	AC150825	Callithri	AC150825	ORGANISM	Homo sapiens
93	432	8.6	235183	14	AC160951	Colobus g	AC160951		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C 94	431.4	8.6	214031	14	AC160952	Colobus g	AC160952		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
C 95	431	8.6	185664	8	AC093249	Homo sapi	AC093249		Hominidae; Homo.
C 96	430.8	8.6	44062	8	AC004517	Homo sapi	AC004517	REFERENCE	1 (bases 1 to 8368)
C 97	430.8	8.6	118396	8	AC004518	Homo sapi	AC004518	AUTHORS	Rieder M.J., Livingston,R.J., Daniels,M.R., Chung,M.-W.,
C 98	430.8	8.6	162701	14	AC073317	Homo sapi	AC073317		Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L., Robertson,P.D.,
99	430.8	8.6	207950	14	AC106886	Homo sapi	AC106886		Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and Nickerson,D.A.
C 100	430.6	8.6	41613	8	AC004790	Homo sapi	AC004790	TITLE	Direct Submission
C 101	430.6	8.6	174304	8	AL450327	Human DNA	AL450327	JOURNAL	Submitted (16-OCT-2003) Genome Sciences, University of Washington,
C 102	430	8.6	174389	14	AC160950	Papio ham	AC160950		1705 NE Pacific, Seattle, WA 98195, USA
C 103	429.8	8.6	156503	8	AC011511	Homo sapi	AC011511	COMMENT	To cite this work please use: NIHGS-SNPs, Environmental Genome
C 104	429.8	8.6	172963	8	AC134866	Homo sapi	AC134866		Project, NIHES E515478, Department of Genome Sciences, Seattle, WA
C 105	429.2	8.6	129577	8	AC004659	Homo sapi	AC004659	FEATURES	(URL: http://egp.gs.washington.edu).
106	429	8.6	167357	8	CNS01DWY	Human chr		source	Location/Qualifiers
107	429	8.6	220206	14	AC140726	Homo sapi	AC140726		1..8368
C 108	428.6	8.6	113744	14	AC008884	Homo sapi	AC008884		/organism="Homo sapiens"
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C 111	428	8.6	163427	8	AC090953	Homo sapi	AC090953	repeat_region	101..257
C 112	427.6	8.6	107320	14	AC011391	Homo sapi	AC011391		/rpt_family="MIR"
113	427.6	8.6	120584	8	AC011342	Homo sapi	AC011342	variation	205
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115	427	8.5	198821	8	AC120057	Homo sapi	AC120057		/frequency="0.01"
C 116	427	8.5	230552	8	AC005098	Homo sapi	AC005098	variation	/replace="a"
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C 120	426.4	8.5	193953	14	AC149623	Papio anu	AC149623	repeat_region	326..538
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C 126	425.2	8.5	125377	14	AC118135	Homo sapi	AC118135	mRNA	/gene="PLA2G1B"
C 127	425.2	8.5	181442	14	AC134875	Homo sapi	AC134875		Join(875..944,2644..2803,3603..3730,6347..6548)
C 128	425.2	8.5	218485	14	AC127470	Pan trogl	AC127470		/gene="PLA2G1B"
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C 133	424.2	8.5	143737	8	AC004867	Homo sapi	AC004867		/product="phospholipase A2, group IB (pancreas)"
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C 135	424.2	8.5	275197	8	AC004166	Homo sapi	AC004166		/db_xref="GI:37953285"
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C 138	423.6	8.5	98117	8	AC003688	Homo sapi	AC003688		AITCSSKNKECAFICNCDRNAICFSKAPYNKAHNLDTKKYCS"
C 139	423.6	8.5	154791	14	AC065933	Homo sapi	AC065933	repeat_region	1174..1307
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C 141	423.4	8.5	152033	8	AC027319	Homo sapi	AC027319		/rpt_type=dispersed
C 142	423.4	8.5	153148	14	AC017030	Homo sapi	AC017030		1286
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C 147	423	8.5	192462	8	CNS01RHC	Human chr			/rpt_family="Alu"
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ALIGNMENTS

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LOCUS Homo sapiens phospholipase A2, group IB (pancreas) (PLA2G1B) gene,
complete cds.
AY438977
ACCESSION AY438977 GI:37953284
VERSION
KEYWORDS
SOURCE Homo sapiens (human)

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RESULT 2
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DEFINITION AC003982
ACCESSION AC003982.1 GI:2769695
VERSION HTG.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominoidea; Homo.
1 (bases 1 to 122302)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
9847074
2 (bases 1 to 122302)
Bradehaw, H., Wu, X. and Ozersky, P.
The sequence of Homo sapiens PAC clone 166H1
Unpublished (1999)
3 (bases 1 to 122302)
Waterston, R.
Direct Submission
Submitted (13-JAN-1998) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 122302)
Waterston, R.
Direct Submission
Submitted (18-MAR-1999) Department of Genetics, Washington
University, 444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY: WUGSC
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:sapiens@watson.wustl.edu

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
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from more than one subclones; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

This clone was originally isolated in the laboratory of Professor Graeme Bell, Howard Hughes Medical Institute and Departments of Biochemistry and Molecular Biology, and Medicine, The University of Chicago, Chicago, IL, USA. The clone was provided by the laboratory of Dr. Roger Cox at The Wellcome Trust Centre For Human Genetics, Oxford, UK. Some contig information was also obtained from Yamagata et al., Nature 384:455-8 (1996).

SOURCE INFORMATION:

This clone was derived from human PAC library RPCI-1, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc.

(<http://www.genomesystems.com>) or Research Genetics, Inc.

(<http://www.resgen.com>); or from Pieter de Jong.

VECTOR: pCYPAC2

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is 278C19; the clone sequenced to the right is 15E1. Actual start of this clone is at base position 1 of 166H1; actual end is at 122302 of 166H1.

FEATURES

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DEFINITION	Sequence 1 from Patent WO0212562.		
ACCESSION	AX377239		
VERSION	AX377239.1		
KEYWORDS	GI:19573528		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Kazemi,A., Kliem,S.E. and Koshy,B.		
AUTHORS	Haplotypes of the pla2g1b gene		
TITLE	Patent: WO 0212562-A 1 14-FEB-2002;		
JOURNAL	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.		
LINEAR	PAT 18-MAR-2002		

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Best Local Similarity 99.8%; Pred. No. 0;				
Matches 4991; Conservative 10; Mismatches 0; Indels 1; Gaps 1;				
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C 94	380.4	7.6	183610	10	ADB96923	Human MDR
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C 103	378.4	7.6	32204	4	Aai57790	Human col
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C 106	378.4	7.6	32204	9	ADB32580	Human nov
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C 111	377.6	7.6	48509	13	ABd33397	Human can
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C 113	375.6	7.5	221600	14	ADx80720	Human neu
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C 115	374.6	7.5	17185	4	Aak75628	Human imm
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C 118	374.2	7.5	12683	4	Aai98939	Human exc
C 119	374.2	7.5	12683	5	Aai63289	Human kid
C 120	374.2	7.5	58845	11	ACN43874	Human gen
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C 125	374	7.5	160552	4	AAD02697	Human gly
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C 127	372.8	7.5	30265	13	ACN37210	Human per
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C 129	372.8	7.5	52677	11	ACN43934	Human gen
C 130	372.8	7.5	87320	14	ADJ12863	Human can
C 131	372.2	7.4	32152	4	Aak89020	Human dig
C 132	372.2	7.4	32152	4	Aak91534	Human dig
C 133	372.2	7.4	32152	4	Aai57791	Human col
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C 145	370.8	7.4	149671	6	ABK84797	Human cdN
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C 148	370.6	7.4	16183	4	Aak74819	Human imm
C 149	370	7.4	22801	14	ADz59535	Secondary
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ALIGNMENTS

RESULT 1
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ID ADJ09983 standard; DNA; 12174 BP.

XX AC ADJ09983
XX AC
XX AC
DT 17-JUN-2004 (first entry)
XX DE Human phospholipase A2 (PLA2G1B) DNA SeqID 1.
XX DE

KW	human; gene; ds; fat reduction; fat deposition; phospholipase A2; PLA2G1B; chromosome 12q24; single nucleotide polymorphism; SNP; appetite suppressant; lipase inhibitor; exercise regimen; obesity; non-insulin dependent diabetes mellitus; NIDDM; cardiovascular disorder; hypertension; antidiabetic.
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XX	08-JAN-2004.
XX	27-JUN-2003; 2003WO-US020831.
XX	27-JUN-2002; 2002US-0392362P.
XX	(SEQU-) SEQUENOM INC.
XX	Adam GIR, Langdown ML, Denissenko MF, Dennis E, Cantor C;
XX	Rubin B;
XX	WPI; 2004-071944/07.
XX	P-PSDB; ADJ09984.
XX	Identifying a candidate therapeutic for fat reduction, useful for treating diabetes, by introducing a test molecule to a system comprising PLA2G1B protein or nucleic acid, and determining the presence of PT interaction between the compounds.
XX	

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Qy 1861 TGGAAATACAACAACACTAGCGGTGCTACTGTGGCTTGGGGGCTCAGGCACCCCCGTGGATG 1920
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Qy 2881 TATCAATTTCTAGTTGGTTCTCAGTAGCGCGGGGAAATATATAGTAACACAGCCATGAT 2940
Dbb 7380 TATCAATTTCTAGTTGGTTCTCAGTAGCGCGGGGAAATATATAGTAACACAGCCATGAT 7439

Qy 2941 TTAGTGTAAATTTTCTTGGTTCTGGSCAGTGTCTCCTTTAAATCCTCAGAACCAACTATG 3000
Dbb 7440 TTAGTGTAAATTTTCTTGGTTCTGGSCAGTGTCTCCTTTAAATCCTCAGAACCAACTATG 7499
Qy 3001 GGATAGGTACAAATTTATCTCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGCTGAGCT 3060
Dbb 7500 GGATAGGTACAAATTTATCTCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAGCTGAGCT 7559
Qy 3061 ATTTGCCCAAGATACACAGCTTGTAAAGTGTGACAGTTTGGGTTTTTTTTTGTGTGT 3120
Dbb 7560 ATTTGCCCAAGATACACAGCTTGTAAAGTGTGACAGTTTGGGTTTTTTTTTGTGTGT 7619
Qy 3121 TTAGAGACAGGGCTTGTCTCTCACCCAGGCATGAGCACAGTGTGTGCAACCATAGGTCA 3180
Dbb 7620 TTAGAGACAGGGCTTGTCTCTCACCCAGGCATGAGCACAGTGTGTGCAACCATAGGTCA 7679
Qy 3181 CTGACGCTCAACCTCTGAGCTCAAGGATCTGTGACCTCAGCCTCCCAAGTAGCTGG 3240
Dbb 7680 CTGACGCTCAACCTCTGAGCTCAAGGATCTGTGACCTCAGCCTCCCAAGTAGCTGG 7739
Qy 3241 GACTAGAGCTGACACACCGCTGCTTAATAAAAAATTTTGTGTAGAGACTGG 3300
Dbb 7740 GACTAGAGCTGACACACCGCTGCTTAATAAAAAATTTTGTGTAGAGACTGG 7799
Qy 3301 TCTTACTAGTTGGCCAGGCTTGTCTTAACTCTCTGGCTTCAAGCAATCTCTCTACTTTG 3360
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Qy 3421 CATTCATCTTCCAAATAGAAATGAAGTCCACAGAACAGGAGTTACTGCCTATTTCTT 3480
Dbb 7920 CATTCATCTTCCAAATAGAAATGAAGTCCACAGAACAGGAGTTACTGCCTATTTCTT 7979
Qy 3481 CCTTTCTTTTGTAGACAGAGTCTCACTTTCATCACTCAACCTCGTTCAGCTCACTGCA 3540
Dbb 7980 CCTTTCTTTTGTAGACAGAGTCTCACTTTCATCACTCAACCTCGTTCAGCTCACTGCA 8039
Qy 3541 ACCTCTGCCCTCCCGGTTCAAGYATTCCTCGCTCAAGCCTCCTGAGTAGTGGAATTA 3600
Dbb 8040 ACCTCTGCCCTCCCGGTTCAAGCGATTCCTCGCTCAAGCCTCCTGAGTAGTGGAATTA 8099
Qy 3601 CAAGGTGACACACATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTAC 3660
Dbb 8100 CAAGGTGACACACATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTAC 8159
Qy 3661 CATGTTGCCCGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCTCGCTCAGTCTCC 3720
Dbb 8160 CATGTTGCCCGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCTCGCTCAGTCTCC 8219
Qy 3721 CAAAGTGTGGAATTAATAGGCTGAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTT 3780
Dbb 8220 CAAAGTGTGGAATTAATAGGCTGAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTT 8279
Qy 3781 TATTGCTATATCCAGAGTCTAGACAGTGTCTGACATATAGTAGTGTCTCAATAATAA 3840
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Dbb 8340 TTTGATGAATGACAGCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTGACA 8399
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Db 8760 ACTTTGGAAGTCAAGGTGGTGGATCACTTGAGGTGAGAAGTTCAGACACAGCCTGGTTC 8819
QY 4321 AATATGCTGAACCCCTATCTCTACTAAATAACAAAATTAAGCTGGTGTAGTGATGCAT 4380
Db |||||
Db 8820 AATATGCTGAACCCCTATCTCTACTAAATAACAAAATTAAGCTGGTGTAGTGATGCAT 8879
QY 4381 GCCTGTAGTCCCACTACTCGGAGGCTGAGGCAAGAGAAATTCCTTGAACCTGGGAGGCA 4440
Db |||||
Db 8880 GCCTGTAGTCCCACTACTCGGAGGCTGAGGCAAGAGAAATTCCTTGAACCTGGGAGGCA 8939
QY 4441 GAGGTTGAGTGAGCGGAGATCCACACTGCACTCCAGCTGGGCGACACAGCGAGACT 4500
Db |||||
Db 8940 GAGGTTGAGTGAGCGGAGATCCACACTGCACTCCAGCTGGGCGACACAGCGAGACT 8999
QY 4501 CTATCTCAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACCTAATAAGAT 4560
Db |||||
Db 9000 CTATCTCAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACCTAATAAGAT 9059
QY 4561 TCCTGAAGGTGAAGCAGAGATACGTAATATATGTAATAAGTTTAAATGCAATTTAACT 4620
Db |||||
Db 9060 TCCTGAAGGTGAAGCAGAGATACGTAATATATGTAATAAGTTTAAATGCAATTTAACT 9119
QY 4621 GTAATCTATTTGTTTATTTTGGTTTAAAGTAACAAGCCAAAGTAATGCAACTTCAA 4680
Db |||||
Db 9120 GTAATCTATTTGTTTATTTTGGTTTATAAAGTAACAAGCCAAAGTAATGCAACTTCAA 9179
QY 4681 ACKTACATAAATATCTATTATGGAAGTGGAAGGATCTATAATCTTACTACCCAAAGA 4740
Db |||||
Db 9180 ACTCTACATAAATATCTATTATGGAAGTGGAAGGATCTATAATCTTACTACCCAAAGA 9239
QY 4741 TAACCAAGTTACATATTCCTCCAGATTTTGGGCGATACACTAGCTTTTTTTTATTTGGGAA 4800
Db |||||
Db 9240 TAACCAAGTTACATATTCCTCCAGATTTTGGGCGATACACTAGCTTTTTTTTATTTGGGAA 9299
QY 4801 AATTTTCATGTGAGGATACCTAATTTTCTAAATGCTATGATAGTATTCATTTAAAG 4860
Db |||||
Db 9300 AATTTTCATGTGAGGATACCTAATTTTCTAAATGCTATGATAGTATTCATTTAAAG 9359
QY 4861 ATGTTTCCATATTTTAAATAACATGCTTTTAAAGTAGAGAACTAGGTTGGGCGATGTCG 4920
Db |||||
Db 9360 ATGTTTCCATATTTTAAATAACATGCTTTTAAAGTAGAGAACTAGGTTGGGCGATGTCG 9419
QY 4921 CTCACGCTGTATCCAGCAGCTTTGGAGGCGGAGGCAATGGATCACTTTGAGGTCGGGA 4980
Db |||||
Db 9420 CTCACGCTGTATCCAGCAGCTTTGGAGGCGGAGGCAATGGATCACTTTGAGGTCGGGA 9479
QY 4981 GTTTGAGACCAAGCTGTGACAA 5001
Db |||||
Db 9480 GTTTGAGACCAAGCTGTGACAA 9500
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RESULT 2

ADI35082

ID ADI35082 standard; DNA; 12174 BP.

XX

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AC ADI35082;
XX 22-APR-2004 (first entry)
XX Human PLA2G1B nucleotide sequence.
XX PLA2G1B ; fat deposition; leanness; polymorphism;
KW non-insulin dependent diabetes mellitus; NIDDM; hyperinsulinemia;
KW hypertension; glucose intolerance; dyslipidemia; hypercoagulability;
KW microalbuminuria; human; gene; ds.
XX Homo sapiens.
OS WO2004002295-A2.
XX 08-JAN-2004.
XX 27-JUN-2003; 2003WO-US020830.
XX 27-JUN-2002; 2002US-0392361P.
XX (SEQU-) SEQUENOM INC.
PI Adam GIR, Langdown ML;
XX WPI; 2004-082843/08.
DR P-PSDB; ADI35083.
XX
PT Diagnosing a predisposition to fat deposition or leanness, useful for
PT diagnosing a predisposition to e.g. diabetes or hypertension, comprises
PT detecting the presence of a polymorphism in the PLA2G1B nucleic acid from
PT the subject.
XX Claim 1; SEQ ID NO 1; 91pp; English.
XX The invention relates to diagnosing a predisposition to fat deposition or
CC leanness in a subject comprising detecting the presence or absence of a
CC polymorphic variation associated with fat deposition at a polymorphic
CC site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a
CC subject, where the presence of the polymorphic variation indicates a
CC predisposition to fat deposition in the subject. The polymorphic
CC variation is a guanine at position 7328 or thymine at position 9182 of
CC the present sequence. The method is useful for diagnosing a
CC predisposition to fat deposition or leanness in a subject, and
CC subsequently for diagnosing a predisposition to non-insulin dependent
CC diabetes mellitus (NIDDM) in a subject and conditions such as
CC hyperinsulinemia, hypertension, glucose intolerance, dyslipidemia,
CC hypercoagulability, or microalbuminuria, which can lead to early
CC prescription of preventive measures. The present sequence represents a
CC human PLA2G1B nucleotide sequence.
XX Sequence 12174 BP; 3217 A; 2992 C; 2738 G; 3215 T; 0 U; 12 Other;
Query Match 100.0%; Score 4997.8; DB 12; Length 12174;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5000; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 CTGGTCATCTCAGTTCTTTTCTCAGCTTGACATGCAAGATGAACCTCTTGTGCTAGCTGT 60
Db |||||
Db 4500 CTGGTCATCTCAGTTCTTTTCTCAGCTTGACATGCAAGATGAACCTCTTGTGCTAGCTGT 4559
QY 61 GCTGCTCAGATGAGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAGCTA 120
Db |||||
Db 4560 GCTGCTCAGATGAGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAGCTA 4619
QY 121 AGATCTCACTCTCTGGAAATGGGGCCACAGGCCACAGCAACAGGATGGCCAGCCCG 180
Db |||||
Db 4620 AGATCTCACTCTCTGGAAATGGGGCCACAGGCCACAGCAACAGGATGGCCAGCCCG 4679
QY 181 CAGTCTCAAWTCGAGTTCCCAAGTGGGCTTAAAGGCTCCTCTATTGGGTTCCCTCAAG 240
Db |||||
Db 4680 CAGTCTCAAWTCGAGTTCCCAAGTGGGCTTAAAGGCTCCTCTATTGGGTTCCCTCAAG 4739
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Qy	241	GCTGGCACTTTTCAACCTCGAAGTCTGAAGTCTGAGTTCAGAAAGCTTGCC	300
Db	4740	GCTGGCACTTTTCAACCTCGAAGTCTGAAGTCTGAGTTCAGAAAGCTTGCC	4799
Qy	301	TTTATTTTCTTTTTCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTTCAGTGGCA	360
Db	4800	TTTATTTTCTTTTTCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTTCAGTGGCA	4859
Qy	361	TGATCATAGCTCACACAGCTTCAACTCTGGGGTCAAGTGATCTCCACCTTACTCA	420
Db	4860	TGATCATAGCTCACACAGCTTCAACTCTGGGGTCAAGTGATCTCCACCTTACTCA	4919
Qy	421	ACTAAGTAGTTCAGCCAACTCTCCCATTTATTTTATTTTATTTTATTTTATTTT	480
Db	4920	ACTAAGTAGTTCAGCCAACTCTCCCATTTATTTTATTTTATTTTATTTTATTTT	4979
Qy	481	TACTTTATTTTATTTTGGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG	540
Db	4980	TACTTTATTTTATTTTGGACGGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGTGGCG	5039
Qy	541	TGATCTCAGATCACTACAACTCTCATCTCTGGGTTCAAATAATTTCTTTGGCTCAGCCT	600
Db	5040	TGATCTCAGATCACTACAACTCTCATCTCTGGGTTCAAATAATTTCTTTGGCTCAGCCT	5099
Qy	601	CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGSCACACACCACCTGCCAGCTAA	660
Db	5100	CTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGSCACACACCACCTGCCAGCTAA	5159
Qy	661	TTTTTTGTGTGTTTTTTTGGTAGACAGGTTTTTACCATGTTGGCCAGGCTGGGTGAC	720
Db	5160	TTTTTTGTGTGTTTTTTTGGTAGACAGGTTTTTACCATGTTGGCCAGGCTGGGTGAC	5219
Qy	721	CTCCCTTTAGATCTCCTCATCTGCTCTATTTCTTCCCTTCTTAATGCAAGTATCCAGT	780
Db	5220	CTCCCTTTAGATCTCCTCATCTGCTCTATTTCTTCCCTTCTTAATGCAAGTATCCAGT	5279
Qy	781	TTCTCTACTTATCACATTTATTTATTTCTTATTTATTTAGACAGAGTCTTGCTTTGT	840
Db	5280	TTCTCTACTTATCACATTTATTTATTTCTTATTTATTTATTTAGACAGAGTCTTGCTTTGT	5339
Qy	841	CGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCATCTGCAAGCTCCAACCTCGGGTT	900
Db	5340	CGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCATCTGCAAGCTCCAACCTCGGGTT	5399
Qy	901	CAGGCCATTTCCGGCTCAGGCTCCCGCTAGCTGGGACTAAAGGGCTGCCACACG	960
Db	5400	CAGGCCATTTCCGGCTCAGGCTCCCGCTAGCTGGGACTAAAGGGCTGCCACACG	5459
Qy	961	CCCCGCTAAATTTTGTATTTTAAAGACGGGGTTTCATCGTGTAGCCAGGATGG	1020
Db	5460	CCCCGCTAAATTTTGTATTTTAAAGACGGGGTTTCATCGTGTAGCCAGGATGG	5519
Qy	1021	TCTCGATCTCATGACCTTGTGATCCGCTCGCTCGGCTCCCAAAGTGTGGGATTCACAG	1080
Db	5520	TCTCGATCTCATGACCTTGTGATCCGCTCGCTCGGCTCCCAAAGTGTGGGATTCACAG	5579
Qy	1081	GCATGACCAAGTCCCGGCTTATCACATTTATTTATTTATTTTCTCTCCCACTA	1140
Db	5580	GCATGACCAAGTCCCGGCTTATCACATTTATTTATTTATTTTCTCTCCCACTA	5639
Qy	1141	GGTTGTAAAGCTCCAATGAGTTTAGAGATTATTTATTTATTTATTTATTTATTTAT	1200
Db	5640	GGTTGTAAAGCTCCAATGAGTTTAGAGATTATTTATTTATTTATTTATTTATTTAT	5699
Qy	1201	TATTTATTTATTTCTGTTCACTGCTGATCTCTAGCTCCTAGGACAGAGCTGGCACAT	1260
Db	5700	TATTTATTTATTTCTGTTCACTGCTGATCTCTAGCTCCTAGGACAGAGCTGGCACAT	5759
Qy	1261	AGTAAGTGCTCAATAAATTTCACTGGATAAACAGTGCAGATAGTTTAAACTATCTGAC	1320
Db	5760	AGTAAGTGCTCAATAAATTTCACTGGATAAACAGTGCAGATAGTTTAAACTATCTGAC	5819
Qy	1321	CTAGGGAGGCTGAGGCAGGAGAAATGGCGTGAAACCCGGGAAGCAGAGTTTTCAGTGAAGCTG	1380

Db	5820	CTAGGGAGGCTGAGGCAGGAGAAATGCGCTGAACCCGGGAGCAGAGTTTTCAGTGAAGCTG	5879
Qy	1381	AAATCGTGTCACTGCACCTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA	1440
Db	5880	AAATCGTGTCACTGCACCTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA	5939
Qy	1441	AAAAAACTATCAGGCTAGCTGGGTGGCACATGCGCTGTAATCTAGCTAGGCGGTAGGG	1500
Db	5940	AAAAAACTATCAGGCTAGCTGGGTGGCACATGCGCTGTAATCTAGCTAGGCGGTAGGG	5999
Qy	1501	TCCCAAGAAAGAAAGAAAGAAAGAAAGAAAGATATATATATATATACACACACAA	1560
Db	6000	TCCCAAGAAAGAAAGAAAGAAAGAAAGAAAGATATATATATATATACACACACAA	6059
Qy	1561	GATATAAACTTTATATATATAAAGTTTTTCATTTAAAAAAAACCTCTACCCACTT	1620
Db	6060	GATATAAACTTTATATATATAAAGTTTTTCATTTAAAAAAAACCTCTACCCACTT	6119
Qy	1621	TCACITTTACCAGTTCTCGGGTCCAAACGCTCTTCAGAGGAGGACGCTGCGAGGGTCAAG	1680
Db	6120	TCACITTTACCAGTTCTCGGGTCCAAACGCTCTTCAGAGGAGGACGCTGCGAGGGTCAAG	6179
Qy	1681	GAGGACGCTGGGACCCCGAGGAGCAGGAAGACAGTGTCTCCCGGGGTGCTGGCAGACC	1740
Db	6180	GAGGACGCTGGGACCCCGAGGAGCAGGAAGACAGTGTCTCCCGGGGTGCTGGCAGACC	6239
Qy	1741	GATTTGAACTCTGGGCTATGTCTTTTGCAGTGGCGCGCCGCMCAGCGGCTACGCCCTC	1800
Db	6240	GATTTGAACTCTGGGCTATGTCTTTTGCAGTGGCGCGCCGCMCAGCGGCTACGCCCTC	6299
Qy	1801	GGGCGCTGGGAGTTCCGCAAAATGATCAAGTGGTGTATCCCGGGAGTGACCCCTT	1860
Db	6300	GGGCGCTGGGAGTTCCGCAAAATGATCAAGTGGTGTATCCCGGGAGTGACCCCTT	6359
Qy	1861	TGGAATACAACTACCGCTCTACTGTGGCTTGGGGGCTCAGGCACCCCGCTGGATG	1920
Db	6360	TGGAATACAACTACCGCTCTACTGTGGCTTGGGGGCTCAGGCACCCCGCTGGATG	6419
Qy	1921	AACTGGCAAGTAAAGTATCGCCTGCGAGGAAATTTGGAGTCCCTCGCGGGCGGGGTG	1980
Db	6420	AACTGGCAAGTAAAGTATCGCCTGCGAGGAAATTTGGAGTCCCTCGCGGGCGGGGTG	6479
Qy	1981	GGGACACGCCAAGGATCTCACAGGATACAAAGGGGACTTGCATATCTGCTAAGGATA	2040
Db	6480	GGGACACGCCAAGGATCTCACAGGATACAAAGGGGACTTGCATATCTGCTAAGGATA	6539
Qy	2041	ACATATTTTCACTCTTGTCAAATAAACAATATGTTCCAAGAGGACCTGTAGCGAACG	2100
Db	6540	ACATATTTTCACTCTTGTCAAATAAACAATATGTTCCAAGAGGACCTGTAGCGAACG	6599
Qy	2101	CACCCGTTTAGAGATGGAAAACATGACGACGTGCAAAAACAGTGGCGGATGTCGCCCTC	2160
Db	6600	CACCCGTTTAGAGATGGAAAACATGACGACGTGCAAAAACAGTGGCGGATGTCGCCCTC	6659
Qy	2161	AGTGGCAGAACTGACCAACAGTAAACATCACAGCAACTATCCACGTGTCATTTTCTAGCA	2220
Db	6660	AGTGGCAGAACTGACCAACAGTAAACATCACAGCAACTATCCACGTGTCATTTTCTAGCA	6719
Qy	2221	GTGGTTGTCACTGCACTTCTGAATACAGGATTTTATGTAATTTTGTGAACCATGTTAAA	2280
Db	6720	GTGGTTGTCACTGCACTTCTGAATACAGGATTTTATGTAATTTTGTGAACCATGTTAAA	6779
Qy	2281	AATCGCTTTAGGACAGGCGGCTGCTCATGCTGTAATCCAGCACTTTGGGAGGCGG	2340
Db	6780	AATCGCTTTAGGACAGGCGGCTGCTCATGCTGTAATCCAGCACTTTGGGAGGCGG	6839
Qy	2341	AGGCGGGGGGATCAGTTGAGGTTCAGAGTTTCAGAGCAGGCTGGCCAAACATGTTGAAACC	2400
Db	6840	AGGCGGGGGGATCAGTTGAGGTTCAGAGTTTCAGAGCAGGCTGGCCAAACATGTTGAAACC	6899
Qy	2401	CTGTCTCTACTAAAAAATAAAAAATTAGCCGGAATGCGCGGACATGCGCGAGCGCTGTAAACCCCA	2460

Qy	4621	GTAACTCTATTGTTTATTTGGTTATAAAGTAACAAGCCAAAGTAATGCAACTTCAA	4680
Db	9120	GTAACTCTATTGTTTATTTGGTTATAAAGTAACAAGCCAAAGTAATGCAACTTCAA	9179
Qy	4681	ACKTACATAAATATCTATTATGGAAGTGAAGGCATCTATATCTACTACCCAAAGA	4740
Db	9180	ACKTACATAAATATCTATTATGGAAGTGAAGGCATCTATATCTACTACCCAAAGA	9239
Qy	4741	TAACCAAGTTACATATTCCTCCAGATTTTGGGGCATACACTAGCTTTTTTTATTCGGAA	4800
Db	9240	TAACCAAGTTACATATTCCTCCAGATTTTGGGGCATACACTAGCTTTTTTTATTCGGAA	9299
Qy	4801	AATTTCCATGTCGAGGCATACCTAAATTTTCTAAATGCTCTATCTAGTATTCATTTAAG	4860
Db	9300	AATTTCCATGTCGAGGCATACCTAAATTTTCTAAATGCTCTATCTAGTATTCATTTAAG	9359
Qy	4861	ATGTTCCATATATTTTAAAAATACATGCTTTTAAAGTAGAGAAACTAGTTGGCATGGTG	4920
Db	9360	ATGTTCCATATATTTTAAANATACATGCTTTTAAAGTAGAGAAACTAGTTGGCATGGTG	9419
Qy	4921	CTCAGCCTGTATCCAGCACTTTGGGAGCCGAGGCAAAATGGATCACCTTGAGTCCGGA	4980
Db	9420	CTCAGCCTGTATCCAGCACTTTGGGAGCCGAGGCAAAATGGATCACCTTGAGTCCGGA	9479
Qy	4981	GTTTGAGACCAGCTGGACAA	5001
Db	9480	GTTTGAGACCAGCTGGACAA	9500
RESULT 3			
ABK47376	ID ABK47376 standard; DNA; 13612 BP.		
XX	AC	ABK47376;	
XX	AC	ABK47376;	
XX	DT	18-JUN-2002 (first entry)	
XX	DE	Human Phospholipase A2, groupIB (PLA2G1B) gene.	
XX	KW	Human; db; gene; SNP; single nucleotide polymorphism; pancreatitis;	
XX	KW	pancreatic cancer; Phospholipase A2 groupIB; PLA2G1B; Gene therapy;	
XX	KW	haplotype; genotype; chromosome 12q23-q24.1; transgenic; drug screening.	
OS	OS	Homo sapiens.	
XX	XX		
FH	Key	Location/Qualifiers	
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FT		/label= SNP	
FT		/note= "Single nucleotide polymorphism"	
FT	variation	replace(3968,A)	
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FT	exon	4053..4086	
FT		/*tag= d	
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FT	intron	4087..5785	
FT		/*tag= e	
FT		/number= 1	
FT	exon	5786..5945	
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FT		/number= 2	
FT	intron	5946..6744	
FT		/*tag= g	
FT		/number= 2	
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FT		/*tag= h	
FT		/label= SNP	
FT		/note= "Single nucleotide polymorphism"	

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FT		/number= 3	
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FT		/*tag= j	
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FT		/note= "Single nucleotide polymorphism"	
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FT		/note= "Single nucleotide polymorphism"	
FT	XX		
PN	WO200212562-A2.		
XX	14-FEB-2002.		
PD			
XX	06-AUG-2001; 2001WO-US024663.		
PF			
XX	04-AUG-2000; 2000US-0223179P.		
PR			
XX	(GENA-) GENAISSANCE PHARM INC.		
PA			
XX			
PI	Kazemi A, Kliem SE, Koshy B;		
XX			
DR	WPI; 2002-303982/34.		
DR	P-PSDB; AAU78667.		
XX			
PT	Novel isolated human Phospholipase A2, Group IB pancreas polynucleotide,		
PT	for therapeutic purposes, for studying expression and function of the		
PT	polynucleotide and for expressing the phospholipase protein.		
XX	Claim 1; Fig 1; 5lpp; English.		
PS			
XX	The invention relates to an isolated human Phospholipase A2, Group IB		
CC	(pancreas) (PLA2G1B) polynucleotide comprising a sequence which is a		
CC	polymorphic variant for a reference sequence for the PLA2G1B gene or its		
CC	fragment, or a polymorphic variant of a reference sequence for a PLA2G1B		
CC	CDNA or its fragment. Also included are haplotyping/genotyping the		
CC	PLA2G1B gene of an individual, predicting the haplotype pair for the		
CC	PLA2G1B gene of an individual, identifying an association between a trait		
CC	and at least one haplotype or haplotype pair of the PLA2G1B gene, an		
CC	isolated genotyping oligonucleotide for detecting a polymorphism in the		
CC	PLA2G1B gene, a recombinant non-human organism transformed or transfected		
CC	with the PLA2G1B sequence, where the organism expresses a PLA2G1B protein		
CC	encoded by the first nucleotide sequence or by the polymorphic variant		
CC	sequence, an isolated polypeptide comprising a sequence which is a		
CC	polymorphic variant of a reference sequence for the PLA2G1B protein or		
CC	its fragment, an anti-PLA2G1B monoclonal antibody, screening for drugs		
CC	targeting PLA2G1B, a computer system for storing and analysing		
CC	polymorphism data for the PLA2G1B gene and a genome anthology for PLA2G1B		
CC	gene. The PLA2G1B variant is useful in studying the expression and		
CC	function of PLA2G1B, and in expressing PLA2G1B protein for use in		
CC	screening for candidate drugs to treat diseases related to PLA2G1B		
CC	activity (e.g. pancreatitis and pancreatic cancer) and for therapeutic		
CC	purposes. The transgenic organism is useful for studying expression of		
CC	the PLA2G1B isogenes in vivo, for in vivo screening and testing of drugs		
CC	targeted against PLA2G1B protein, and for testing the efficacy of		
CC	therapeutic agents and compounds in a biological system. The antibody is		
CC	useful for studying the effect of the variation on the biological		
CC	activity of PLA2G1B as well as on the binding affinity of candidate drugs		
CC	targeting PLA2G1B. The present sequence is the PLA2G1B gene which is		
CC	located on chromosome 12q23-q24.1		
XX			
SQ	Sequence 13612 BP; 3637 A; 3290 C; 3070 G; 3615 T; 0 U; 0 Other;		
Query Match 99.8%; Score 4986.8; DB 6; Length 13612;			
Best Local Similarity 99.8%; Pred. No. 0;			

Matches 4993; Conservative 8; Mismatches 0; Indels 1; Gaps 1;			
Qy	1	CTGGTCATCTCAG-TTCTTTTCTCAGCTTGACCTGCAAGATGAACCTCTTGCTAGCTG	59
Db	4015	CTGGTCATCTCAGTTCTTTTCTCAGCTTGACCTGCAAGATGAACCTCTTGCTAGCTG	4074
Qy	60	TGCTGCTCACAGGTAGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAAGCT	119
Db	4075	TGCTGCTCACAGGTAGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTGAAGCT	4134
Qy	120	AAGATCTCACTCTCTGGAAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCC	179
Db	4135	AAGATCTCACTCTCTGGAAATGGGGCCACAGGCCACAGCAACAGGGATGGCCAGCC	4194
Qy	180	GCAAGTCTCAAWTCAGAGTTCCCAAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAA	239
Db	4195	GCAAGTCTCAAWTCAGAGTTCCCAAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCCTCAA	4254
Qy	240	GGCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCTGAGCTAAGAAAGCTTGC	299
Db	4255	GGCTGGCACTTTTCAACCTGCAAGTCTGAACTCAGATTGCTGAGCTAAGAAAGCTTGC	4314
Qy	300	CTTTATTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAAGTGC	359
Db	4315	CTTTATTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAAGTGC	4374
Qy	360	ATGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTC	419
Db	4375	ATGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTC	4434
Qy	420	AACCTAAGTAGTTAGGCAATCTCCCAATTTATTTTATTTTATTTTATTTTATTTTATTT	479
Db	4435	AACCTAAGTAGTTAGGCAATCTCCCAATTTATTTTATTTTATTTTATTTTATTTTATTT	4494
Qy	480	TTACTTTATTTTATTTTGAAGGGGCTCACTCTGTGGCCAGGCTGGAGTGGGTGGC	539
Db	4495	TTACTTTATTTTATTTTGAAGGGGCTCACTCTGTGGCCAGGCTGGAGTGGGTGGC	4554
Qy	540	GTGATCTCAGATCACTACACCTCCATCTCTGGGTTCAAATATTTCTTTGCTCAGCC	599
Db	4555	GTGATCTCAGATCACTACACCTCCATCTCTGGGTTCAAATATTTCTTTGCTCAGCC	4614
Qy	600	TCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCATGCCCCAGCTA	659
Db	4615	TCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCATGCCCCAGCTA	4674
Qy	660	ATTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTCACATGTTGGCCAGGCTGGGTGA	719
Db	4675	ATTTTGTGTGTTTTTTTGGTAGAGACAGGTTTTTCACATGTTGGCCAGGCTGGGTGA	4734
Qy	720	CTTCCCTTTTATGATTTCTCTCATCTGCTCTATTCTTCCCTTTCTAAATGCAATCCAG	779
Db	4735	CTTCCCTTTTATGATTTCTCTCATCTGCTCTATTCTTCCCTTTCTAAATGCAATCCAG	4794
Qy	780	TTTCTCTTACTTATCACATTTTATTTATTTCTTATTTATTTGAGACAGAGTCTTGCTTTG	839
Db	4795	TTTCTCTTACTTATCACATTTTATTTATTTCTTATTTATTTGAGACAGAGTCTTGCTTTG	4854
Qy	840	TCGCCAAGGCTGAGTACAGTGTGGATCTCGGCTCACTGCAAGCTTCACTGCTGGGT	899
Db	4855	TCGCCAAGGCTGAGTACAGTGTGGATCTCGGCTCACTGCAAGCTTCACTGCTGGGT	4914
Qy	900	TCACGCCATTCTCCGCTCAGCTCCCAAGTAGCTGGGACTAAAGCGCTGCCACAC	959
Db	4915	TCACGCCATTCTCCGCTCAGCTCCCAAGTAGCTGGGACTAAAGCGCTGCCACAC	4974
Qy	960	GCCCCGCTAAATTTTGTATTTTATTAAGAGCGGGTTTCTATCGTGTAGCCAGGATG	1019
Db	4975	GCCCCGCTAAATTTTGTATTTTATTAAGAGCGGGTTTCTATCGTGTAGCCAGGATG	5034
Qy	1020	GTCTCGATCTCATGACCTTGTGATTCGGCTCGCTCGGCTCCCAAGTGTGGGATTACA	1079
Db	5035	GTCTCGATCTCATGACCTTGTGATTCGGCTCGCTCGGCTCCCAAGTGTGGGATTACA	5094
Qy	1080	GGCATGAGCCACCGTGCCGGCTTATACATTTTATTTATTTATTTTCTCTCCACT	1139
Db	5095	GGCATGAGCCACCGTGCCGGCTTATACATTTTATTTATTTATTTTCTCTCCACT	5154
Qy	1140	AGGTTGTAACTCCATAGGTTAGAGATTTATTTATTTATTTATTTATTTATTTA	1199
Db	5155	AGGTTGTAACTCCATAGGTTAGAGATTTATTTATTTATTTATTTATTTATTTA	5214
Qy	1200	TTATTTATTTATTTATTTCTCTGCTGCTATCTCTAGCTCCTAGGACAGGCTGGCACA	1259
Db	5215	TTATTTATTTATTTATTTCTGCTGCTGCTATCTCTAGCTCCTAGGACAGGCTGGCACA	5274
Qy	1260	TAGTAAAGTCTCAATAAATTTTCACTGGGATAAAGTGCAGATAGTTTAAAACTATCTGA	1319
Db	5275	TAGTAAAGTCTCAATAAATTTTCACTGGGATAAAGTGCAGATAGTTTAAAACTATCTGA	5334
Qy	1320	CCTAGGGAGGCTGAGGACAGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGAGTGAGCT	1379
Db	5335	CCTAGGGAGGCTGAGGACAGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGAGTGAGCT	5394
Qy	1380	GAAATCGTGTCACTGCACCTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA	1439
Db	5395	GAAATCGTGTCACTGCACCTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAAAA	5454
Qy	1440	AAAAAACTATCAGGCTTAGCTGGGTGGCACATGCTGTAATCTCTAGCTGAGCGGTAGG	1499
Db	5455	AAAAAACTATCAGGCTTAGCTGGGTGGCACATGCTGTAATCTCTAGCTGAGCGGTAGG	5514
Qy	1500	GTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGATATATATATATATACACACAA	1559
Db	5515	GTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGATATATATATATATACACACAA	5574
Qy	1560	AGATATAAATTTTATATATATATAAAGTTTTCATTTAAAAAATAAATAAATAAATAAATAA	1619
Db	5575	AGATATAAATTTTATATATATATAAAGTTTTCATTTAAAAAATAAATAAATAAATAAATAA	5634
Qy	1620	TTTCACTTTTACCAAGTTTCTTGGGTCCAAACGGTCTTTCAGAGGAGGAGCTGGCAGGCTCAG	1679
Db	5635	TTTCACTTTTACCAAGTTTCTTGGGTCCAAACGGTCTTTCAGAGGAGGAGCTGGCAGGCTCAG	5694
Qy	1680	GGAGGAGGCTGGGACCCGAGGAGCAGAAAGGAGTGTGTCCCGGGGTGTGGCAGAC	1739
Db	5695	GGAGGAGGCTGGGACCCGAGGAGCAGAAAGGAGTGTGTCCCGGGGTGTGGCAGAC	5754
Qy	1740	CGATTTGAACCTCTGCTATGTCTTCTTGAGTGGCCGCGGAGCAGCGGCTCAGCCCT	1799
Db	5755	CGATTTGAACCTCTGCTATGTCTTCTTGAGTGGCCGCGGAGCAGCGGCTCAGCCCT	5814
Qy	1800	CGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGGTATCCCGGGGAGTGACCCCTTV	1859
Db	5815	CGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGGTATCCCGGGGAGTGACCCCTTV	5874
Qy	1860	TTTGAATACAACTTACGGCTGTCTGTGGTGTGGGGGTTCAGGCAACCCCGTGGAT	1919
Db	5875	TTTGAATACAACTTACGGCTGTCTGTGGTGTGGGGGTTCAGGCAACCCCGTGGAT	5934
Qy	1920	GAACTGGACAAAGTAAAGTATCCGCTGCAAGAAATTTGAGTGGCTTGGGGGGGGGT	1979
Db	5935	GAACTGGACAAAGTAAAGTATCCGCTGCAAGAAATTTGAGTGGCTTGGGGGGGGGT	5994
Qy	1980	GGGGCAGCAGCAAGGATCTCAGAGGATACAAAGGGGACTTGGCATATCTGCTAAGGAT	2039
Db	5995	GGGGCAGCAGCAAGGATCTCAGAGGATACAAAGGGGACTTGGCATATCTGCTAAGGAT	6054
Qy	2040	AACATATTTTCACTCTTGTCAAAATAAACAATATTTTCCAAAGAGACCTGTAGGCAAC	2099
Db	6055	AACATATTTTCACTCTTGTCAAAATAAACAATATTTTCCAAAGAGACCTGTAGGCAAC	6114
Qy	2100	GCACCCGTTAGAGTGGAAACAATGACCGCTGCAAAACAGTGGGCGATGCTGCCCTC	2159
Db	6115	GCACCCGTTAGAGTGGAAACAATGACCGCTGCAAAACAGTGGGCGATGCTGCCCTC	6174

QY 2160 CAGTGCAGAAATGAGCAACAGTAATAACATCACAGCAACTATCCACGCTGTCATTTCTAGC 2219
DB 6175 CAGTGGCAGAAATGAGCAACAGTAATAACATCACAGCAACTATCCACGCTGTCATTTCTAGC 6234
QY 2220 AGTGGTTGTCACTGCACCTTCTCTGAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAA 2279
DB 6235 AGTGGTTGTCACTGCACCTTCTGAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAA 6294
QY 2280 AAATCGTTTTCAGGCCAGCGCGGTGGCTCATCGCTGTAATCCAGCATTTGGGAGGCC 2339
DB 6295 AAATCGTTTTCAGGCCAGCGCGGTGGCTCATCGCTGTAATCCAGCATTTGGGAGGCC 6354
QY 2340 GAGCGCGCGGATCACTTGAGGTCAGAGTTCCAGACCAAGCTCGGCCAACATGGTGAAC 2399
DB 6355 GAGCGCGCGGATCACTTGAGGTCAGAGTTCCAGACCAAGCTCGGCCAACATGGTGAAC 6414
QY 2400 CCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCTGTAAACCCC 2459
DB 6415 CCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCGCTGTAAACCCC 6474
QY 2460 AGCTACTTGGGAGACTGAGTTGAGGTTTCAGTGAGCAAGGTCGTCACTGCTGTCCA 2519
DB 6475 AGCTACTTGGGAGACTGAGTTGAGGTTTCAGTGAGCAAGGTCGTCACTGCTGTCCA 6534
QY 2520 GCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTCAATAATATATGAT 2579
DB 6535 GCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTCAATAATATATGAT 6594
QY 2580 AAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTTGGCGAAGT 2639
DB 6595 AAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTTGGCGAAGT 6654
QY 2640 CATCCCCACCTGTCTCGAGAGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACT 2699
DB 6655 CATCCCCACCTGTCTCGAGAGTGGCAGGTGAGGCTGACCTATTGCTCTGCACTTACT 6714
QY 2700 CCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACATGACAACCTGTAYGA 2759
DB 6715 CCTATCTCAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGACATGACAACCTGTAYGA 6774
QY 2760 CCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMCCGTTACACCCACCTTA 2819
DB 6775 CCAGGCCAAGAAGCTGGACAGCTGTAAATTTCTGCTGGACAMCCGTTACACCCACCTTA 6834
QY 2820 TTCAATCTCGTGTCTGGCTCGCNAATCACTGTACGAGTAGGTTTATCCCTTCTTGTGAC 2879
DB 6835 TTCAATCTCGTGTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTGTGAC 6894
QY 2880 CTATGAATTTCTAGTTGGTTCTCAGTAGCGCGGGGAAATAATAGTAAACAACAGCCATGA 2939
DB 6895 CTATGAATTTCTAGTTGGTTCTCAGTAGCGCGGGGAAATAATAGTAAACAACAGCCATGA 6954
QY 2940 TTTAGTGTAAATTTTCTGTTCTGGCAGTGTCTCTTTTAACTCTCAGAACCAACTAT 2999
DB 6955 TTTAGTGTAAATTTTCTGTTCTGGCAGTGTCTCTTTTAACTCTCAGAACCAACTAT 7014
QY 3000 GGGATAGTCAATATTCCTCACTTAACAGATAGAAACTGAGGCTCAGAGGCTGAGC 3059
DB 7015 GGGATAGTCAATATTCCTCACTTAACAGATAGAAACTGAGGCTCAGAGGCTGAGC 7074
QY 3060 TATTTGCCCAAGATCACACAGCTTGAAGTGGTGACAGTTGGGTTTTTTTTTTGTTGTG 3119
DB 7075 TATTTGCCCAAGATCACACAGCTTGAAGTGGTGACAGTTGGGTTTTTTTTTTGTTGTG 7134
QY 3120 TTTAGAGACAGGTTCTGTCTGTCAACAGGATGAGCACAGTGGTGCAACCATAGGTC 3179
DB 7135 TTTAGAGACAGGTTCTGTCTGTCAACAGGATGAGCACAGTGGTGCAACCATAGGTC 7194
QY 3180 ACTGCAAGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAGCTCCCAAGTAGCTG 3239
DB 7195 ACTGCAAGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAGCTCCCAAGTAGCTG 7254
QY 3240 GGACTACGAGCGTGCAACCAAGCCCTGGCTAAATTAATAAATAATTTTTTTGTAGAGACTGG 3299

DB 7255 GGACTACGAGCGTGCAACCAAGCCCTGGCTAAATTAATAAATAATTTTTTTGTAGAGACTGG 7314
QY 3300 GTCTTTACTACGTTGGCGAGGCTTGTCTTAAACTCTCTGGCTTCAAGCAATCTCTTACCTT 3359
DB 7315 GTCTTTACTACGTTGGCGAGGCTTGTCTTAAACTCTCTGGCTTCAAGCAATCTCTTACCTT 7374
QY 3360 GGCATCCCAAGTGTGGGATTAAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTT 3419
DB 7375 GGCATCCCAAGTGTGGGATTAAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTT 7434
QY 3420 ACATTTCCATCTTTTCCAAATAGAAATGTAAGATCCACAGAACAGGGATTTACTGCTATTTTCT 3479
DB 7435 ACATTTCCATCTTTTCCAAATAGAAATGTAAGATCCACAGAACAGGGATTTACTGCTATTTTCT 7494
QY 3480 TCCTTTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCTCGTTCAGTCTACTGCG 3539
DB 7495 TCCTTTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCTCGTTCAGTCTACTGCG 7554
QY 3540 AACCTCTGCTCCCGGTTCAAGYATTTCTCTGCTGAAGCTCTCTGAGTAGCTGGAAT 3599
DB 7555 AACCTCTGCTCCCGGTTCAAGCGATTTCTCTGCTGAAGCTCTCTGAGTAGCTGGAAT 7614
QY 3600 ACAAGCGTGCAACCATGCTTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTTA 3659
DB 7615 ACAAGCGTGCAACCATGCTTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTTA 7674
QY 3660 CCATGTTGCCAGGCTGCTCAAACTCTGACCTCAAGTGATCTGCTGCTGCTCAGTCTC 3719
DB 7675 CCATGTTGCCAGGCTGCTCAAACTCTGACCTCAAGTGATCTGCTGCTGCTCAGTCTC 7734
QY 3720 CCATAAGTCGGAATTAAGGCGTGAGTCACCTGCTGCGCGATTTACTGCTTATTTTCT 3779
DB 7735 CCATAAGTCGGAATTAAGGCGTGAGTCACCTGCTGCGCGATTTACTGCTTATTTTCT 7794
QY 3780 TTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATATAGTAGTCTCAATAAATA 3839
DB 7795 TTATTTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATATAGTAGTCTCAATAAATA 7854
QY 3840 ATTGATGAATGACAGCCTAGATATAAATTTCTTTTCTTTTAAACAATCTTGAC 3899
DB 7855 ATTGATGAATGACAGCCTAGATATAAATTTCTTTTCTTTTAAACAATCTTGAC 7914
QY 3900 AACTTTGACAGATAAATAACAATCTTGCAATCTGCTTTTCTCACTTATCACTTGTATGAC 3959
DB 7915 AACTTTGACAGATAAATAACAATCTTGCAATCTGCTTTTCTCACTTATCACTTGTATGAC 7974
QY 3960 TTTTTCATATTCCTCAAACTTTATTTGTTACTGTTTTCATTTGTTACTATTTTAGTCA 4019
DB 7975 TTTTTCATATTCCTCAAACTTTATTTGTTACTGTTTTCATTTTCTTTTAAACAATCTTGAC 8034
QY 4020 CTGAATAATATGGCTTAATTTGCTTATACATCTCTGCTCCACTTTAGAGGCCAAAT 4079
DB 8035 CTGAATAATATGGCTTAATTTGCTTATACATCTCTGCTCCACTTTAGAGGCCAAAT 8094
QY 4080 TACAAATCTGATGAAGCTATGAACCTCTCCAGAGAGAAATACACACACACACACAC 4139
DB 8095 TACAAATCTGATGAAGCTATGAACCTCTCCAGAGAGAAATACACACACACACACAC 8154
QY 4140 TCACACACAGTTTTTTTTTAAATTTGTTGCAATTAAGCAAGAAACCTGCAATTAGAGGATGT 4199
DB 8155 TCACACACAGTTTTTTTTTAAATTTGTTGCAATTAAGCAAGAAACCTGCAATTAGAGGATGT 8214
QY 4200 TTGTTTCATATTAATTAATAATAACTCAGTTGGGCAAGTCAAGCTGTAAACACACAG 4259
DB 8215 TTGTTTCATATTAATTAATAATAACTCAGTTGGGCAAGTCAAGCTGTAAACACACAG 8274
QY 4260 TACTTTGGAGTCCCAAGGTTGGGTGATCACTTTGAGGTGAGAGTTCCGAGACCGCTGCT 4319
DB 8275 TACTTTGGAGTCCCAAGGTTGGGTGATCACTTTGAGGTGAGAGTTCCGAGACCGCTGCT 8334
QY 4320 CAATATGTTGAAACCCCTATCTCTACTAAATAATACAAAAATTAGCTGGGTGTAGTAGTCA 4379

8335 CAATATGGTGAACCCCTATCTCTCTATAAAAAATAGCTGGGTGATGCA 8394
4380 TGCTCTAGTCCAGCTACTCGGAGGCTGAGCAGAGAATTTGCTTGAACCTGGGAGC 4439
8395 TGCTCTAGTCCAGCTACTCGGAGGCTGAGCAGAGAATTTGCTTGAACCTGGGAGC 8454
4440 AGAGGTTGCAGTGAGCGAGATCCCACTGCTCCAGCTCGGCGGACACAGCGAGAC 4499
8455 AGAGGTTGCAGTGAGCGAGATCCCACTGCTCCAGCTCGGCGGACACAGCGAGAC 8514
4500 TCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAATAAAGA 4559
8515 TCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAAATAAAGA 8574
4560 TTCTCAAGGTAGCAGATAGTAAATTTATATGTAATAAAGTTTAAATGATTTTAA 4619
8575 TTCTCAAGGTAGCAGATAGTAAATTTATATGTAATAAAGTTTAAATGATTTTAA 8634
4620 TGTAAATCTTATTTGTTTATTTGTTTATAAAGTAAACAAAGCCAAAGTAATGCACTTCA 4679
8635 TGTAAATCTTATTTGTTTATTTGTTTATAAAGTAAACAAAGCCAAAGTAATGCACTTCA 8694
4680 AACKTACATAAATATCTATATGGAAGTGAAGGCATCTATATCTCTACTACCCAAAG 4739
8695 AACTCTACATAAATATCTATATGGAAGTGAAGGCATCTATATCTCTACTACCCAAAG 8754
4740 ATAACAGTTACATATCTCTCAGATTTTGGGGCATACACTAGCTTTTTTATTTGGGA 4799
8755 ATAACAGTTACATATCTCTCAGATTTTGGGGCATACACTAGCTTTTTTATTTGGGA 8814
4800 AAATTTCCATGTGCGAGCATACCTAATTTTCTAATGTCTATGTAGTATTCATTTAAG 4859
8815 AAATTTCCATGTGCGAGCATACCTAATTTTCTAATGTCTATGTAGTATTCATTTAAG 8874
4860 GATGTTCCATAATTTTAAATACATGCTTTAAAGTAGAGAACTAGGTGGGCATGGTG 4919
8875 GATGTTCCATAATTTTAAATACATGCTTTAAAGTAGAGAACTAGGTGGGCATGGTG 8934
4920 GCTCAGCCTGTATCCAGCAGCTTTGGGAGGCGGAGGAAATGGATCACTTCAGGTCGG 4979
8935 GCTCAGCCTGTATCCAGCAGCTTTGGGAGGCGGAGGAAATGGATCACTTCAGGTCGG 8994
4980 AGTTTGAGACCGCCTGGACAA 5001
8995 AGTTTGAGACCGCCTGGACAA 9016
RESULT 4
ID AAA35101 standard; DNA; 3375 BP.
XX AAA35101;
AC AAA35101;
XX 28-JUL-2000 (first entry)
XX Human adenosine receptor related polynucleotide SEQ ID NO:2790.
DE Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX Homo sapiens.
XX WO200009525-A2.
PN 24-FEB-2000.
XX 03-AUG-1999; 99WO-US017712.

03-AUG-1998; 98US-0095212P.
(UYEC-) UNIV EAST CAROLINA.
Nyce JW;
WPI; 2000-205971/18.
New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.
Disclosure; Page 1056-1057; 1343pp; English.
The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytosstatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukaemias, lymphomas, carcinomas, and cancers which may metastasise to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3232 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;
Query Match 53.8%; Score 2690.8; DB 3; Length 3375;
Best Local Similarity 98.5%; Pred No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;
QY 1 CTGGTCACTCAGTTCTTTTCTACCTTGACTGCAAGATGAAACTCTTTGCTAGCTGT 60
Db 500 CTGGTCACTCAGTTCTTTTCTACCTTGACTGCAAGATGAAACTCTTTGCTAGCTGT 559
QY 61 GCTGCTCAGTAGGCAAGTCTCCCGGCTCCACCGCTTTCTCTCCCAAGTGA 120
Db 560 GCTGCTCAGTAGGCAAGTCTCCCGGCTCCACCGCTTTCTCTCCCAAGTGA 619
QY 121 AGATCTCACTCTCTGGAATGGGGCCACAGCCACAGCAACAGGGATGGCCAGCCCG 180
Db 620 AGATCTCACTCTCTGGAATGGGGCCACA---CACAGCAACAGGGATGGCCAGCCCG 676
QY 181 CAGTCTCAAWTCGAGGTTCCCAAGTGGGGCTTAAGGGCTCTCTATTGGGGTTCCCTCAAG 240
Db 677 CAGTCTCAAWTCGAGGTTCCCAAGT---GGGCTTAAGGGCTCTCTATTGGGGTTCCCTCAAG 735
QY 241 GCTGCGACTTTTCAACCTGCAAGTCTGCACTGCAATGCTCCCTGAGCTAAGAAGCTGCC 300
Db 736 GCTGCGACTTTTCAACCTGCAAGTCTGCACTGCAATGCTCCCTGAGCTAAGAAGCTGCC 795
QY 301 TTTATTTCTTTTCCAGACAGGGTCTTGCTCTATACCCAGGCTGGAGTTCAAGTGCCA 360
Db 796 TTTATTTCTTTTCCAGACAGGGTCTTGCTCTATATACCCAGGCTGGAGTTCAAGTGCCA 855
QY 361 TGATCATAGTCAACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCCACCTTACTCA 420

Db 856 |||||TGATCATAGCTCACCAGACTTCCAACCTCGTGGGCTCAAGTGATCCTCCACCTTACTCA 915
Qy 421 ACTAAGTAGTAGGCAACTCCCACTTATTTTATTTATTTTATTTTAAATTTTATTTTATTTT 480
Db 916 ACTAAGTAGTAGGCAACTCCCACTTATTTTATTTTATTTTATTTTAAATTTTATTTTATTTT 975
Qy 481 TACTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 540
Db 976 TACTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1034
Qy 541 TGATCTCAGATCACTCAAACTCCATCTCCTCGGTTCAAATAATTTCTTTGGCTCAGCCT 600
Db 1035 TGATCTCAGATCACTCAAACTCCATCTCTCT-GGTTCAATAATTTCTTTGGCTCAGCCT 1093
Qy 601 CTCAAAGTAGCTGGACCTTGAGTCTCTCAAGTAGCTGGCACACACCACTATGCCAGCTAA 660
Db 1094 CTCAAAGTAGCT-GGACTTGTAGCTCTCAAGTAGCTGGCACACACCACTATGCCAGCTAA 1152
Qy 661 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 1153 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1212
Qy 721 CTCCTTTTAGATTCTCTCATCTGCTCTATTTCTTCCCTTTCT-AATGCAGTATCCAG 779
Db 1213 CTCCTTTTAGATTCTCTCATCTGCTCTATTTCTTCCCTTTCTAAATGCAGTATCCAG 1272
Qy 780 TTTCTCTTACTTATCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 839
Db 1273 TTTCTCTTACTTATACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1332
Qy 840 TCGCAGGCTGGAGTACAGTGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
Db 1333 TCGCAGGCTGGAGTACAGTGTGGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 1392
Qy 900 TCACGCCATTCTCCGCTCAGCCTCCCACTAGTGGACTAAAGCGCGCTGCCACCAC 959
Db 1393 TCACGCCATTCTCCGCTCAGCCTCCCACTAGTGGACTAAA-GCGCTGCCACCAC 1451
Qy 960 GCGCGCTAAATTTTGTATTTTAAATAAGAGGGGTTTCATGTTAGCCAGGATG 1019
Db 1452 GCGCGCTAAATTTTGTATTTTAAATAAGAGGGGTTTCATGTTAGCCAGGATG 1511
Qy 1020 GTCTCGATCTCATGACCTGTGATCGCGCTCGCTCCCAAGTGTGGGATTACA 1079
Db 1512 GTCTCGATCTCATGACCTGTGATCGCGCTCGCTCCCAAGTGTGGGATTACA 1569
Qy 1080 GGATAGCCACCGTGCCTGCGGCTTATCAATTTATTTATTTATTTATTTATTTATTTATTTATTT 1139
Db 1570 GGATAGCCACCGTGCCTGCGGCTTATCAATTTATTTATTTATTTATTTATTTATTTATTTATTT 1629
Qy 1140 AGGTTGTAAGCTCCATGAGGTTAGAG---ATTATTTATTTATTTATTTATTTATTTATTTATTT 1196
Db 1630 AGGTTGTAAGCTCCATGAGGTTAGAGTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1689
Qy 1197 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1256
Db 1690 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1749
Qy 1257 ACATAGTAAGTGTCAATAAATTTCACTGGATAAAGTGCAGATAGTTTAAAACTATC 1316
Db 1750 ACATAGTAAGTGTCAATAAATTTCACTGGATAAAGTGCAGATAGTTTAAAACTATC 1809
Qy 1317 TGACCTAGGAGGCTGAGGAGGAGATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA 1376
Db 1810 TGACCTAGGAGGCTGAGGAGGAGATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA 1869
Qy 1377 GCTGAATCGTGTCACTGTCACTCCAACTGGGCAACAGACCAAGACTCCATCTCAAAAAA 1436
Db 1870 GCTGAATCGTGTCACTGTCACTCCAACTGGGCAACAGACCAAGACTCCATCTCAAAAAA 1929
Qy 1437 AAAAAAATACTATCAGGCTAGCTGGGTGGCACATGCCCTGTAAATCCTAGCTGAGCGGT 1496
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Db 1930 AAAAAAATACTATCAGGCTAGCTGGGTGGCACATGCCCTGTAAATCCTAGCTGAGCGGT 1989
Qy 1497 AGGTTCCAGAGAAGAAGAAAGAAAGAGATATATATATATATATATATATATATATATATATATAT 1556
Db 1990 AGGTTCCAGAGAAGAAGAAAGAAAGAGATATATATATATATATATATATATATATATATATATAT 2049
Qy 1557 CAAAGATATAAACTTTTATATATATAAAGTTTTCATTTAAAAAATAAACTCTTACCC 1616
Db 2050 CAAAGATATAAACTTTTATATATAAAGTTTTCATTTAAAAAATAAACTCTTACCC 2108
Qy 1617 ACTTTTCACTTTACAGGTTCTGGGTCCAAACGGTCTTTCAGAGGAGCAGCTGGCAGGGT 1676
Db 2109 ACTTTTCACTTTACAGGTTCTGGGTCCAAACGGTCTTTCAGAGGAGCAGCTGGCAGGGT 2168
Qy 1677 CAGGAGGAGCGTGGGACCCGAGGAGCAGAAAGCAGTGTCCCGGGGTGCTGGCA 1736
Db 2169 CAGGAGGAGCGTGGGACCCGAGGAGCAGAAAGCAGTGTGTCCCGGGGTGCTGGCA 2228
Qy 1737 GACCGATTGAACTCTGGCTATGTCTTTTCAGTGGCCCGCCGCMCAGCGGCATCAGC 1796
Db 2229 GACCGATTGAACTCTGGCTATGTCTTTTCAGTGGCCCGCCGACAGCGGCATCAGC 2288
Qy 1797 CCTCGGGCGTGTGGAGTTCCGCAAAATGATCAAGTGGTGTATCCCGGGAGTGACCC 1856
Db 2289 CCTCGGGCGTGTGGAGTTCCGCAAAATGATCAAGTGGTGTATCCCGGGAGTGACCC 2348
Qy 1857 TTTTGTGGAATCAACAACTACGGCTGTCTGTGGCTTGGGGGCTCAGGACACCCCGTG 1916
Db 2349 TTTTGTGGAATCAACAACTACGGCTGTCTGTGGCTTGGGGGCTCAGGACACCCCGTG 2408
Qy 1917 GATGAACCTGGACAAGTGAATCCGCTGCAAGGAAAAATTTGAGTGCCTGCCGGGGCGG 1976
Db 2409 GATGAACCTGGACAAGTGAATCCGCTGCAAGGAAAAATTTGAGTGCCTGCCGGGGCGG 2468
Qy 1977 GGTGGGCA-CACGCCAAGGATCTCAGAGGATCAAAAGGGGACTTGCAATATCTGCTAA 2035
Db 2469 GGTGGGCAACCAAGGATCTCAGAGGATCAAAAGGGGACTTGCAATATCTGCTAA 2528
Qy 2036 GGATGAATATTTTCACTCTTGTCAAATAAATAATATGTTCCAAAGAGACCTGTAGC 2095
Db 2529 GGATGAATATTTTCACTCTTGTCAAATAAATAATATGTTCCAAAGAGACCTGTAGC 2588
Qy 2096 GAAACGACCCCTTAGAGATGAAACAATGACCGACGTGCAAAACAGTGGGCGATGCTGC 2155
Db 2589 GAAACGACCCCTTAGAGATGAAACAATGACCGACGTGCAAAACAGTGGGCGATGCTGC 2648
Qy 2156 CCTCAGTGGAGATGTAGCAACAGTAAACATCAGCAATCTCCAGCTGTCTTTTC 2215
Db 2649 CCTCAGTGGAGATGTAGCAACATTAACATCAGCACTATCCAGCTGTCTTTTC 2708
Qy 2216 TAGCAGTGTGTCTCACTGCACCTTCT-GAATACAGATTTTACTGTATTCTTTGCAACCAT 2274
Db 2709 TAGCAGTGTGTGTCTCACTGCCTTCTTGGNATACAGATTTTACTGTATTCTTTGCAACCAT 2768
Qy 2275 GTTAAAAATCGCTTTTTCAGGCCAGCGCGTGCCTCATGCTGTAAATCCAGCACTTTGGG 2334
Db 2769 GTTAAAAATCGCTTTTTCAGGCCAGCGCGTGCCTCATGCTGTAAATCCAGCACTTTGGG 2828
Qy 2335 AGCGCAGCGCGCGGATCAGTTGAGTTCAGAGTTCAGAGCAGCGCTGGCCAACTGGT 2394
Db 2829 AGCGCAGCGCGCGGATCAGTTGAGTTCAGAGTTCAGAGCAGCGCTGGCCAACTGGT 2888
Qy 2395 GAAACCTGTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2454
Db 2889 GAAACCTGTCTCTACTAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2948
Qy 2455 ACCCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGTTCGTCTACTGCT 2514
Db 2949 ACCCCAGCTACTTTGGGAGACTGAGTTGGAGGTTTTCAGTGAGCCAAAGTTCGTCTACTGCT 3007
Qy 2515 GTCCAGCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAA 2574
Db 3008 GTCCAGCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAA 3067
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QY 2575 ATGATAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAGCATCTTGGC 2634
 Db 3068 ATGATAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAGCATCTTGGC 3127
 QY 2635 GAAGTCATCCCACTGTTCTCTGAGAGTGGGAGGTGAGGCTGACCTATTGCTTGGC 2694
 Db 3128 GAAGTCATCCCACTGTTCTCTGAGAGTGGGAGGTGAGGCTGACCTATTGCTTGGC 3187
 QY 2695 TTACTCTATCTCAGCTGTCCTCCACATTTCCAGTGTGCGAGACATGACAACTGC 2754
 Db 3188 TTACTCTATCTCAGCTGTCCTCCACATTTCCAGTGTGCGAGACATGACAACTGC 3247
 QY 2755 TAYGACCGCCCAAGAGTGGACAGCTGTAATTTCTCTGACAAACCGTACACCCAC 2814
 Db 3248 TAGGACCGCCCAAGAGTGGACAGCTGTAATTTCTCTGACAAACCGTACACCCAC 3307
 QY 2815 ACCTATTCACTCTGCTCTGCTCGGCAATCACTGTAGCAGTAGGTTATCCCTTCC 2874
 Db 3308 ACCTATTCACTCTGCTCTGCTCGGCAATCACTGTAGCAGTAGGTTATCCCTTCC 3367
 QY 2875 TTGACCTA 2882
 Db 3368 TTGACCTA 3375

RESULT 5
 AAF21223
 ID AAF21223 standard; DNA; 3375 BP.
 XX AAF21223;
 XX AAF21223;
 DT 14-MAR-2001 (first entry)
 XX Human low adenine antisense oligonucleotide related sequence #2790.
 DE Low adenine antisense oligonucleotide; phosphorothioate; allergy;
 XX human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; anasthetic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary vasoconstriction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX Homo sapiens.
 XX WO200062736-A2.
 PN 26-OCT-2000.
 PD 24-MAR-2000; 2000MO-US008020.
 PF 06-APR-1999; 99US-0127958P.
 PR (UYEC-) UNIV EAST CAROLINA.
 XX (NYCE/) NYCE J W.
 PA Nyce JW;
 PI WPI; 2000-679539/66.
 XX Low adenine (A) content antisense oligonucleotides which do not trigger
 PT adenine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX Disclosure; Page 1135-1136; 1592pp; English.
 PS The present invention describes low adenine (A) content antisense
 XX oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.

CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, anasthetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;
 Query Match 53.8%; Score 2690.8; DB 3; Length 3375;
 Best Local Similarity 98.5%; Pred. No. 0;
 Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;
 QY 1 CTGGTCATCTCAGTCTTTTCTCCTGACCTGACGAGATGAACCTCTTGTGCTAGCTGT 60
 Db 500 CTGGTCATCTCAGTCTTTTCTCCTGACCTGACGAGATGAACCTCTTGTGCTAGCTGT 559
 QY 61 GCTGCTCAGGTAGGCAAGTCTCCCGGCTCCACCGGCTTCTCTCCCAAGTGAAGCTA 120
 Db 560 GCTGCTCAGGTAGGCAAGTCTCCCGGCTCCACCGGCTTCTCTCCCAAGTGAAGCTA 619
 QY 121 AGATCTCACTCTCTGGAAATGGGGGCGCAGGCCACAGCAACAGGATGGCCAGCCCG 180
 Db 620 AGATCTCACTCTCTGGAAATGGGGGCGCACA---CACAGCAACAGGATGGCCAGCCCG 676
 QY 181 CAGTCTCAATCGAGGTTCCAGTGGGCTTAAAGGCTCTCTATTGGGGTTCCTCTCAAG 240
 Db 677 CAGTCTCAATCGAGGTTCCAGTGGGCTTAAAGGCTCTCTATTGGGGTTCCTCTCAAG 735
 QY 241 GCTGGCAGCTTTTCAACCTGCAAGTCTGAACCTCAGATTGCTGAGCTAAGAAAGCTTGCC 300
 Db 736 GCTGGCAGCTTTTCAACCTGCAAGTCTGAACCTCAGATTGCTGAGCTAAGAAAGCTTGCC 795
 QY 301 TTTATTTTCTTTTCCAGACAGGCTTTGCTATFACCCAGGCTGAGTTCAGTGGCA 360
 Db 796 TTTATTTTCTTTTCCAGACAGGCTTTGCTATFACCCAGGCTGAGTTCAGTGGCA 855
 QY 361 TGATCATAGTCCACACAGCTTCCAGTCTGGGCTCAAGTATCTCCACCTTACTCA 420
 Db 856 TGATCATAGTCCACACAGCTTCCAGTCTGGGCTCAAGTATCTCCACCTTACTCA 915
 QY 421 ACTAAGTAGTTAGGCAATCTCCCATTTATTTATTTATTTATTTATTTATTTATTT 480
 Db 916 ACTAAGTAGTTAGGCAATCTCCCATTTATTTATTTATTTATTTATTTATTTATTT 975
 QY 481 TACTTTATTTATTTTGGAGCGGGCTCACTCTGTGCGCCAGGCTGAGTGGGCGG 540
 Db 976 TACTTTATTTATTTTGGAGCGGGCTCACTCTGTGCG---CCAGGCTGAGTGGGCGG 1034
 QY 541 TGATCTCAGTCACTACACCTCCATCTCTCTGGGTTCAATTAATTTCTCTTGGCTCAGCCT 600
 Db 1035 TGATCTCAGTCACTACACCTCCATCTCTCTGGGTTCAATTAATTTCTCTTGGCTCAGCCT 1093

Db 3248 TACGACCAGCCGAAGCTGGAGACGTGTAATTTCTGCTGGACAACCGGTACACCCAC 3307

QY 2815 ACCTATTTCATCTACTGCTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874

Db 3308 ACCTATTTCATCTACTGCTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3367

QY 2875 TTGACCTA 2882

Db 3368 TTGACCTA 3375

RESULT 6

ABZ96917

ID ABZ96917 standard; DNA; 3375 BP.

XX AC ABZ96917;

XX DE 17-OCT-2003 (first entry)

XX DE Human nucleic acid sequence.

XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX WO200285308-A2.

XX PN 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

XX ubiquinone.

XX PS Disclosure; SEQ ID NO 12159; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 10; Length 3375;

Best Local Similarity 98.5%; Pred. No. 0;

Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

QY 1 CTGGTCACTCAGTCTCTTTTCTACCTTGACATGCAAGATGAAACTCCTTTGCTAGCTGT 60

Db 500 CTGGTCACTCAGTCTCTTTTCTACCTTGACATGCAAGATGAAACTCCTTTGCTAGCTGT 559

QY 61 GCTGCTCAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTAGCTA 120

Db 560 GCTGCTCAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCCCAAGTAGCTA 619

QY 121 AGATCTCACTCTCTCTGGAATGGGGCCACAGGCCACAGCAACACAGGGATGGCCAGCCCG 180

Db 620 AGATCTCACTCTCTCTGGAATGGGGCCACA ---CACAGCAACACAGGGATGGCCAGCCCG 676

QY 181 CAGTCTCAAWTCGAGGTTCCAGTGGGCTTAAGGGCTCTCTATTTGGGGTTCCCTCAAG 240

Db 677 CAGTCTCAAWTCGAGGTTCCAGTGGGCTCTCTATTTGGGGTTCCCTCAAG 735

QY 241 GCTGGCAGCTTTTCAACCTGCAAGTCTGAACTCAGATTCGCTGAGCTAAGAAGCTTGC 300

Db 736 GCTGGCAGCTTTTCAACCTGCAAGTCTGAACTCAGATTCGCTGAGCTAAGAAGCTTGC 795

QY 301 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTTCAGTGGCA 360

Db 796 TTTATTTTCTTTTCCAGACAGGGTCTTGCTCTATTAACCCAGGCTGGAGTTTCAGTGGCA 855

QY 361 TGATCATAGTCCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA 420

Db 856 TGATCATAGTCCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA 915

QY 421 ACTAAGTAGTAGGCCAATCTCCATTTATTTATTTATTTATTTATTTATTTATTTATTT 480

Db 916 ACTAAGTAGTAGGCCAATCTCCATTTATTTATTTATTTATTTATTTATTTATTTATTT 975

QY 481 TACTTTATTTATTTTGAGACGGGCTCACTCTGTGCGCCAGGCTGGAGTGGGGTGGCG 540

Db 976 TACTTTATTTATTTTGAGACGGGCTCACTCTGTGCG ---CGAGGCTGGAGTGGGGTGGCG 1034

QY 541 TGATCTCAGATCACTACAACTCTCTCGGGTTCAAATAAATTTCTTTGGCTCAGCCT 600

Db 1035 TGATCTCAGATCACTACAACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1093

QY 601 CTCAGTAGCTGGGACTGTGTAGCTCTCAAGTAGCTGGGACACACACCACTGCCAGCTAA 660

Db 1094 CTCAGTAGCTGGGACTGTGTAGCTCTCAAGTAGCTGGGACACACCACTGCCAGCTAA 1152

QY 661 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720

Db 1153 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1212

QY 721 CTCCTCTTTAGATTCCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 779

Db 1213 CTCCTCTTTAGATTCCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1272

QY 780 TTTCTCTACTTATACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 839

Db 1273 TTTCTCTACTTATACATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1332

QY 840 TCGCCAAGGCTGGAGTACAGTGTGCTCGGCTCACTGCAAGCTCCACCTGTGGGT 899

Db 1333 TCGCCAAGGCTGGAGTACAGTGTGCTCGGCTCACTGCAAGCTCCACCTGTGGGT 1392

QY 900 TCACGCCATTTCTCCCGCTCAGCCTCCCGAGTAGCTGGGACTAAAGGGCGCTGCCACCA 959

Db 1393 TCACGCCATTTCTCCCGCTCAGCCTCCCGAGTAGCTGGGACTAAA -GCGCCTGCCACCA 1451

QY 960 GCGCCGCTAAATTTTGTATTTTAAATAAGACGGGGTTTCATCGTGTGTAGCAGGATG 1019

Db 1452 GCGCCGCTAAATTTTGTATTTTAAATAAGACGGGGTTTCATCGTGTGTAGCAGGATG 1511

Qy	1020	GTCTCGATCTCATGACCTTGATCCGCTCGCCTCGCCCTCCAAAGTGTGGGATTACA	1079
Db	1512	GTCTCGATCTCATGACCTTGATCCGCTCGCCTCGCCCTCCCAA--TGCTGGATTACA	1569
Qy	1080	GGCATGAGCCACCGTGGCCGCTTATCATTATTATTATTATTATTATTATTATTATTATT	1139
Db	1570	GGCATGAGCCACCGTGGCCGCTTATCATTATTATTATTATTATTATTATTATTATTATT	1629
Qy	1140	AGGTGTAGCTCATGAGGTTAGAG---ATTATTATTATTATTATTATTATTATTATTATT	1196
Db	1630	AGGTGTAGCTCATGAGGTTAGAGTTATTATTATTATTATTATTATTATTATTATTATT	1689
Qy	1197	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	1256
Db	1690	TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT	1749
Qy	1257	ACATAGTAAGTGTCAATAAATATTCACTGGATAAAGAGTGCAGATAGTTTAAACATATC	1316
Db	1750	ACATAGTAAGTGTCAATAAATATTCACTGGATAAAGAGTGCAGATAGTTTAAACATATC	1809
Qy	1317	TGACCTAGGAGGCTGAGGAGAGAAATGCGGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1376
Db	1810	TGACCTAGGAGGCTGAGGAGAGAAATGCGGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1869
Qy	1377	GCTGAATCGTGTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAA	1436
Db	1870	GCTGAATCGTGTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAA	1929
Qy	1437	AAAAAAAACCTATCAGCGCTAGCTGGGTGGACATGCCCTGTAACTCTAGCTGAGCGGT	1496
Db	1930	AAAAAAAACCTATCAGCGCTAGCTGGGTGGACATGCCCTGTAACTCTAGCTGAGCGGT	1989
Qy	1497	AGGTGCCAGAGAAGAGAGAAAGAGAGAGATATATATATATATATATATATATATAT	1556
Db	1990	AGGTGCCAGAGAAGAGAGAAAGAGAGAGATATATATATATATATATATATATATAT	2049
Qy	1557	CAAGATATAAATTTATATATATAAAGTTTCAATTAATAAATAAATAAATAAATAAATA	1616
Db	2050	CAAGATATAAATTTATATATATAAAGTTTCAATTAATAAATAAATAAATAAATAAATA	2108
Qy	1617	ACTTTCACTTTACAGGTTCTCGGTCACACGCTTTTCAGAGGAGGAGCTGGCAGGGGT	1676
Db	2109	ACTTTCACTTTACAGGTTCTCGGTCACACGCTTTTCAGAGGAGGAGCTGGCAGGGGT	2168
Qy	1677	CAGGAGGACGCTGGGACCCGAGGAGAGAGGAGGAGTGTGTCCCGGGGTGCTGGCA	1736
Db	2169	CAGGAGGACGCTGGGACCCGAGGAGAGAGGAGGAGTGTGTCCCGGGGTGCTGGCA	2228
Qy	1737	GACCGATTTGAATCTCGGCTATGCTTCTTGCAAGTGCAGGCGCCGCMCAGCGGCATCAGC	1796
Db	2229	GACCGATTTGAATCTCGGCTATGCTTCTTGCAAGTGCAGGCGCCGCMCAGCGGCATCAGC	2288
Qy	1797	CCTCGGCGGTGTGGCAGTTCCGCAAAATGATCAAGTGCAGTGCAGGCGGAGTGACCCC	1856
Db	2289	CCTCGGCGGTGTGGCAGTTCCGCAAAATGATCAAGTGCAGTGCAGGCGGAGTGACCCC	2348
Qy	1857	TTVTTGAATACAAACACTACGGCTGCTACTGTGGCTTGGGGGGCTCAGGCACCCCGGTG	1916
Db	2349	TTCTTGAATACAAACACTACGGCTGCTACTGTGGCTTGGGGGGCTCAGGCACCCCGGTG	2408
Qy	1917	GATGAACCTGGACAGTAAGTGAATCCGCTCAGGAAATTTGGAGTGCCTCGCGGGGGCGG	1976
Db	2409	GATGAACCTGGACAGTAAGTGAATCCGCTCAGGAAATTTGGAGTGCCTCGCGGGGGCGG	2468
Qy	1977	GGTGGGGCA-CAGCCCAAGGATCTCAGAGGCATACAAAGGGGACTTGCATATCTGCTAA	2035
Db	2469	GGTGGGGCACCGCAAGGATCTCAGAGGCATACAAAGGGGACTTGCATATCTGCTAA	2528
Qy	2036	GGATAACATATTTTCACTCTGTCAAAATAAATAATATTTTCCAGAGGAGCCCTGTAGC	2095
Db	2529	GGATAACATATTTTCACTCTGTCAAAATAAATAATATTTTCCAGAGGAGCCCTGTAGC	2588

Qy	2096	GAACGACCCCTTAGAGATGGAACAATGACCGAGTGCACAAACAGTGGGCGATGCTGC	2155
Db	2589	GAACGACCCCTTAGAGATGGAACAATGACCGAGTGCACAAACAGTGGGCGATGCTGC	2648
Qy	2156	CCTCCAGTGGCAGAAATGTAGCAACAGTAAACATCAGCAATATCCAGTGTCAATTTTC	2215
Db	2649	CCTCCAGTGGCAGAAATGTAGCAACATTAACATCAGCAATATCCAGTGTCAATTTTC	2708
Qy	2216	TAGCAGTGGTGTCTACTGCACCTTCT-GAATACAGATTTTACTGTATTTCTTGAACCAT	2274
Db	2709	TAGCAGTGGTGTCTACTGCCCTTCTCGAAATACAGATTTTACTGTATTTCTTGAACCAT	2768
Qy	2275	GTAAAAAATCGCTTTTCAGGCCAGCGGTGCTCATGCTGTAAATCCAGACATTTGGG	2334
Db	2769	GTAAAAAATCGCTTTTCAGGCCAGCGGTGCTCATGCTGTAAATCCAGACATTTGGG	2828
Qy	2335	AGGCCAGCGCGGCGGATCATCTTGAGGTCAGAGTTTCAGACACAGCTGGCCAAATGGT	2394
Db	2829	AGGCCAGCGCGGCGGATCATCTTGAGGTCAGAGTTTCAGACACAGCTGGCCAAATGGT	2888
Qy	2395	GAACCCCTGTCTCTACTAAAAAATACAAAAATTTAGCCGACATGTTGGCGAGCGCTGTA	2454
Db	2889	GAACCCCTGTCTCTACTAAAAAATACAAAAATTTAGCCGACATGTTGGCGAGCGCTGTA	2948
Qy	2455	ACCCAGCTTACTTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGGTCGTCACTGCT	2514
Db	2949	ACCCAGCTTACTTTGGGAGACTGAGTTGGAGGTTTCA-TGAGCCAAAGGTCGTCACTGCT	3007
Qy	2515	GTCCAGCTGGGTAAACAGACAACTCTGTCTCAAAAAAATAAATGCTTTCAATAATAT	2574
Db	3008	GTCCAGCTGGGTAAACAGACAACTCTGTCTCAAAAAAATAAATGCTTTCAATAATAT	3067
Qy	2575	ATGATAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTGGC	2634
Db	3068	ATGATAAAGGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAAGCATCTTGGC	3127
Qy	2635	GAAGTCATCCCCACCTGTTCTTGAGAGTGGGAGGCTGAGGCTGACCTATTGCTCTGCAC	2694
Db	3128	GAAGTCATCCCCACCTGTTCTTGAGAGTGGGAGGCTGAGGCTGACCTATTGCTCTGCAC	3187
Qy	2695	TTACTCTTATCTCAGCTGTCTCCACCTTTCCAGGTCGTCAGACACATGACAACTGC	2754
Db	3188	TTACTCTTATCTCAGCTGTCTCCACCTTTCCAGGTCGTCAGACACATGACAACTGC	3247
Qy	2755	TAYGACCGAGCAAGAGCTGGACAGCTGTAATTTCTGTCGACAMMCCGTACACCCAC	2814
Db	3248	TACGACCGAGCAAGAGCTGGACAGCTGTAATTTCTGTCGGACAAACCCGTACACCCAC	3307
Qy	2815	ACCTATTATCTCTGCTCTGGCTCGGCAATCAGCTGTAGCAGTAGGTTTATCCCTTCC	2874
Db	3308	ACCTATTATCTCTGCTCTGGCTCGGCAATCAGCTGTAGCAGTAGGTTTATCCCTTCC	3367
Qy	2875	TTGACCTA 2882	
Db	3368	TTGACCTA 3375	
RESULT 7			
ABD20766			
ID	ABD20766	standard; DNA; 3375 BP.	
XX	AC	ABD20766;	
XX	DT	29-JUL-2004 (first entry)	
XX	DE	Human pulmonary and inflammatory target DNA #377.	
XX	KW	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;	
KW	KW	respiratory tract inflammation; adenosine sensitivity; lung; cancer;	
KW	KW	surfactant depletion; antiallergic; antiinflammatory; antispasmodic;	
KW	KW	analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;	
KW	KW	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;	
KW	KW	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;	

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW pulmonary transplantation rejection; ds.
XX Homo sapiens.
XX W0200285309-A2.
XX 31-OCT-2002.
XX 23-APR-2002; 2002WO-US013143.
XX 24-APR-2001; 2001US-0286036P.
XX (EPIC-) EPIGENESIS PHARM INC.
XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI: 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX Claim 15; SEQ ID NO 12159; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 3375 BP; 837 A; 866 C; 764 G; 908 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 11; Length 3375;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

QY 1 CTGGTCATCTCAGTCTTTTCTCACCTTGACTGCTCAAGATGAACCTCTTGCTGCTAGCTGT 60
DB |||||
500 CTGGTCATCTCAGTCTTTTCTCACCTTGACTGCTCAAGATGAACCTCTTGCTGCTAGCTGT 559
QY 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCTCCCAAGTAGCTA 120
DB |||||
560 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGCTTCTCTCTCCCAAGTAGCTA 619
QY 121 AGATCTCACTCTCTGGAATGGGGGCCACAGGGCCACAGCAAGGATGGCCAGCCCG 180

DB |||||
620 AGATCTCACTCTCTGGAATGGGGCCACA---CACAGCAACAGGATGGCCAGCCCG 676
QY |||||
181 CAGTCTCAANTCGAGGTCCAGTGGGCTTAAGGGCTCTCTATTGGGGTTCCTCAAG 240
DB |||||
677 CAGTCTCAANTCGAGGTTCCTCAGT-GGGCTTAAGGGCTCTCTATTGGGGTTCCTCAAG 735
QY |||||
241 GCTGGCAGCTTTTCAACCTGCAAGTCTGAACCTCAGATTGCCTGAGCTAAGAAAGCTTGCC 300
DB |||||
736 GCTGGCAGCTTTTCAACCTGCAAGTCTGAACCTCAGATTGCCTGAGCTAAGAAAGCTTGCC 795
QY |||||
301 TTATTTTCTTTTCCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAAGTGCA 360
DB |||||
796 TTATTTTCTTTTCCAGACAGGGTCTTGCTCTATTAACCCAGGCTGGAGTTCAAGTGCA 855
QY |||||
361 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGTATCTCCCACTTACTCA 420
DB |||||
856 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGTATCTCCCACTTACTCA 915
QY |||||
421 ACTAAGTAGTTAGGCCAATCTCCCAATTTATTTATTTATTTATTTATTTATTTATTT 480
DB |||||
916 ACTAAGTAGTTAGGCCAATCTCCCAATTTATTTATTTATTTATTTATTTATTTATTT 975
QY |||||
481 TACTTTATTTATTTTGGACGGGCTCACTCTGTGCGCCAGGCTGGAGTCCGGTGGCG 540
DB |||||
976 TACTTTATTTATTTTGGACGGGCTCACTCTGTGCG-CCAGGCTGGAGTCCGGTGGCG 1034
QY |||||
541 TGATCTCAGTCACTACAACTCCATCTCTGGGTTCCTCAATTAATTTCTTCTGCTCAGCCT 600
DB |||||
1035 TGATCTCAGTCACTACAACTCCATCTCTCT-GGTTCAAATTAATTTCTTCTGCTCAGCCT 1093
QY |||||
601 CTCAGTAGTCTGGGACTTGTAGCTCTCAAGTAGTGGCACACACACCACTGCCAGCTAA 660
DB |||||
1094 CTCAGTAGTCT-GGACTTGTAGCTCTCAAGTAGTGGCACACACCACTGCCAGCTAA 1152
QY |||||
661 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
DB |||||
1153 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1212
QY |||||
721 CTCCTTTTAGATTCTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 779
DB |||||
1213 CTCCTTTTAGATTCTCTCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1272
QY |||||
780 TTTCTCTACTTATCACTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 839
DB |||||
1273 TTTCTCTACTTATCACTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1332
QY |||||
840 TCGCAAGGCTGGAGTACAGTGGTGGTCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 899
DB |||||
1333 TCGCAAGGCTGGAGTACAGTGGTGGTCTCGGCTCACTGCAAGCTCCACCTGCTGGGT 1392
QY |||||
900 TCACGCCATTCTCCCGCTCAGCTCCCGCTCAGCTGGGACTAAAGGGCTGCCACCCAC 959
DB |||||
1393 TCACGCCATTCTCCCGCTCAGCTCCCGCTCAGCTGGGACTAAA-GCGCTGCCACCCAC 1451
QY |||||
960 GCGCCGCTAAATTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1019
DB |||||
1452 GCGCCGCTAAATTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1511
QY |||||
1020 GTCTCGATCTCATGACCTTGTGATCCGCTCGCTCCCGCTCCCAAGTGTGGGATTACA 1079
DB |||||
1512 GTCTCGATCTCATGACCTTGTGATCCGCTCGCTCCCGCTCCCAAA--TGCTGGGATTACA 1569
QY |||||
1080 GGCATGAGCCACCGTCCCGGCTTATCACATTTATTTATTTATTTATTTATTTATTTATTT 1139
DB |||||
1570 GGCATGAGCCACCGTCCCGGCTTATCACATTTATTTATTTATTTATTTATTTATTTATTT 1629
QY |||||
1140 AGTTTGAAGCTCCATGAGTTAGAG---ATTATTTATTTATTTATTTATTTATTTATTTATTT 1196
DB |||||
1630 AGTTTGAAGCTCCATGAGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1689
QY |||||
1197 TTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1256

1690	TTATATTATTTATATATCTGTTCTACCTGCTGTATATCTCTAGCTCCTTAGACAGAGCCTGGC	1749	
Qy	1257	ACATAGTAAGTGTCTCAATAAATATTTACTCGATAAAACAGTGCAGATAGTTTAAAACTATC	1316
	1750	ACATAGTAAGTGTCTCAATAAATTTACTCGATAAAACAGTGCAGATAGTTTAAACTATC	1809
	1317	TGACCTAGGAGGCTGAGGCAGGAGAAATGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1376
	1810	TGACCTAGGAGGCTGAGGCAGGAGAAATGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA	1869
Qy	1377	GCTGAAATCGTGTCACTGCACTCCAACTCGGCCAACAGACAAGACTCCATCTCAAAAA	1436
	1870	GCTGAAATCGTGTCACTGCACTCCAACTCGGCCAACAGACAAGACTCCATCTCAAAAA	1929
	1437	AAAAAAAACCTATCAGCGCTAGCTGGTGGCACATCGCTGTAATCTTAGCTCAGGCGGT	1496
	1930	AAAAAAAACCTATCAGCGCTAGCTGGTGGCACATCGCTGTAATCTTAGCTCAGGCGGT	1989
Qy	1497	AGGTCCCGAAGAAGAAAGAAAAAGAAAGAGATATATATATATACACACACA	1556
	1990	AGGTCCCGAAGAAGAAAGAAAAAGAAAGAGATATATATATATACACACACA	2049
	1557	CAAAAGATATAAACTTTATATATATAAAGTTTTCTATTAATAAAAAAAAACCTCTACCC	1616
	2050	CAAAAGATATAAACTTTATATATAAAGTTTTCTATT-AAAAAAAACCTCTACCC	2108
Qy	1617	ACTTTCACTTTACCAGGTTCTCGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGCGAGGGT	1676
	2109	ACTTTCACTTTACCAGGTTCTCGGGTCCAAACGGTCTTCAGAGGAGGCAGCTGCGAGGGT	2168
	1677	CAGGAGGCAGCGTGGACCCCGAGGAGCAGGAAGCAGTGTGTCCCGGGGTGCTGGCA	1736
	2169	CAGGAGGCAGCGTGGACCCCGAGGAGCAGGAAGCAGTGTGTCCCGGGGTGCTGGCA	2228
Qy	1737	GACCGATTTGAACTCTCGCTGATGTCTTTCTTGCAGTGCGCCCGCGMCACGGGATCAGC	1796
	2229	GACCGATTTGAACTCTCGCTGATGTCTTTCTTGCAGTGCGCCCGCGMCACGGGATCAGC	2288
	1797	CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCGTGATCCCGGGAGTGACCC	1856
	2289	CCTCGGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGCGTGATCCCGGGAGTGACCC	2348
Qy	1857	TTTGTGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGACCCCGGTG	1916
	2349	TTCTTGGAATACAACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGACCCCGGTG	2408
	1917	GATGAACCTGGCAAGTAAGTGTATCCGCTCGAGGAAAAATTGGAGTGCTCCCGGGGGCGG	1976
	2409	GATGAACCTGGCAAGTAAGTGTATCCGCTCGAGGAAAAATTGGAGTGCTCCCGGGGGCGG	2468
Qy	1977	GGTGGGGCA-CACGCCAAGGATCTCAGAGGCATACAAAGGGACTTGCATATCTGCTAA	2035
	2469	GGTGGGGCACACGCCAAGGATCTCAGAGGCATACAAAGGGACTTGCATATCTGCTAA	2528
	2036	GGATAACATATTTTCACTCTTGTCAAATAAAACAAATATGTTCACAGAGGACCCCTGTAGC	2095
	2529	GGATAACATATTTTCACTCTTGTCAAATAAAACATATGTTCACAGAGGACCCCTGTAGC	2588
Qy	2096	GAACGCACCCCGTTAGAGATGGAAAAATGACCGACCTGCAAAACAGTGGGGGATGCTGC	2155
	2589	GAACGCACCCCGTTAGAGATGGAAAAATGTACCGACCTGCAAAACAGTGGGGGATGCTGC	2648
	2156	CCTCCAGTGGCAGAAATGTAGGCAAGTAAACATCACAGCAACTATCCAGTGTCAATTTTC	2215
	2649	CCTCCAGTGGCAGAAATGTAGGCAACATTAACATCACAGCAACTATCCAGTGTCAATTTTC	2708
Qy	2216	TAGCAGTGGTGTCACTGCACCTTCT-GAATACAGGATTTTACTGTATTTCTTGCAACCAT	2274
	2709	TAGCAGTGGTGTCACTGCACCTTCTCGAATACAGGATTTTACTGTATTTCTTGCAACCAT	2768
	2275	GTTMAAAATCGCTTTCAGGCACGCGCGGTGGCTCATGCCCTGTAAATCCCAAGCACTTTGGG	2334
	2769	GTTMAAAATCGCTTTCAGGCACGCGCGGTGGCTCATGCCCTGTAAATCCCAAGCACTTTGGG	2828

Qy	2335	AGCCGAGCGGCGCGAATCACTTGAGGTGAGGTGAGAGTTTCGAGACGAGCTGCGCCAAACATGGT	2394
Db	2829	AGCCGAGCGGCGCGGATCACTTGAGGTGAGGTGAGAGTTTCGAGACGAGCTGCGCCAAACATGGT	2888
Qy	2395	GAACCCCTGCTCTACTATAAAATACAAAAATTTAGCCGACATGGTGGCGAGCGCCTGTA	2454
Db	2889	GAACCCCTGCTCTACTATAAAATACAAAAATTTAGCCGACATGGTGGCGAGCGCCTGTA	2948
Qy	2455	ACCCGAGCTACTTTGGGAGACTGAGTTTGGAGTTTTCAGTGAGCCCAAGGTGCTGTCACTGCT	2514
Db	2949	ACCCGAGCTACTTTGGGAGACTGAGTTTGGAGTTTTCAGTGAGCCCAAGGTGCTGTCACTGCT	3007
Qy	2515	GTCGAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATAT	2574
Db	3008	GTCGAGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCAATAAATAT	3067
Qy	2575	ATGATAAAGGACTTATATTTTTTCAAGCATAGGATCATTTCTCCTGAAGCATCTTGGC	2634
Db	3068	ATGATAAAGGACTTATATTTTTTCAAGCATAGGATCATTTCTCCTGAAGCATCTTGGC	3127
Qy	2635	GAAGTCATCCCCACCTGTTCTCGAGAGTGGCGAGGTGAGGGCTGACCTATTGCTCTGCAC	2694
Db	3128	GAAGTCATCCCCACCTGTTCTCGAGAGTGGCGAGGTGAGGGCTGACCTATTGCTCTGCAC	3187
Qy	2695	TTACTCTCTATCTCAGCTGCTCCCTCCCACTTTCCAGGTGCTGCGCAGACACATGACAACCTGC	2754
Db	3188	TTACTCTCTATCTCAGCTGCTCCCTCCCACTTTCCAGGTGCTGCGCAGACACATGACAACCTGC	3247
Qy	2755	TAYGACGAGCCGAAGAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCGTACACCCAC	2814
Db	3248	TACGACGAGCCGAAGAGCTGGACAGCTGTAAATTTCTGCTGGACACACCCGTCACACCCAC	3307
Qy	2815	ACCTATTCTACTCGTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC	2874
Db	3308	ACCTATTCTACTCGTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC	3367
Qy	2875	TTGACCTTA 2882	
Db	3368	TTGACCTTA 3375	
RESULT 8			
AAA35103			
ID	AAA35103 standard; DNA; 6771 BP.		
XX			
AC	AAA35103;		
XX			
DT	28-JUL-2000 (first entry)		
XX			
DE	Human adenosine receptor related polynucleotide SEQ ID NO:2792.		
XX			
KW	Human; adenosine receptor; low adenosine antisense oligonucleotide;		
KW	phosphorothioate; impaired respiration; inflammation; allergy;		
KW	allergic disease; bronchoconstriction; inhibitor; antiinflammatory;		
KW	antiallergic; antiasthmatic; cytosstatic; analgesic; impaired airway;		
KW	lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;		
KW	respiratory distress syndrome; pain; cystic fibrosis; emphysema;		
KW	pulmonary hypertension; chronic obstructive pulmonary disease; COPD;		
KW	cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200009525-A2.		
XX			
PD	24-FEB-2000.		
XX			
PF	03-AUG-1999; 99WO-US017712.		
XX			
PR	03-AUG-1998; 98US-0095212P.		
XX			
PA	(UYEC-) UNIV EAST CAROLINA.		
XX			

QY	1557	CAAGATATAA	CTTTATATATA	TATAAAGTTT	TTTCATTAAAAA	AAAAAACCTCTACCC	1616
Db	2612	CAAGATATAA	CTTTATATATA	TATAAAGTTT	TTTCATT-AAAAA	AAAAAACCTCTACCC	2670
QY	1617	ACTTTCACTT	TACAGGTTCT	CTGGGTC	CAACGGTCTT	CAGAGGAGCAGCTGCGAGGGT	1676
Db	2671	ACTTTCACTT	TACAGGTTCT	CTGGGTC	CAACGGTCTT	CAGAGGAGCAGCTGCGAGGGT	2730
QY	1677	CAGGAGGACG	TGGGACCGG	AGGAGCAGG	AGGAGCAGTGT	TCCCCGGGGTCTGGCA	1736
Db	2731	CAGGAGGACG	TGGGACCGG	AGGAGCAGG	AGGAGCAGTGT	TCCCCGGGGTCTGGCA	2790
QY	1737	GACCGATTTC	GAACCTCTCG	GTATGCTT	CTTTCAGTGGC	CGCCGCMCAGCGGCATCAGC	1796
Db	2791	GACCGATTTC	GAACCTCTCG	GTATGCTT	CTTTCAGTGGC	CGCCGCMCAGCGGCATCAGC	2850
QY	1797	CTCTGGCCGT	GTGGCAGTT	CCGCAAAAT	GATCAAGTGC	TGATCCGGGGAGTGACCC	1856
Db	2851	CTCTGGCCGT	GTGGCAGTT	CCGCAAAAT	GATCAAGTGC	TGATCCGGGGAGTGACCC	2910
QY	1857	TTTGTGAAT	TACACAACT	AGGCTGCTAC	TGTGGCTTGGG	GGGCTCAGGCACCCCGTG	1916
Db	2911	TTCTTGAAT	TACACAACT	AGGCTGCTAC	TGTGGCTTGGG	GGGCTCAGGCACCCCGTG	2970
QY	1917	GATGAAC	TGGACAA	GTAAAGT	GATCCGCTCG	CAGGAAATTTGGAGTGCCTCGCGGGCGG	1976
Db	2971	GATGAAC	TGGACAA	GTAAAGT	GATCCGCTCG	CAGGAAATTTGGAGTGCCTCGCGGGCGG	3030
QY	1977	GGTGGGCA	-CAGCC	AAAGATCT	CACGAGGCAT	TACAAAGGGACTTGCATATCTGCTAA	2035
Db	3031	GGTGGGCA	-CAGCC	AAAGATCT	CACGAGGCAT	TACAAAGGGACTTGCATATCTGCTAA	3090
QY	2036	GGATAACAT	TTTTTCACT	CTTGTCAAT	TAACAAATAT	TTTCCAGAGGACCTCTAGC	2095
Db	3091	GGATAACAT	TTTTTCACT	CTTGTCAAT	TAACAAATAT	TTTCCAGAGGACCTCTAGC	3150
QY	2096	GAACGCA	CCCCGTT	TAGAGAT	TGAAACAAT	CACGACGCTGCAAAACAGTGGCGGATGCTGC	2155
Db	3151	GAACGCA	CCCCGTT	TAGAGAT	TGAAACAAT	CACGACGCTGCAAAACAGTGGCGGATGCTGC	3210
QY	2156	CTCCAGT	GGCAGAA	TTAGCAAC	AGTAAACAT	CACAGCAACTATCCACGTGCTATTTTC	2215
Db	3211	CTCCAGT	GGCAGAA	TTAGCAAC	AGTAAACAT	CACAGCAACTATCCACGTGCTATTTTC	3270
QY	2216	TAGCAGT	GGTGTG	TCACCTGC	ACCTTCT-CAAT	CAGGATTTTACTGTATTTCTTGCACCAT	2274
Db	3271	TAGCAGT	GGTGTG	TCACCTGC	ACCTTCT-CAAT	CAGGATTTTACTGTATTTCTTGCACCAT	3330
QY	2275	GTTAAAAAT	CGCTTTC	CAGGCGC	GGCGGTGG	CTCATGCTGTAATCCACAGCACTTTGGG	2334
Db	3331	GTTAAAAAT	CGCTTTC	CAGGCGC	GGCGGTGG	CTCATGCTGTAATCCACAGCACTTTGGG	3390
QY	2335	AGGCCGAGG	GGGGCGG	ATCATCTT	GAGTCAAGG	ATTTCGACACAGCCTTGCCCAACATGGT	2394
Db	3391	AGGCCGAGG	GGGGCGG	ATCATCTT	GAGTCAAGG	ATTTCGACACAGCCTTGCCCAACATGGT	3450
QY	2395	GAACCCCTG	TCTCTACT	TAATAAAT	TACAAAAAT	TAGCCGGACATGTTGGCGGCGCCTGTA	2454
Db	3451	GAACCCCTG	TCTCTACT	TAATAAAT	TACAAAAAT	TAGCCGGACATGTTGGCGGCGCCTGTA	3510
QY	2455	ACCCGACG	TACTTGGG	AGACTGAG	TTCAGTGG	AGCCAAAGTTCGTGTCACTGCT	2514
Db	3511	ACCCGACG	TACTTGGG	AGACTGAG	TTCAGTGG	AGCCAAAGTTCGTGTCACTGCT	3569
QY	2515	GTCCAGC	CTGGTAA	CAGACAA	CTGTCTCA	AAAAAATATGCTTTCAATAAATAT	2574
Db	3570	GTCCAGC	CTGGTAA	CAGACAA	CTGTCTCA	AAAAAATATGCTTTCAATAAATAT	3629
QY	2575	ATGATAA	AGGACCT	TATATTTT	TTTCAAGCC	ATAGGATCAATTTCTCCTGAAGCATCTTGGC	2634
Db	3630	ATGATAA	AGGACCT	TATATTTT	TTTCAAGCC	ATAGGATCAATTTCTCCTGAAGCATCTTGGC	3689

RESULT 9

AAF21225

ID AAF21225 standard; DNA; 6771 BP.

XX AAF21225;

XX AC AAF21225;

DT 14-MAR-2001 (first entry)

XX Human low adenosine antisense oligonucleotide related sequence #2792.

DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytosatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.

XX Homo sapiens.

OS WO200062736-A2.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008020.

PF 06-APR-1999; 99US-0127958P.

XX (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

PI Nyce JW;

XX WPI; 2000-679539/66.

DR Low adenosine (A) content antisense oligonucleotides which do not trigger

XX adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
PS Disclosure; Page 1137-1139; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytosatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and

[illegible]

2791 GACCGATTTGAACCTCTGGCTATGTTCTTTGCAGTGGCGCCGCCGACAGCGGCATCAGC 2850
1797 CTTGGGCGGTGGGAGTTCCGCAAAATGATCAAGTGGTGTATCCGGGGAGTGACCCC 1856
2851 CCTCGGGCGGTGGGAGTTCCGCAAAATGATCAAGTGGTGTATCCGGGGAGTGACCCC 2910
1857 TTTTGTGAATACAACTACCGCTGCTACTGTGGCTTGGGGGGCTCAGGCACCCCGGTG 1916
2911 TTCTTGGNATACAACTACGCTGCTACTGTGGCTTGGGGGGCTCAGGCACCCCGGTG 2970
1917 GATGAATGGCAAGTAAGTATCGCCTGTCAGGAAATTTGGAGTGCCTGCGGGGGCGG 1976
2971 GATGAATGGCAAGTAAGTATCGCCTGTCAGGAAATTTGGAGTGCCTGCGGGGGCGG 3030
1977 GGTGGGGCA-CAGCCNAGATCTCAGGAGCATACAAAGGGACATTGCATATCTCTAA 2035
3031 GGTGGGGCACCGCCAAAGATCTCAGGAGCATACAAAGGGACATTGCATATCTCTAA 3090
2036 GGATAACATATTTTCACTCTTGTCAAATAAAATATGTTCCAAAGAGGACCTGTAGC 2095
3091 GGATAACATATTTTCACTCTTGTCAAATAAAATATGTTCCAAAGAGGACCTGTAGC 3150
2096 GAACGCAACCCGTTAGAGATGSAACAAATGACCGAGCTGCAAAACAGTGGCGATCTGC 2155
3151 GAACGCAACCCGTTAGAGATGSAACAAATGACCGAGCTGCAAAACAGTGGCGATCTGC 3210
2156 CTTCCAGTGCAGAAATGACCAAGTAAACATCACAGCACTATCCAGTGTCTATTTTC 2215
3211 CTTCCAGTGCAGAAATGACCAAGTAAACATCACAGCACTATCCAGTGTCTATTTTC 3270
2216 TAGCAGTGGTGTCTACCTGCACTTCT- GAATACAGGATTTTACTGTATTCTTCAACCAT 2274
3271 TAGCAGTGGTGTCTACCTGCACTTCTTGGAAATACAGATTTTACTGTATCTTGCACCAT 3330
2275 GTTAAAAATCGCTTTACGGCCAGCGCGGTGCATGCTGTAATCCAGCACTTTTGGG 2334
3331 GTTAAAAATCGCTTTACGGCCAGCGCGGTGCATGCTGTAATCCAGCACTTTTGGG 3390
2335 AGCCGAGGCGGGGATCACTTGAGTCAAGGATTCGAGCAGCAGCTGGCCAACTGTT 2394
3391 AGCCGAGGCGGGGATCACTTGAGTCAAGGATTCGAGCAGCAGCTGGCCAACTGTT 3450
2395 GAAACCTGTCTCTACTTAAAAATACAAAAATTTAGCGGACATGTTGGGAGCGCTGTA 2454
3451 GAAACCTGTCTCTACTTAAAAATACAAAAATTTAGCGGACATGTTGGGAGCGCTGTA 3510
2455 ACCCAGCTACTTGGGAGCTGAGTTGGAGTTTCAAGTGGCAAGTCTGTGCTACTGCT 2514
3511 ACCCAGCTACTTGGGAGCTGAGTTGGAGTTTCA-TGAGCCAAGTCTGTGCTACTGCT 3569
2515 GTCCAGCTGGTTACAGACCACTCTGTCTCAAAAAAATAATGCTTTCAATAATAT 2574
3570 GTCCAGCTGGTTACAGACCACTCTGTCTCAAAAAAATAATGCTTTCAATAATAT 3629
2575 ATGATAAAGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAAGCATTTTGGC 2634
3630 ATGATAAAGACTTATATTTTCAAGCCATAGGATCATTTCTCTGAAGCATTTTGGC 3689
2635 GAAGTCAATCCCACTGTTCTCAGAGTGGGAGGTGAGGCTGACCTATTGCTCTGCAC 2694
3690 GAAGTCAATCCCACTGTTCTCAGAGTGGGAGGTGAGGCTGACCTATTGCTCTGCAC 3749
2695 TTACTCTATCTCAGTGTCTCTCCCACTTTCCAGTGTCTGCAGACATGACACTGC 2754
3750 TTACTCTATCTCAGTGTCTCTCCCACTTTCCAGTGTCTGCAGACATGACACTGC 3809
2755 TAYGACCAGCCCAAGAGCTGGACGCTGTAATTTCTGCTGCAAMCCGTACACCCAC 2814
3810 TAGACCAAGCCCAAGAGCTGGACGCTGTAATTTCTGCTGCAACCCCGTACACCCAC 3869
2815 ACCTATTATCTACTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874
3870 ACCTATTATCTACTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3929

QY 2875 TTGACCTA 2882
Db 3930 TTGACCTA 3937

RESULT 10
AB296919
ID AB296919 standard; DNA; 6771 BP.
XX
AC AB296919;
XX
DT 17-OCT-2003 (first entry)
XX
Human nucleic acid sequence.
XX
Human; antisense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
Homo sapiens.
OS
XX
WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.
XX
Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12161; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 6771 BP; 1815 A; 1570 C; 1439 G; 1947 T; 0 U; 0 Other;

Query Match 53.8%; Score 2690.8; DB 10; Length 6771;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 2846; Conservative 6; Mismatches 18; Indels 18; Gaps 13;

QY 1 CTGGTCATCTCAGTTCCTTTTCTCACCTTGACTGCAAGATGAACACTCCTTGTGCTAGCTGT 60
Db 1062 CTGGTCATCTCAGTTCCTTTTCTCACCTTGACTGCAAGATGAACACTCCTTGTGCTAGCTGT 1121
QY 61 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGGCTTCTCTCCCAAGTGAGCTA 120
Db 1122 GCTGCTCACAGGTAGGCAAGTCTCCCGGCTCCACCGGCTTCTCTCCCAAGTGAGCTA 1181
QY 121 AGATCTCACTCTCTGGAATGGGGGCCACAGGGCCACAGCAAAACAGAGGATGGCCAGCCCCG 180
Db 1182 AGATCTCACTCTCTGGAATGGGGGCCACA---CACAGCAAAACAGAGGATGGCCAGCCCCG 1238
QY 181 CAGTCTCAAWTCGAGGTCCCAAGTGGGGCTTAAGGGCTCCTCTATTGGGGTTCCTCTCAAG 240
Db 1239 CAGTCTCAAWTCGAGGTTCCTCACT-GGGCTTAAGGGCTCCTCTATTGGGGTTCCTCTCAAG 1297
QY 241 GCTGGCACTTTTTCACAGCTGCAAGTCTGAACCTCAGATTGCTGAGCTAAGAAAGCTTGCC 300
Db 1298 GCTGGCACTTTTTCACAGCTGCAAGTCTGAACCTCAGATTGCTGAGCTAAGAAAGCTTGCC 1357
QY 301 TTTATTCTTTTTCAGACAGGGTCTTGCTCTATCACCCAGGCTGGAGTTCAGTGCCA 360
Db 1358 TTTATTCTTTTTCAGACAGGGTCTTGCTCTATAACCCAGGCTGGAGTTCAGTGCCA 1417
QY 361 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCTCCACCTTACTCA 420
Db 1418 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCTCCACCTTACTCA 1477
QY 421 ACTAAGTAGTTAGGCAATCTCCATTTATTTTATTATTTTAAATTTTATTTTATTTT 480
Db 1478 ACTAAGTAGTTAGGCAATCTCCATTTATTTTATTATTTTAAATTTTATTTTATTT 1537
QY 481 TACTTTATTTTATTTTGGAGCGGGCTCACTCTGTCGGCCAGGCTGGAGTGGGGCG 540
Db 1538 TACTTTATTTTATTTTGGAGCGGGCTCACTCTGTCG-CCAGGCTGGAGTGGGGTGGGC 1596
QY 541 TGATCTCAGATCACTCAACCTCCATCTCCTGGGTTCAAAATAATTTCTTTCCTCAGCCT 600
Db 1597 TGATCTCAGATCACTCAACCTCCATCTCT-GGTTCAAATAATTTCTTTCCTCAGCCT 1655
QY 601 CTCAGTAGCTGGGACTGTAGCTCTCAAGTAGCTGGGCAACACCACTATGCCAGCTAA 660
Db 1656 CTCAGTAGCT-GGACTGTGTAGCTCTCAAGTAGCTGGGCAACACCACTATGCCAGCTAA 1714
QY 661 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 1715 TTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1774
QY 721 CTCCTCTTTAGATTCCTCATCTCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 779
Db 1775 CTCCTCTTTAGATTCCTCATCTCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1834
QY 780 TTTCTTACTTATCAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 839
Db 1835 TTTCTCTACTTATACACTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1894
QY 840 TCGCCAAGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGTGGGT 899
Db 1895 TCGCCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCCACCTGTGGGT 1954
QY 900 TCAGGCACTTCTCCCGCTCAGCCTCCCGAGTAGCTGGGACTAAAGGCGCTGCCACCAAC 959
Db 1955 TCAGGCACTTCTCCCGCTCAGCCTCCCGAGTAGCTGGGACTAAA-GCGCCTGCCACCAAC 2013
QY 960 GCGCCGCTAAATTTTGTATTTTAAATAAGCGGGTTTCACTGTGTAGCAGGATG 1019
Db 2014 GCGCCGCTAAATTTTGTATTTTAAATAAGCGGGTTTCACTGTGTAGCAGGATG 2073
QY 1020 GTCTCGATCTCATGACCTGTGATCGCTCGCCTCGCCTCCCAAGTCTGGGATTACA 1079
Db 2074 GTCTCGATCTCATGACCTGTGATCGCTCGCCTCGCCTCGCCTCCCAAA--TGCTGGATTACA 2131

QY 1080 GGCATGAGCCACCGTCCCGGCTTATCACATTTATTTATTTATTTTCTCTCCCACT 1139
Db 2132 GGCATGAGCCACCGTCCCGGCTTATCACATTTATTTATTTATTTTCTCTCCCACT 2191
QY 1140 AGTTTGTAAAGCTCCATGAGGTTAGAG---ATTATTTATTTATTTATTTATTTATTTA 1196
Db 2192 AGTTTGTAAAGCTCCATGAGGTTAGAGATTATTTATTTATTTATTTATTTATTTATTTA 2251
QY 1197 TTATTTATTTATTTATTTATTTCTGTTCACTGCTGATCTCTAGCTCCTAGGACAGAGCTGGC 1256
Db 2252 TTATTTATTTATTTATTTATTTCTGTTCACTGCTGATCTCTAGCTCCTAGGACAGAGCTGGC 2311
QY 1257 ACATAGTAAGTCTCAATAAATATTTCACTGGATAAACAGTGCAGATAGTTTAAAACTATC 1316
Db 2312 ACATAGTAAGTCTCAATAAATATTTCACTGGATAAACAGTGCAGATAGTTTAAAACTATC 2371
QY 1317 TGACCTAGGGAGGCTGAGGCAGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA 1376
Db 2372 TGACCTAGGGAGGCTGAGGCAGAGAAATGGCGTGAACCCGGGAAGCAGAGTTTGCAGTGA 2431
QY 1377 GCTGAAATCGTCTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAA 1436
Db 2432 GCTGAAATCGTCTCACTGCACTCCAACTGGGCAACAGAGCAAGACTCCATCTCAAAAAA 2491
QY 1437 AAAAAAATACTATCAGGCCTAGCTGGGTGGCACAATGCTGTAATCTCTAGCTGAGCGGT 1496
Db 2492 AAAAAAATACTATCAGGCCTAGCTGGGTGGCACAATGCTGTAATCTCTAGCTGAGCGGT 2551
QY 1497 AGGTCCTCCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGATATATATATATACACACA 1556
Db 2552 AGGTCCTCCAGAAGAAAGAAAGAAAGAAAGAAAGAAAGATATATATATATACACACA 2611
QY 1557 CAAAGATATAAACTTTATATATATAAAGTTTTTCATTTAAAAAATAAACTCTTACCC 1616
Db 2612 CAAAGATATAAACTTTATATATAAAGTTTTTCATTTAAAAAATAAACTCTTACCC 2670
QY 1617 ACTTTCACTTTACAGGTTCTGGTCCAAAGCTTTTTCAGAGGAGCAGCTGGCAGGGT 1676
Db 2671 ACTTTCACTTTACAGGTTCTGGTCCAAAGCTTTTTCAGAGGAGCAGCTGGCAGGGT 2730
QY 1677 CAGGAGGAGCGTGGGACCCGAGGAGCAGAAAGCAGTGTCTCCCGGGGTGCTGGCA 1736
Db 2731 CAGGAGGAGCGTGGGACCCGAGGAGCAGAAAGCAGTGTGTCTCCCGGGGTGCTGGCA 2790
QY 1737 GACCATTTGAACCTCTGCTATGCTTTCTTGCAGTGGCGCGCMCAAGCGGCACTCAGC 1796
Db 2791 GACCATTTGAACCTCTGCTATGCTTTCTTGCAGTGGCGCGCGCMCAAGCGGCACTCAGC 2850
QY 1797 CCTCGGGCGGTGTCAGTTCGCAAAATGATCAAAGTGGTATCCCGGGGAGTGACCCC 1856
Db 2851 CCTCGGGCGGTGTCAGTTCGCAAAATGATCAAAGTGGTATCCCGGGGAGTGACCCC 2910
QY 1857 TTTTGGAAATCAACAACTACGGCTGCTACTGTGGGCTTGGGGGCTCAGGCAACCCCGTG 1916
Db 2911 TTTTGGAAATCAACAACTACGGCTGCTACTGTGGGCTTGGGGGCTCAGGCAACCCCGTG 2970
QY 1917 GATGAACCTGGACAAGTAAAGTATCGCTCGCAGGAAAAATTTGGAGTGCCTGCGCGGGCGG 1976
Db 2971 GATGAACCTGGACAAGTAAAGTATCGCTCGCAGGAAAAATTTGGAGTGCCTGCGCGGGCGG 3030
QY 1977 GGTGGGCA-CACGCCAAGGATCTCACAGGCATACAAAGGGGACTTGCATATCTGCTAA 2035
Db 3031 GGTGGGCA-CACGCCAAGGATCTCACAGGCATACAAAGGGGACTTGCATATCTGCTAA 3090
QY 2036 GGATAACATATTTTTCACCTCTGTAATAATAAATAATGTTTCCAAGAGGCCCTGTAGC 2095
Db 3091 GGATAACATATTTTTCACCTCTGTAATAATAAATAATGTTTCCAAGAGGCCCTGTAGC 3150
QY 2096 GAAACGACCCCTTAGAGATGGAAACATGACCGACGTGCAAAACAGTGGGCGATGCTGTC 2155
Db 3151 GAAACGACCCCTTAGAGATGGAAACATGACCGACGTGCAAAACAGTGGGCGATGCTGTC 3210
QY 2156 CCTCAGTGGCAGAAATGTAGCAACAGTAAGAAATCAACAGCAACTATCCACGTGTCTTTTC 2215

Db	1239	CAGTCTCAATTCGAGGTTCCAGT- GGGCTTAAGGGCTCTCTATTGGGGTTCCCTCAAG	1297
Qy	241	GCTGGCACTTTTCAAACTGCAAGTCTGAATCTAGATTGCTGAGCTAAGAAAGCTTGCC	300
Db	1298	GCTGGCACTTTTCAAACTGCAAGTCTGAATCTAGATTGCTGAGCTAAGAAAGCTTGCC	1357
Qy	301	TTTATTTCCTTTTTCAGACAGAGGTCCTGCTCTATCACCAGAGCTGGAGTTGAGTGCCA	360
Db	1358	TTTATTTCCTTTTTCAGACAGAGGTCCTGCTCTATCACCAGAGCTGGAGTTGAGTGCCA	1417
Qy	361	TGATCATAGCTCACACAGCTTCCAAATCTGFGGGCTCAAGTGATCTCCACCACTTACTCA	420
Db	1418	TGATCATAGCTCACACAGCTTCCAAATCTGFGGGCTCAAGTGATCTCCACCACTTACTCA	1477
Qy	421	ACTAAGTAGTTAGGCCAATCTCCATTTATTATTTATTTATTTATTTATTTATTTATTT	480
Db	1478	ACTAAGTAGTTAGGCCAATCTCCATTTATTATTTATTTATTTATTTATTTATTTATTT	1537
Qy	481	TACTTTATTTATTTTGGACAGGGGCTCACTGTGCGCCAGAGCTGGAGTGGGTGGG	540
Db	1538	TACTTTATTTATTTTGGACAGGGGCTCACTGTGCG- CCAAGGCTGGAGTGGGTGGG	1596
Qy	541	TGATCTCAGATCACTACAACCTCAATCTCTGGGTTCAAATTAATTCCTTCGCTCAGCCT	600
Db	1597	TGATCTCAGATCACTACAACCTCAATCTCTCT- GGTTCAAATAATTCCTTCGCTCAGCCT	1655
Qy	601	CTCAAGTAGCTGGGACTTTGAGTCTCTCAAGTAGCTGGCACACACCACTGCCCAGCTAA	660
Db	1656	CTCAAGTAGCT- GGACTTGTAGTCTCTCAAGTAGCTGGCACACACCACTGCCCAGCTAA	1714
Qy	661	TTTTTTGTGTGTTTTTTTGGTAGACAGGTTTTCCATGTTGGCCAGGCTGGGTGAC	720
Db	1715	TTTTTTGTGTGTTTTTTTGGTAGACAGGTTTTTCACCATGTTGGCCAGGCTGGGTGAC	1774
Qy	721	CTCCCTTTAGATTCTCCTCATCTGCTCTATTCTTCCCTTTCT- AATGCAGTATCCAG	779
Db	1775	CTCCCTTTTAGATTCTCCTCATCTGCTCTATTCTTCCCTTTCTAATATGCAGTATCCAG	1834
Qy	780	TTTTCTTACTTATCACATTTTATTATTCTTATTATTATTGACAGAGTCTTGCTTTG	839
Db	1835	TTTTCTTACTTATCACATTTTATTATTCTTATTATTATTGACAGAGTCTTGCTTTG	1894
Qy	840	TGCGCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGTCTCCACCTGCTGGT	899
Db	1895	TGCGCAAGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGTCTCCACCTGCTGGT	1954
Qy	900	TCAGCCATCTTCCGGCTCAGCCTCCCGAGTAGCTGGGACTAAGGCGCTGCCACCAC	959
Db	1955	TCAGCCATCTTCCGGCTCAGCCTCCCGAGTAGCTGGGACTAAA- CGCGCTGCCACCAC	2013
Qy	960	GCCCGCTAAATTTTTTTGTTATTTTAAATAAGACGGGTTTCATCGTGTAGCCAGATG	1019
Db	2014	GCCCGCTAAATTTTTTTGTTATTTTAAATAAGACGGGTTTCATCGTGTAGCCAGATG	2073
Qy	1020	GTCTCGATCTCATGACCTTGTGATCCGCCTGCCTCGGCTCCCAAAGTGTGGGATTACA	1079
Db	2074	GTCTCGATCTCATGACCTTGTGATCCGCCTGCCTCGGCTCCCAA- - TCCTGGAATTACA	2131
Qy	1080	GGCATGAGCCACCGTGGCGGCTTATCATATTATTATTATTATTGTTTTTCTCTCCCACT	1139
Db	2132	GGCATGAGCCACCGTGGCGGCTTATCATATTATTATTATTATTGTTTTTCTCTCCCACT	2191
Qy	1140	AGGTTGTAAGCTCCATCAGGTTAGAG- - -ATTATTATTATTATTATTATTATTATTA	1196
Db	2192	AGGTTGTAAGCTCCATGAGGTTAGAGATTATTATTATTATTATTATTATTATTATTA	2251
Qy	1197	TTATTATTATTATTATCTGTTCACTGCTGATCTCTAGCTCCTAGGACAGAGCTGGC	1256
Db	2252	TTATTATTATTATTATCTGTTCACTGCTGATCTCTAGCTCCTAGGACAGAGCTGGC	2311
Qy	1257	ACATAGTAAGTGTCAATAAATATTCTCGATAAACAAGTGCAGATAGTTTAAAACTATC	1316
Db	2312	ACATAGTAAGTGTCAATAAATATTCTCGATAAACAAGTGCAGATAGTTTAAAACTATC	2371

Qy	1317	1318	1319	1320	1321	1322	1323	1324	1325	1326	1327	1328	1329	1330	1331	1332	1333	1334	1335	1336	1337	1338	1339	1340	1341	1342	1343	1344	1345	1346	1347	1348	1349	1350	1351	1352	1353	1354	1355	1356	1357	1358	1359	1360	1361	1362	1363	1364	1365	1366	1367	1368	1369	1370	1371	1372	1373	1374	1375	1376	1377	1378	1379	1380	1381	1382	1383	1384	1385	1386	1387	1388	1389	1390	1391	1392	1393	1394	1395	1396	1397	1398	1399	1400	1401	1402	1403	1404	1405	1406	1407	1408	1409	1410	1411	1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500	1501	1502	1503	1504	1505	1506	1507	1508	1509	1510	1511	1512	1513	1514	1515	1516	1517	1518	1519	1520	1521	1522	1523	1524	1525	1526	1527	1528	1529	1530	1531	1532	1533	1534	1535	1536	1537	1538	1539	1540	1541	1542	1543	1544	1545	1546	1547	1548	1549	1550	1551	1552	1553	1554	1555	1556	1557	1558	1559	1560	1561	1562	1563	1564	1565	1566	1567	1568	1569	1570	1571	1572	1573	1574	1575	1576	1577	1578	1579	1580	1581	1582	1583	1584	1585	1586	1587	1588	1589	1590	1591	1592	1593	1594	1595	1596	1597	1598	1599	1600	1601	1602	1603	1604	1605	1606	1607	1608	1609	1610	1611	1612	1613	1614	1615	1616	1617	1618	1619	1620	1621	1622	1623	1624	1625	1626	1627	1628	1629	1630	1631	1632	1633	1634	1635	1636	1637	1638	1639	1640	1641	1642	1643	1644	1645	1646	1647	1648	1649	1650	1651	1652	1653	1654	1655	1656	1657	1658	1659	1660	1661	1662	1663	1664	1665	1666	1667	1668	1669	1670	1671	1672	1673	1674	1675	1676	1677	1678	1679	1680	1681	1682	1683	1684	1685	1686	1687	1688	1689	1690	1691	1692	1693	1694	1695	1696	1697	1698	1699	1700	1701	1702	1703	1704	1705	1706	1707	1708	1709	1710	1711	1712	1713	1714	1715	1716	1717	1718	1719	1720	1721	1722	1723	1724	1725	1726	1727	1728	1729	1730	1731	1732	1733	1734	1735	1736	1737	1738	1739	1740	1741	1742	1743	1744	1745	1746	1747	1748	1749	1750	1751	1752	1753	1754	1755	1756	1757	1758	1759	1760	1761	1762	1763	1764	1765	1766	1767	1768	1769	1770
----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

QY 2395 GAAACCTGCTCTACTAATAAATACAAAAATAGCGGACATGGTGGCGAGCGCTGTA 2454
DB |||||||
QY 3451 GAAACCTGCTCTACTAATAAATACAAAAATAGCGGACATGGTGGCGAGCGCTGTA 3510
DB |||||||
QY 2455 ACCCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGGTGCTGTCACCTGCT 2514
DB |||||||
QY 3511 ACCCCAGCTACTTGGGAGACTGAGTTGGAGGTTTCA-TGAGCCAAAGGTGCTGTCACCTGCT 3569
DB |||||||
QY 2515 GTCAGCCTGGTAACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTCAATAATAT 2574
DB |||||||
QY 3570 GTCAGCCTGGTAACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTCAATAATAT 3629
DB |||||||
QY 2575 ATGATAAAGGACTTATATTTTTCAGGCCATAGGATCATTTCTCTGAAGCATCTTGGC 2634
DB |||||||
QY 3630 ATGATAAAGGACTTATATTTTTCAGGCCATAGGATCATTTCTCTGAAGCATCTTGGC 3689
DB |||||||
QY 2635 GAAGTCATCCCCACTGTTCTCGAGAGTGGCGAGGTGAGGCTGACCTATTGCTCTGCAC 2694
DB |||||||
QY 3690 GAAGTCATCCCCACTGTTCTCGAGAGTGGCGAGGTGAGGCTGACCTATTGCTCTGCAC 3749
DB |||||||
QY 2695 TTACTCTATCTGAGTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC 2754
DB |||||||
QY 3750 TTACTCTATCTGAGTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGC 3809
DB |||||||
QY 2755 TAYGACCAGGCCAAGAGCTGGACAGCTGTAATTTCTGCTGGACAMMCGTACACCCAC 2814
DB |||||||
QY 3810 TAGACACGCGCAAGAGCTGGACAGCTGTAATTTCTGCTGGACAAACCCGTACACCCAC 3869
DB |||||||
QY 2815 ACCTATTATCATCTGCTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 2874
DB |||||||
QY 3870 ACCTATTATCATCTGCTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCC 3929
DB |||||||
QY 2875 TTGACCTA 2882
DB |||||||
QY 3930 TTGACCTA 3937
DB |||||||

RESULT 12
ABD33466/c
ID ABD33466 standard; DNA; 42360 BP.
XX
AC ABD33466;
XX
XX 18-NOV-2004 (first entry)
XX Human cancer-associated (CA) gene HD07-089.
DE Human cancer-associated protein; CAP; cancer-associated gene; CA; gene;
XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX Homo sapiens.
XX WO2004058146-A2.
XX
XX 15-JUL-2004.
XX
XX 15-DEC-2003; 2003WO-US040081.
XX
XX 17-DEC-2002; 2002US-00322281.
XX (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Malandro MS;
XX WPI; 2004-499109/47.
XX Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX
XX Claim 16; SEQ ID NO 618; 182pp; English.
XX The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates

CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 42360 BP; 11698 A; 9658 C; 10445 G; 10559 T; 0 U; 0 Other;
Query Match 9.1%; Score 456.6; DB 13; Length 42360;
Best Local Similarity 99.8%; Pred. No. 3.5e-74;
Matches 456; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4545 ACAAACTAATAAGATTCTCTGAAGTAAAGCAGAGATACGTAATATATGTAATAAGTT 4604
DB |||||||
QY 4605 TAAATGCAATTTTAACTGTAATCTTATTTTGGTTATAAAAGTAAACAGCCAA 4664
DB |||||||
QY 42300 TAAATGCAATTTTAACTGTAATCTTATTTTGGTTATAAAAGTAAACAGCCAA 42241
DB |||||||
QY 4665 AGTAATGCAACTTCAAACTCTACATAAATATCTATTGGAAGTGAAGGCATCTATAA 4724
DB |||||||
QY 42240 AGTAATGCAACTTCAAACTCTACATAAATATCTATTGGAAGTGAAGGCATCTATAA 42181
DB |||||||
QY 4725 TCCTACTACCAAGATTAACAGATTACATATTCTCCAGATTTTTGGGCGATACACTAGC 4784
DB |||||||
QY 42180 TCCTACTACCAAGATTAACAGATTACATATTCTCCAGATTTTTGGGCGATACACTAGC 42121
DB |||||||
QY 4785 TTTTATTTTGGGAAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGCTCTATGT 4844
DB |||||||
QY 42120 TTTTATTTTGGGAAATTTCCATGTGCAGGCATACCTAAATTTTCTAAATGCTCTATGT 42061
DB |||||||
QY 4845 AGTATTCCATTTAAGGATGTTCCATAATTTTAAATACATCTTTAAAGTAGAGAACT 4904
DB |||||||
QY 42060 AGTATTCCATTTAAGGATGTTCCATAATTTTAAATACATCTTTAAAGTAGAGAACT 42001
DB |||||||
QY 4905 AGTTGGGCGATGGTGGCTCACGCTGTATCCAGCACATTGGGAGCCGAGGCNAATGCA 4964
DB |||||||
QY 42000 AGTTGGGCGATGGTGGCTCACGCTGTATCCAGCACATTGGGAGCCGAGGCNAATGCA 41941
DB |||||||
QY 4965 TCACCTTGAGGTCGGAGTTTGAGACCAGCCTGGACAA 5001
DB |||||||
QY 41940 TCACCTTGAGGTCGGAGTTTGAGACCAGCCTGGACAA 41904
DB |||||||

RESULT 13
ADP13332/c
ID ADP13332 standard; DNA; 126990 BP.
XX
XX ADP13332;
AC
DT 26-AUG-2004 (first entry)
XX Renal cell carcinoma differentially expressed gene #68.
DE
XX ds; diagnosis; non-blood disease; solid tumor; gene expression;
KW peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer;
KW head/neck cancer; differential expression.
XX Homo sapiens.
XX WO2004048933-A2.
XX 10-JUN-2004.
PD

XX 21-NOV-2003; 2003WO-US037481.
 XX PF
 XX PR 21-NOV-2002; 2002US-0427982P.
 XX PR 03-APR-2003; 2003US-0459782P.
 XX PA (AMHP) WYETH.
 XX PA (TWIN/) TWINE N C.
 XX PA (BURC/) BURCZYNSKI M B.
 XX PA (TREP/) TRSPLICCHIO W L.
 XX PA (DORN/) DORNER A.
 XX PA (STOV/) STOVER J A.
 XX PA (SLON/) SLONI D K.
 XX PI Twine NC, Burczynski ME, Trepicchio WL, Dorner A, Stover JA;
 XX PI Sloni DK;
 XX DR WPI; 2004-460799/43.
 XX PT Diagnosing non-blood disease such as solid tumor, involves comparing
 PT differential expression profile of specific genes in peripheral blood
 PT sample of subject with reference expression profile of specific genes.
 XX PS Disclosure; SEQ ID NO 68; 350pp; English.
 XX SS
 CC The invention relate to a method of diagnosing (M1) non-blood disease
 CC such as solid tumor by providing peripheral blood sample of human having
 CC non-blood disease, and comparing an expression profile of specific genes
 CC in the peripheral blood sample to reference expression profile of the
 CC genes, where each of the genes is differentially expressed in peripheral
 CC blood mononuclear cells (PBMCs) of patients having the disease as
 CC compared to PBMCs of normal humans. The method is useful for diagnosing
 CC non-blood disease such as solid tumor. The solid tumor is chosen from
 CC renal cell carcinoma (RCC), prostate cancer and head/neck cancer. The
 CC peripheral blood sample comprises enriched PBMCs. The peripheral blood
 CC sample is a whole blood sample (claimed). (M1) is useful for identifying
 CC genes that are differentially expressed in peripheral blood samples
 CC isolated at different stages of progression, development or treatment of
 CC RCC and/or other solid tumors. This sequence corresponds to a gene that
 CC is differentially expressed and detected by the method of the invention.
 CC (Note: this sequence is not given as part of the printed specification
 CC but was obtained from WIPO in electronic format at
 CC ftp.wipo./pub/published_pct_sequences).
 XX SQ Sequence 126990 BP; 36683 A; 27389 C; 27065 G; 35853 T; 0 U; 0 Other;
 Query Match 8.9%; Score 444.4; DB 12; Length 126990;
 Best Local Similarity 54.1%; Pred. No. 7.2e-72;
 Matches 1225; Conservative 3; Mismatches 987; Indels 51; Gaps 14;
 QY 2291 AGCCAGGCGGTGCTCATGCTCTAATCCAGCAGCTTGGAGGCGGCGGCGG 2350
 DB 28169 AGCCAGGCGGTGATGGCTCATGCTCTGATCCAGCAGCTTGGAGGCGGCGGCGG 28110
 QY 2351 ATCAGCTTGAGGTGAGGTTGAGACAGCCTGGCCAAATGGTGAACCTGTCTCTAC 2410
 DB 28109 ATCAGCTGAGGTGAGGTTGAGACAGCCTGGCCAAATGGTGAACCTGTCTCTAC 28050
 QY 2411 TAAAAAATACAAAAATATAGCCGACATGGTGGCGAGCGGC-----TGTAACCCAGCTAC 2465
 DB 28049 T-AAAAAATACAAAAATATAGCCGCGGTGGTGGCAGACACATATAGTCTAGTCTAGCTAC 27991
 QY 2466 TTGGGAGACTGAGTTGGAGTTTCAGTGAGCCAGGTGCTGTGTCACCTGCTCCAGCTGG 2525
 DB 27990 TTGGGAGGCTGAGCGGGGAATCGTTTGAACCCGGAGGTGAGGCTGAAGTGAGCTGAG 27931
 QY 2526 GTAAACAGCAACTCTGTCTCAAA-----AAAAAAAATGCTTCAATATAATATATATAA 2581
 DB 27930 ATCACACCACTGCACTCCAGCTTGGTACAGCAGCAGGCTCATCTCAAAAACAATG 27871
 QY 2582 AAGGACTATATATTTTTCAAGCCATAGGATCATTTCTCTGGAAGCATCTTGGCGAAGTCA 2641
 DB 27870 GTGGGCGAGGCGGCTGAGTCAAGTCAATATCCAGCACTTTGGGAGGCGCAAGGCGGC 27811

QY 2642 TCCCCACCTGTTCTCTGAGAGTGGGCGAGGTGAGGCTGACCTATTGCTCTGCACTTACTCC 2701
 DB 27810 AGATCATGAGGTGAGGAGATCAAGACCATCTCTGGCTAACCGGTAAACCCCGTCTCTAC 27751
 QY 2702 TATCTCAGCTGCTCCCTCCACTTTCCAGGTGCTGCAGACACATGACAACCTCTCTAYGACC 2761
 DB 27750 TAAAAAATACAAAAATATAGCCGCGCATCTGTGTGGCGCTGTATATCCAGCTACTTGGG 27691
 QY 2762 AGCCCAAGAGCTGCAGACAGCTGTAATTTCTGTCTGCACAMMCCGTACACCCACACTATT 2821
 DB 27690 AGGCTGAGCGGGAGAAATGGCGTGAACCCGGGAGCGGAGCTTTGCAGGAGCGGAGATCG 27631
 QY 2822 CATACTCTGCTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCTCCCTCTCTTGACCT 2881
 DB 27630 CACTCTCGCTCCCATTTCCAGCTGGGAGACAGAGTGAGACTCCATCTCAAAAACAAAACA 27571
 QY 2882 ATGAATTTAGTTGTTCTCAGTAGGCGGGGGGAAATAATAGTAAAC-----AACAG 2933
 DB 27570 AAACAAAAACAAAGTGGTGGGCGCATCTCTTAATCTCTAGCTACTTGGAGGCTGAG 27511
 QY 2934 CCATGATTTAGTGTAAATTTCTTGGTCTGGCAGTGTCTCTTAACTCTCAGAACAA 2993
 DB 27510 GCAGGAGAAATCGCTTGAACCCCGGAGGAGGCTGCAGTGAGCCAGATCACCACTG 27451
 QY 2994 CACTATGGATAGGT-ACAAATTTATCTCTCACTTAACAGATAAGAAAACTGAGGCTCAGAG 3052
 DB 27450 TACTCAGCCTGGGTGACAGAACGAGACTCTCCATAAGTTTCATAGTAAATAACACCAAT 27391
 QY 3053 GCTGAGCTATTGGCCAAAGATCACAGCTTGTAGTGGTGACAGTTTGGGTTTTTTTTT 3112
 DB 27390 TCTAATCCGACACCGCAAGATTTACTCTAGCCTTCCACCATGTCCATATCTTTAACTCTT 27331
 QY 3113 GTTGTGTTAGACAGAGGCTTCTCTCTGTCACCCAGCATGACGACAGTGGTCAACC 3172
 DB 27330 TCTCTAATGCTGAGATGAGTCTCACTCTGTCTCACCAGCTGGAGTGAGTGGTGATC 27271
 QY 3173 ATAGTCTACTGAGCCTCAACCTCTCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAA 3232
 DB 27270 TCA-----CCTCCACTCCAGGTTCAAGGATTTCTCTGCTCAGCTCC- TG 27223
 QY 3233 GTAGCTGGAGTACGAGCGTGCACCAACGCTCTGGCTTAATTAATAAATTTTTTTGAG 3292
 DB 27222 GTAGCTGGGAATACAGGCGTGCACCACTATGCGCGCTAAATTTTTTATA--TTTTCAGTAG 27165
 QY 3293 AGACTGGGTCTTACTAGCTTGGCAGGCTTGTCTTAACTCTGCTTCAAGCAATCTCTC 3352
 DB 27164 AGTCGAGTTTCCACCATGTTTCCAGGCTGGTCTCAAACTCTCTGACCTCAAGTGATCCAC 27105
 QY 3353 CTACCTTGGCATCCCAAGTGTCTGGGATTACAGGCGGTGAGCCACCATGTGCGGCTACTTTA 3412
 DB 27104 CGCCGCGAGCTCCCAACGCTGCTGGGATAATAGGGGTGAGCCACTGCGACCTGGCTTCT 27045
 QY 3413 TTTCTTTATCATTTCCATCTTTTCCAAATAGAAATGTAAGATCCACAGAGGATTAATCGCT 3472
 DB 27044 GTACTCTTTTATCTATTTTCACTGGTCTGTTCTTTGGTTTTCAGTATCATAGTACTTTG 26985
 QY 3473 ATTTCTTCTTTCTTTTGTGAGACAGAGTCTCATCTTATCACCTCAACCTCCGTTCCAG 3532
 DB 26984 TTTCTGTAGCTTAAATAAT--ATATATTTTAAAGCTGGAATGACGTGGCATGATCTCAGC 26927
 QY 3533 TCACCTGCACTCTCGCTCCCGGTTTCAAGTGATTCTCTCTGCTTAAGCCTCTCTGAGTAGC 3592
 DB 26926 TCACCTGCACTCTCGCTCCAGCTCCAGGCTCAAAATTTTCTGTGACTCAGCTCTCTGAGTAGC 26867
 QY 3593 TGGAAATTAAGCGGTGCACCACTGCTTGGCTAAATTTTTTGTATTTTTTGTAGCAGAGTAGG 3652
 DB 26866 TGGGATTAAGCGAGGCGCACCACTGCTGCTCAAACTCTGACCTCAAGTGTATCTGCTGCTCT 26808
 QY 3653 GGTTTTACATGTTGCCCGAGGCTGTCTCAAACTCTGACCTCAAGTGTATCTGCTGCTGCT 3712
 DB 26807 AGTTTTCACCATGTTTCTTCTAGGCTGATCTTAACTCTGACCTCGAGTGTATCCGCGCGT 26748


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QY 3581 CTCTCAGTAGCTGGAATTACAAAGCGTGACACCATGCTTGCTTAATTTTGTATTTT 3640
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18577 CTCCCAAGTAGCTGGAGCTACAGGCATGCCACCCACCTGGCTAA- TTTTGTATTTT 18635
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3641 TAGCAGAGATGGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCGACCTCAAGTG 3700
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18636 TAGTAGACAGCGGGTTTCAACATGCTGGCAGGCTGGTCTCGAACTCTTGACCTC- GTG 18693
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3701 ATCTGCTGCTCAGTCTCCCAAGTGTGGAAATTATAGCGGTGAGTCACTGCTGCTGC 3760
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18694 ATCCACCCGCTCAGCTTCCAAAGTGTGGGATTACAGCATGAGCCACCATACCTGGC 18753
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3761 CGATTACTGTCTATTTT-----CTTATTGTCTATATCCCCAGATCTAGAGCAGTGTCTG 3814
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18754 CAGGAAGTACAGAGTTTATAGAGACATCTTCTGAAATAGGGTGGTGGCCCTCATTTATTC 18813
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3815 ACATATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAATTTCTT 3874
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18814 ATTAATGCTATTCTTCCAAACCCGGGAACCAATAAGATGTATAGCATGGCATCCCTC 18873
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3875 TTTCTTTTTTAAACAATCTTGACAACCTTTGCAGAAATAAATACAATCTTGCAATCTGCT 3934
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18874 ATGATCTGAAGTTACTGTGCGTAACGTGCGGTCCCATTCGATTTGGGATTTGGGGGATGCC 18933
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3935 TTTTCACTTATCA- CCTTGTATGACTTTTTCATATTGCTCAAACTTTATTGTTACTG 3993
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18934 TGCACGTGTCTGTATGCTGTCATGCTGCGGTGCCATCAGTCTGTGAGCTCCCTCT 18993
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3994 TTTTTCATTTTACTTATTTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCTT 4053
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 18994 GGGCTTGGCGCTTTTCTCATCTTCTGTTATTTCTCAGCAGCTTTGTGTAACATACCTGGC 19053
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4054 CTGCTCCACTTTAGAGGCCAAATTTACAAATCTGATGAAGCTATGACCTCTCCCC 4113
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19054 ACTCAATGAATTTAAATAATCTGAAGCGGGGTGGGGGAGCTTGTCAATATAGCCCC 19113
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4114 AGAGAAATACACACACACACACACTCACACAGTTTTTTTTTAATGTTGCAACTAA 4173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19114 ACCTTGTTTGCCCCCTTGGACTTGATTAAGCCGTTTGTGCTATGCATATGTCATCTCTT 19173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4174 GACAAAGAACTGCATTAGAGGATGTTTGTTCATATTAATTAATAATAACTCA----- 4226
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19174 TTCTAGCAATGAGTTACTTTGGATGAATAGGCAGATCTCTTGGTTAAACCATAAAGACAG 19233
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4227 GTTGGGCACAGTCACTCAAGCCTGTAACACAGTACTTTTGGAGTCCAAGTGGTGGAT 4286
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19234 GCTGGGCGGGTGGCTCACATCTGTAAATCCAGCAGCTTTGAGAGCGCGAGGGCGAGAT 19293
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4287 CACTTGAGGTGAGAAGTTTCAGACCCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTA 4346
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19294 CACTTGAGGTTAGAAGTTTCATACCGCTGGCCACATGGTGAACCCCAATCTCTACTA 19353
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4347 AAAATACAAAATTAGTGGGTGTATGTATGTCATGCTGTGATGCTCCAGCTACTCGGGAGG 4406
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19354 AAAATACAAAATTAGCCGAGTGGGTGGCGCATGCTGTAAATCTCTAGCTACTTGGGAGG 19413
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4407 CTGAGCCAGAGATTTGCTTGAACCTGGGAGGAGAGGTGTCAGTGAAGCCGAGATCCCAC 4466
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19414 CTGAGGAGGAGAAATCGCTTGAACCCGGGAGGTGAAGCTTTTCAGTGAAGCCGAGATTTGTC 19473
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4467 CACTGCACTCCAGCCTGGGCGCACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAA 4526
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19474 CATTACACTCCAGCCTGGGCAACAGAGCGAGACTGTGCTCATAATGAACCCATAAAG 19533
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4527 ATA 4529
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 19534 ACA 19536
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 15

ACN43914/c

ID ACN43914 standard; DNA; 160482 BP.

XX

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AC ACN43914;
XX 18-NOV-2004 (first entry)
XX Human genomic sequence hCG26773.
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX Homo sapiens.
XX WO2003073826-A2.
XX 12-SEP-2003.
XX 28-FEB-2003; 2003WO-US006235.
XX 01-MAR-2002; 2002US-00087192.
XX (SAGR-) SAGRES DISCOVERY.
XX Morris DW;
XX WPI; 2003-328604/31.
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
XX Claim 1; SEQ ID NO 100; Opp; English.
XX The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) as a biochip; carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
XX SQ Sequence 160482 BP; 44060 A; 32143 C; 33530 G; 49875 T; 0 U; 874 Other;
Query Match 8.7%; Score 434.2; DB 11; Length 160482;
Best Local Similarity 60.2%; Pred. No. 5.7e-70;
Matches 888; Conservative 1; Mismatches 525; Indels 61; Gaps 8;
QY 3106 TTTTTCCTGTTGTTTAGAGACAGGCTTCTGCTGTACCCAGCATGACAGCTGG 3165
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5181 TGTTCCTGATACGGAGTCTTCTGTTGCCCCAGCTGGATGTCAGTGG 5122
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3166 TGCAACCATAGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGC 3225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5121 CATGATCTCGGCTCACTGAAACCTCTGCTCTGGTTCACGTGATTCCTGCTCAGCA 5062
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3226 CTCCTCAAGTAGCTGGAGTACGAGCGTGACCAACACGCTGG--CTAATTAATAAATAAT 3283
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5061 CTCCTCAAGTAGCTGGAGTACAGGGCTGAGCCACCATGCTGGCCCTAATGTTTGTAT 5002
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3284 TTTTTCAGAGTGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCTCGGCTTCAA 3343
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5001 TTTTAGTAGAGAC-AGGTTTCGCTACATTTGGTCAGCTAGTCTCAAACTCTTCACTCAA 4943
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3344 GCAATCCTCTTACCTTGGCATCCCAAGTGTCTGGGATTAACAGGGTGAGCCACCATGTGC 3403
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4942 GTGATCCGCTGCTTGTATGATACCAAGTGTCTGGGATACAGATGTGAGCCACCCGCC 4883
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3404 GGCTACTTATTTCTTTTACATTCATCTTTCCAAATAGAATGTAAAGTCCACAGAACAGGA 3463
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4882 GGCCAGTCATTCACCTTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTCT 4823
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 5387 TGTTGTTGAGAGGGGCTCGCTATGT-----GGCTGGTCTTCAACTCTCGGCTCAAG 5334
Qy 3345 CAATCTCTCCCTACCTTGGCATCCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGGC 3404
Db 5333 TGATCTCTCCACCTCGGCTCTCAAGCGTGGGATTCAGGTTCCAGCTCTACACCCA 5274
Qy 3405 GCTACTTATTTCTTT-----ACATTCCTATCTTTCC 3434
Db 5273 GCTCATAAATACTTTTTAAATACCAGATAATCTTGCTGCTGCCAAAGAACAACTTTT 5214
Qy 3435 AATAGATGTAAGATCACAGACAGGATTAAGCTATTTCTTCTCTCTTTTCTTTTGA 3494
Db 5213 ACTTGCTCCCAATCTAAAGAAATAGGACTATAG---ACTTGATTTCTTTTTTTTAA 5157
Qy 3495 GACAGAGTCTCACTTTCATCACTCAACCTCCGTTTCAG-----CTCACTGCA 3540
Db 5156 GGTGGAGTATGTCTGCTGCCTAGGCTTGAGTGCAAGTGTGATCTTGCACTCACTGCA 5097
Qy 3541 ACCTTGCTCCCGGTTCAAGYGATTCCTCGCTAAGCCTCTCGAGTAGCTGGAATTA 3600
Db 5096 ACCTCTCTCTCTGGGTTCAAGCGATTCTCTGCTCAGCCTCCAGAGTAGCTGGGACTG 5037
Qy 3601 CAAGCGTGACACCACTGCTTGCTGCTAATTTTTTGTATTTTAGCAGAGATGGGTTTAC 3660
Db 5036 CAGGTGCGCTCCACCGCCAGCTAATTTTTTATATTTTAGTAGAGATGGGTTTTCAC 4977
Qy 3661 CATGTTGCCAGGCTGCTCAAACTCTCAAGTCTCAAGTCTGCTGCTCAGTCTCC 3720
Db 4976 CACTTGGCCAGGCTGCTCGAACTCTGAGCTCAAGTATCACTGCTCGACTCC 4917
Qy 3721 CAAAGTCTGGAATTAAGCGTGAAGTCACTGTGCTCGGCGGATTACTGTCTATTTCTT 3780
Db 4916 CAAAGCGCTGGGATTAAGCATGAGCAATGCACTGCGTGAAGGATAAATTTCTTCTC 4857
Qy 3781 TATTGCTATATCCAGATCTAGACGATGCTGACATATAGTAGGTGCTCAATAATAA 3840
Db 4856 TTTTTTAGCAATTTCTTCTGGTCAATACAGCCA-----TGCTGGTACATACA 4810
Qy 3841 TTGATGAATCACAGCCTAGATATAAATTTCTTTTCTTTTAAACAATCTTGACA 3900
Db 4809 TGTTTTCTGGCTGATTTGACCTGTGACTTTCTTTCTTCTTCTTCTTCTCTCT 4750
Qy 3901 ACTTTCAGAAATAAATACAATCTTGCAATCTGCTTTTTCATTCATCACCTGTATGACT 3960
Db 4749 CTCTCTCTCTT---CTCTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4692
Qy 3961 TTTTCATATGCTCTCAACCTTATTTGTTACTGTTTTCATTTGTTACTATTTTAGTAC 4020
Db 4691 TTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 4632
Qy 4021 TGAATAATATGGCTTAATTTGCTTATACATCTCTCTGCTCCACTTTTAGAAGGCCAAATTT 4080
Db 4631 CTTCCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4584
Qy 4081 ACAAAATCTGATGAAGCTATGAACCTCTCTCCAGAGAAATACACACACACACACT 4140
Db 4583 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4524
Qy 4141 CACACACAGTTTTTTTTTAATGTTTGAACCTAGACAGAACTGCATTAGAGATGTT 4200
Db 4523 TCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4471
Qy 4201 TGTTCTATATTAATAAATACTCAGTTGGGCACAGTGAAGTCAAGCTCTGAACACAGT 4260
Db 4470 CTTTTCTTTTTTAAATATAGAGACAGCCAGGTCGGTGGCTGACGCTGTATCTCCAC 4411
Qy 4261 ACTTTGAAGTCAAAGTGGGTGGATCACTTGAAGTGAAGTTCCAGACCAAGCTGGTC 4320
Db 4410 ACTTTGGAGGCCAAGCGGGCGGATCACTTGAGGTGAGGTTCAAGACCAAGCTGGCC 4351
Qy 4321 AATATGGTGAACCTCTCTCTCTAAATAATAAATAAATAGCTGGGTGATGATGAT 4380
Db 4350 AACATGGTGAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4291

Qy 4381 GCTGTAGTCCAGCTACTCGGAGGCTGAGCAAGAGAAATTCCTTGAACCTGGGAGGCA 4440
Db 4290 GCTGTATCCAGCTACTTGGAGGCTGAGCAGGAGAAATCCCTTGAACCCAGGAGCG 4231
Qy 4441 GAGTTGCTAGTGAAGCGAGATCCACCACTGACCTCCAGCTCCAGCTGGCGACACAGCGAGCT 4500
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Db 4170 CCATCTCAAAATAAATAAATAAATAAATAA 4141

RESULT 17
ADP45591
ID ADP45591 standard; DNA; 92500 BP.
XX
XX ADP45591;
XX AC
XX DT 26-AUG-2004 (first entry)
XX
DE Human intercellular adhesion molecule ICAM-1/ICAM-4/ICAM-5 gDNA.
XX breast cancer; cytostatic; gene therapy; human;
KW intercellular adhesion molecule; ICAM-1; human rhinovirus receptor; BB2;
KW CD54; cell surface glycoprotein P3 58; ICAM-4;
KW Landsteiner-Wiener blood group; ICAM-5; telencephalin; chromosome 19p13;
KW ds; gene; SNP; single nucleotide polymorphism.
XX Homo sapiens.
XX
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DB |||||
QY 2462 CTACTTTGGGAGACT-----GAGTTGGAGTTTCAGTGAG 2495
DB |||||
QY 2496 CCAAGGTCTGTCTACTGCTGTCCAGCTGGTAAACAGAGC--AATCTGTCTCAAAAAA 2553
DB |||||
QY 17289 CTGAGATCGCGCATTTGCACTCCAGGCTGGGCACAGAGCGAATCCGTCTCGAAAAA 17348
QY 2554 AAAAAATGCTTTCAATAAATATATGATAAAGAGCTTATATTTTCAAGCCATPAGGATCA 2613
DB |||||
QY 17349 AAAAAAATACACACACACACAAAAAATGTGTTAAATGCTTAACTACACAAAAATGAT 17408
QY 2614 TTTCTCTGAAGCATCTTGGCGAAGTCATCCCACTGTTCTCTGAGAGTGGGAGGTGAG 2673
DB |||||
QY 17409 AATCAGATAAATATGCAATTTATTAGAGAACTGCATGTTGGTCAGTCCAGTCCCTGCAGA 17468
QY 2674 GGCTGACCTATTGCTGTGCACTTACTCTCTACTCTCAGCTGCTCCCTCCCACTTTCCAGGTGC 2733
DB |||||
QY 17469 GGGAAATCCAGCATGACCTCATCTACTCTGTAAGACAGAGCAATCCTGTGTTTATT 17528
QY 2734 TGCCAGACACATGACAACTGCTAYGACCGCCAGCAAGAGCTGACAGCTGTAAATTTCTG 2793
DB |||||
QY 17529 TTTTAAGATGATCTCACTCTGTGTCAGACTGGAGTGGAGTGGCATGATCTCAGCCCT 17588
QY 2794 CTGGACAMMCGGTACACCCACACTATTATCATCTGCTGTCTGGCTCGGCAATCACTGT 2853
DB |||||
QY 17589 CTGCCACTCCACTTCCGGGTTCAAGAGATTCTCATGCTCAGCCCTCCTGAGTAGCTGA 17648
QY 2854 AGCAGTAGTTTATCCCTTCTTGACCTATGAAATCTAGTGGTCTCAGTAGGCCGGG 2913
DB |||||
QY 17649 GATTACAGGCTGTGCGCTCCATGCCAGCTAAATTTTTTATTATTACTAGAGATGAGTT 17708
QY 2914 GGAATAATAGTAACAAACGCCATGATTAGTGTAAATTTCTTGTTCTGGCAGTGTG 2973
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QY 17709 TCACCAAGTTGGGAGGCG-----GTCTCAAACTCTGACCTCAAGTGATCCAC 17758
QY 2974 TCCTTTAATCCTCAGAACAACTATGGGATAGGTACAATATTCCTCACTTAAACAGATAA 3033
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QY 17759 CCACCTCGGCTCCGGAAGTGTGGGATGACAGGTGC-----CTGGTTCAGCAAC 17807
QY 3034 GAAAACTGAGGCTCAGAGGCTGAGCTATTTGCCCAAGATCAACAGCTTGTAAAGTGGT 3093
DB |||||
QY 17808 TGTGTTTACATACATACATTTTATCTGCTGCTCAGCATGGTCAAGCCCTCCACTT----- 17863
QY 3094 ACAGTTTGGGTTTTTTTTTTGTTTGTAGACACAGGCTTGTGCTCTGTCAACCCAGGCA 3153
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QY 17864 ---TTTAAATTTTATTATTATTATTTTGTGAGACAGAGTCTCACCTGTGTGCCAGGTT 17920
QY 3154 TGAGCACAGTGGTGCAACCATAGTCTACCTGAGGCTCAACCTCTGAGCTCAAGGATCT 3213
DB |||||
QY 17921 GGAGTCCAGTGGGCTGATTTCCGCTCAGTCAACCTCTACTTCCAGGTTTCAGCAATTC 17980
QY 3214 GCTGACCTCAGCTCCCAAGTACTGGGACTAGAGGTGCACACAGCGCTGGCTAAT 3273
DB |||||
QY 17981 TCCTGCTCAGCTTCCCGAGTCTGGGATTTACAGGCCCGCTGCCACACACTAGCTAAT 18040
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QY 3334 CTGGCTTCAAGCAATCCTCCTACTTGGGCAATCCAAAGTCTGGGATTTACAGGGGTGAGC 3393
DB |||||
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QY 18159 CACTGCACAGGCTTAAATTTTATTATTATTATTATTATTATTATTATTATTAGAGA----- 18213
QY 3454 AGAACAGGATTAAGTCTATTTTCTTCTCTTTCTTTTGTGAGACAGAGTCTCATCTTCATC 3513

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QY 3634 GTATTTTATAGCAGAGATGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCC 3693
DB |||||
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QY 3694 TCAAGTGATCTGCCCTGCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGAATCACTCT 3753
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QY 3754 GCCTGGCGATTACTGTCTATTTTCTTTATTG--CTATATCCCCAGATCTAGACAGTGT 3811
DB |||||
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QY 3812 CTGACATATAGTAGTGTCTCAATAAATAATTGATGAATGCACAGGCTAGATATAAATTT 3871
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QY 4052 CTCCTGCTCCACTTTAGAAAGGCCAAATTTTACAATCTGATGAAGACTATGAACCTCTCC 4111
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QY 19077 GCAAGAGATTTCTTGAACCTGGGAGTAGAGGTTGAGTGGAGCCGAGATTCACCACTG 19136
QY 4472 CACTCCAGCTGGGCGACACAGCAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531
DB |||||
QY 19137 CACTCCAGCTGGGCGAGGAGTGAGACCTCACAAAAATTTTACATAAATAAATAA 19196
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Db 19197 AACTAAATAAAATACAA 19215
RESULT 18
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ID ADX98568 standard; DNA; 92600 BP.
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DT 05-MAY-2005 (first entry)
XX Human intercellular adhesion molecule (ICAM1, ICAM4, ICAMS) genomic DNA.
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XX
XX SNP detection; breast tumor; endocrine disease;
KW gynecology and obstetrics; neoplasm; cytostatic; metastasis;
KW gene therapy; RNA interference; intercellular adhesion molecule; ICAM1;
KW ICAM4; ICAM5; chromosome 19; ds; SNP; single nucleotide polymorphism.
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QY 2854 AGCAGTAGGTTATCCCTTCTTGAACCTATGAAATTCAGTGTGTTCTCAGTAGGCGGGG 2913
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QY 3034 GAAACTGAGGCTCAGAGGCTGAGCTATTTGCCCAAGATCACACAGCTTGTAAAGTGTG 3093
Db 17899 TGTGTTTAGACATACACATTTTATCTGCTGCTCAGCAATGTCAGCCCTCCACTT----- 17954
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CC	infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above CC conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Qy	3554 GGGTTCAAGYGATTCCTCGCTAAGCCTCCTGAGTAGCTGGAATACAAGGTGCACCA 3613
Db	70718 GGGTTCAAGAGATTCCTGCGCTCAGCCTCTGAGTAGCTGGACTACAGGACCCGCGCA 70777
Qy	3614 CCATGCTTGGCTAAATTTTTTGTATTTTATAGCAGAGATGGGGTTTTACCATTGTGCCCAGG 3673
Db	70778 CCACATCCGGCTAAATTTTTTGTATTTTATAGTAGATAGGGTTTCGTATGTTGGCCAGG 70837
Qy	3674 CTGCTCTCAAACTCGTCAACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAGTGTGGAA 3733
Db	70838 CTGGTCT'CAAACTCCTGACCTC--GTGATCCGACTGCCTCAGCCTCCCAAGTGTGCGGA 70895
Qy	3734 TTATAGCGGTGAGTCACTGTGCCTGGCCGATTACTGCTATTTTTCTTTATTCCTATATCC 3793
Db	70896 TTACAGGTGTGAGCCACCACTCGG-----CAATAATTTTTTAAGGTATAAA 70944
Qy	3794 CCAGATCTGAGCAGTGTCTGACATATPAGTGGTGTCTCAATAATAATPAGTAATGCAC 3853
Db	70945 ATGTCCAGAGACCAAAAAGGTCAAGAACCACTGCTTTTAAATACATAAATGAT-----ATC 70999
Qy	3854 AGCCTAGATATAACTTTTCTTTTTTCTTTTTTAAAAACAATCTTGACAACTTTTGAGATA 3913
Db	71000 AAACCTTTTATATTATTTCAAAATTACTTTTAAAAAANTTCAACACAGAGCATAG-CTC 71058
Qy	3914 AATACAATCTTGCAATCTGCTTTTTTCACTTATCACCTTGTTATGACTTTTTCATATGCC 3973
Db	71059 CATGAAGCAGAGGTTTTCTTTTTTGTTTTTTATTTATTTATGGAACCTAAGTCCCTAGAACAA 71118

PA (ISIS-) ISIS PHARM INC.
PI Bennett CF, Freier SM;
XX WPI; 2003-256431/25.
XX New antisense oligonucleotide compounds, useful for the diagnosis,
PT prevention and/or treatment of conditions with aberrant expression or
PT activity of CoREST, such as developmental and/or hyperproliferative
PT disorders.
XX Example 15; SEQ ID NO 11; 145pp; English.
XX The invention relates to a new antisense compound comprising 8-50
CC nucleobases in length targeted to a nucleic acid molecule encoding a co-
CC repressor for RE1 silencing transcription factor (CoREST), where the
CC compound specifically hybridises with and inhibits the expression of
CC CoREST. The CoREST antisense oligonucleotide has any of 72 specifically
CC claimed sequences of 20 bp, given in the specification. The methods and
CC compositions of the present invention are useful for the diagnosis, and
CC prevention and/or treatment of diseases or conditions associated with
CC aberrant expression or activity of CoREST, such as a developmental
CC disorder and/or a hyperproliferative condition like neuronal cancer. The
CC current sequence represents the human CoREST genomic DNA sequence that
CC was used to design antisense oligonucleotides of the invention.
XX
SQ Sequence 139257 BP; 35155 A; 29706 C; 30833 G; 43561 T; 0 U; 2 Other;
Query Match 8.3%; Score 416; DB 10; Length 139257;
Best Local Similarity 54.0%; Pred. No. 1.2e-66;
Matches 1222; Conservative 3; Mismatches 948; Indels 89; Gaps 15;
2291 AGCCAGGCGCGTGCTATGCTGTAATCCAGCACCTTTGGAGGCGCGAGCGGCGG 2350
63398 AGGCTGAGCATAGTGGCTATACCTGTAATCTTAGCACTTTGGAGGCTGAGCGCAGCGA 63457
2351 ATCACTTGAGCTCAGGATTCGAGACCGCTGGCGAGCGCTGTAACCCAGCTACTTTGGG 2470
63518 T-A-A-A-A-A-T-A-C-A-A-A-A-T-A-G-C-G-G-T-G-T-G-T-C-A-G-A-G-G-T-G-T-A-T-C-C-A-G-C-T-A-C-T-C-A-G-S 63576
2471 AGACTGA-GTTGGAGTTTCAGTGAGCCAAAGTGTGCTCACTGCTGTGAGCCCTGGGTAA 2529
63577 AGGCTGAGGCAAGAGAATTCCTTGAACCTGGGAGGTGGAGGTTGCGGTGAGTCGAGATCG 63636
2530 CAGAGCAACTCTGCTCAAAAAAATAATGCTTCAATAAATATATGATAAAGGACTT 2589
63637 CGGCACCTGCACTCGAGCTGGGCAACAGAGTGAGACTTTTGTGCACACACACACAC 63696
2590 ATATTTTTCAGCCATAGGATCATTTCTCTGAAGCATCTTTGGCGAAGTCATCCCCACC 2649
63697 ACACACACACACACACAGCTGAATAAACCCTATGAACC--AACTAATGCACTGGATTC 63754
2650 TGTTCTGAGAGTGGGAGGTGAGGCTGACCTATTGCTCTGCACTTACTCTATCTAG 2709
63755 CAAAAATTAAGATCTGTGTAAGTTGTAATGTTTCTTGATGTACCCATTTATTTTGA 63814
2710 CTGTCCCTCCACTTTTCCAGGTGCTGCCA-GACACATGACAACTGTGAYGACCAGCCAA 2768
63815 TGAACACAGATTCCTTTTCATCTTTGAAATCACTTTTGTCTGAGATTTTTTATTTTTT 63874
2769 GAAGCTGGACAGCTGTAATTTCTGCTGGACAMMCGGTACACCCACACCTATTCATPACT 2828
63875 TTTTTTTTTTGGAGACAGAGTCTCGTGTGCGCCAGAGCTGAGTGCGTGTGATC 63934
2829 GTGCTGTGGCTCGGCAATCACTGTAGCAGT-AGGTTTATCCCTTCCCTTGACCTATGAAT 2887
63935 TAGGCTCACTGCAACCTCCACCTCCGGGTTCAAGCGAATTCCTCGCTCAGCCTCCTGA 63994
2888 TCTAGTTGGTTCTCAGTAGCCGGGGAAATAATAGTAACACAGCCATGATTTAGTGT 2947

Db 63995 GTAGCTAGGATATAGGCATGTGCCACCACACTCAGCTAAATTTTGTATTTCAGTAGAGG 64054
Qy 2948 TAATTTTCTTGTTCTGGCAGTGTCTCTTTAAATCTCAGAACCAACTATGAGGATAGG 3007
Db 64055 TAGGGTTTTCACCATGTAGGCCAGGCTGGTCTCAAACTCCTGACCTCAAGCGATCCGCTG 64114
Qy 3008 TACAATATCTCACTTAACAGATPAAGAACTAGGCTCAGAAGGCTGAGCTATTGCCC 3067
Db 64115 CTCAGCTCCCTGAGTATTGGGATTTATAGGTGTAGCCAC-----GGTGTCCCGC 64164
Qy 3068 CAAGATCACACAGCTTGTAAAGTGTGACAGTTGGGTTTTTTTTTGTGTTGTTTAGAGA 3127
Db 64165 CAAGCTGAGACATTTTAAAGAAATGTTTCTGTTTTTGTATTGTTGTTTAGAGA 64224
Qy 3128 CAGGCTCTGTCTGTCAACCAGGATGAGCACAGTGTGTGCAACCATAGGTCACTGCAGC 3187
Db 64225 TGGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGTGCCA-----TCACGTGCAAC 64277
Qy 3188 CTCACCTCTGAGCTCAAGGATCTGTGACCTCAGCTCCCAAGTAGCTGGGACTAGC 3247
Db 64278 CTCGCTCTCTGGGTTCAAGCAATTTCTCTGTTCAGGCTCTCTAGGTAACTGGGACTGA 64337
Qy 3248 AGCGTGCAACCACCGCTGCTGAATTAATAAAAAATTTTTTGTAGAGACTGGGTCTTACT 3307
Db 64338 GCGTTGCCACCATATACCTGGCTGATTTTGTATTTTA-GTAGAGATGGGGTTTACC 64396
Qy 3308 AGTTTGGCAGGCTGTCTTAAACTCTGGCTTCAAGCAATCTCTCCTACCTTGGGACTCC 3367
Db 64397 ATGTTGGCAGGCTGCTTGAACCTTCTGAC--TCAAGCGATCTACCCACCTCAGCCTCC 64455
Qy 3368 AAAGTCTGGGATACAGGGGTGAGCCACCACCTGTGCGGCTACTTATTTCTTTCATTCCA 3427
Db 64456 AAAGTCTGGGATTAATCTCCACAGCACCTGTCTGAAAAGGTTTCTTTTCTTTCTTTT 64515
Qy 3428 TCTTTTCAATAGATGTAAGATCCACAGAACAGGATTAATGCGCTATTTTCTTCTCTTTCT 3487
Db 64516 TTTTTTGAGATCAGGTCTCACTCTGTGCGCCAGGCTGTAGTGCAGTCGCGCAATC---- 64570
Qy 3488 TTTTTGAGACAGAGTCTCACTTTCATCACTCAACCTCCGTTTCAGCTCACTGCAACCTCTG 3547
Db 64571 -----TCAGCTCACTGCAACCTCCG 64590
Qy 3548 CTTCCGGGTTCAAGYGATTCCTCGCTTAAGCTCCTGAGTGTGAAATTTACAAGGT 3607
Db 64591 CTTCCAGGTTTCAGGTGATTCCTTGGCTCAGCTCCTCCACAGCGGTGGATTTCAAGCAT 64650
Qy 3608 GCACCACCATGCTTGGCTAAATTTTTTGTATTTTATAGCAGAGATGGGGTTTTTACCATGTTG 3667
Db 64651 ACACCACCATGATGGCTCA-TTTTTGTATTTTATAGTAGAGA-GGGGTTTCAACATGTTG 64708
Qy 3668 CCAGGCTGGTCTCAAACTCTGACCTCAAGTGTCTGCTGCTCAGTCTCCTCCAAAGTG 3727
Db 64709 GCCAGGATGGTGGCAACTCTCTGACCTCATGTGATCCACCGCATCAGCCTCCCAAAGTG 64768
Qy 3728 CTGGAATTAAGCGGTGAGTCACTGTGCTGCGCGATTAATGCTCTATTTCTTTTATTTGCT 3787
Db 64769 CTGGGATTAAGCGGTGATCACTCCACTGGCTAGAAACATCTTCTTAAGGCTATCTT 64828
Qy 3788 ATATCCCCAGATCTAGACAGTGTCTGACATATAGTAGGTGCTCAATAAATAATGATGA 3847
Db 64829 TTTTTTTTTTCTTATATAATTTAGTTGACTATGTAAACCCCAAAACACATAGGGTAGAA 64888
Qy 3848 A-----TGACAGCTTAGATATAAATCTTCTTTTCTTTTAAAAACAATCTTGACAACT 3903
Db 64889 ACTCGTGAATAATTTTTTGGAGATATCTTTTGAAGATGTTGTGCGCTCAGCGTCTGGAT 64948
Qy 3904 TTGCAGATAAATACAATCTTGCATTTCTGTTTTTCACTTATCACTTGTATGACTTTT 3963
Db 64949 ATGGATGTGCTGTAGTGTGATGATGATTTAGGATTTCCCACTGTATGATGCTTT 65008
Qy 3964 TCATATTCCTCAAACTTTTATTTGTTACTGTTTTTTCATTGTTA--CTATTTTAGTCA 4020

PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244817P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 03-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX
XX Disclosure; SEQ ID NO 32692; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK51921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the

CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 17170 BP; 4466 A; 4250 C; 4340 G; 4114 T; 0 U; 0 Other;
Query Match 8.3%; Score 415.6; DB 4; Length 17170;
Best Local Similarity 54.4%; Pred. No. 1.1e-66;
Matches 1324; Conservative 2; Mismatches 916; Indels 190; Gaps 17;
QY 2279 AAAATCGCTTTCAGGCCAGGCGCGTGCATGCTGTAAATCCAGACACTTTTGGAGGC 2338
DB 13306 AAAATGAAGTCAAGCGCGGTGCGGTGCTACGCTGTAAATCCAGACACTTTTGGAGGC 13365
QY 2339 CGAGCGCGCGGATCACTTGGAGTTCAGAGCTCAGAGCCAGCTGGCCAAATGTGAAA 2398
DB 13366 TGAGGTGGCAGATAAACCCTGAGGTCAAGAGTTCAAGACCAGCCTGGCCAAATGCGGAAA 13425
QY 2399 CCCTGTCTTACTAAAAAATACAAAAATAGCCGACATGTGTGGGAGCGCCTGTAAACC 2458
DB 13426 CCCTGTCTTAC-CAAAAAATACAAAACTTAATGGGCATGTGTGGCCCATGCTGTAAACC 13484
QY 2459 CAGCTACTTGGGAGACTGAG-----TTGGAGGTTTCAGT 2492
DB 13485 CAGCTACTCGCGCGCTGAGGAGGAGAAATCACTGAACCCAGGATGTGGAGTTGCAGA 13544
QY 2493 GAGCCAAGTCTGTCTCACTGTCTCCAGCTGGGTAACAGAGCAACTCTGTCTCAAAAAA 2552
DB 13545 GAGCCGAGCTTGTGCCACTGCACTTCAGCTGGGTGACAGAGCAAGACTCTGTCTCAAAA 13604
QY 2553 AAAAAATGTTTCAATAAATATATATGATAAAGGACTTATATTTTTCAAGCCATAGGATC 2612
DB 13605 AAAAAAGAAAGTCAGTTGCTCAAGGCCATTCCAACCTCAACATT-----CACACTCGGGTC 13659
QY 2613 ATTTCTCTGAAGCATCTTGGCGAAGTCATCCCCACCTGTTCTCGAGAGTGGCGAGGTGA 2672
DB 13660 TTTTGATACCAACGCCAGGCGTGAATAATGATCAACTGTTT--TTAGATGGAGAACTGA 13717
QY 2673 GGGCTGACCTATTGCTGCACTTACTCTATCTCAGCTGTCTCCCTCCCACTTTCCAGGTG 2732
DB 13718 GGCATGGA--AGGGCAGTGTCTCGCACCAGTGTCTGCTGGGACTCACCTCGGGGAAC 13775
QY 2733 CTGCCAGACACATGACAACTGCTATGACAGGCCCAAGAGCTGGACAGCTGTAAATTCT 2792
DB 13776 GAGGAGGGGATTGCTCTTGTG---GGACTGGAGAGCTGATGGATTTAGAAAGCTTGTGG 13831
QY 2793 GCTGGACAMMCGTACACCCACACCTATTCTACTCTGCTCTGGCTCGGCAATCACCTG 2852
DB 13832 GCAGGACACCGTGTCTCAGAGCTGGGCTGGGAGAGTAACACAGCTCTGCAATCA---- 13887
QY 2853 TAGCAGTAGGTTTATCCCTTCCTTGACCTATGAATTTCTAGTTGGTTCTCAGTAGGCCGG 2912
DB 13888 -----AAAAAGCTTAG 13898
QY 2913 GGGAAATATAGTAACAACAGCCATGATTAGTGTAAATTTCTTGGTTCTCGGCAGTGT 2972
DB 13899 CCCCAGTGAGACAAACAGCATCTACTTTCCTCTACTGAGCTCCAGAGCAGAGGCTAACTA 13959
QY 2973 CTCCTTTAATCTCAGAACACACTATGGGATAGGTACAAATTTATCTCACTTTAAACAGATA 3032
DB 13959 AGCCTCAGCTTCTACTTCTGCCATGAGAGTGAANAATCTAACTTACCATGTTGTCGTAA 14018
QY 3033 AGAAACTGAGCTCAGAGGCTGAGCTATTTCGCCAAGATCACACAGCTTGTAAAGTGT 3092
DB 14019 GGATGCCAATTCGAAAGGCCACTTGTCTTGTCCACTGTGGGGGTGCCAGTGTAAAGAAATA 14078
QY 3093 GACAGTTTGGGTTTTTTTTTTTGTGTTTGTAGAGACAGGCTCTTCTCTGTCAACCCAGC 3152
DB 14079 CAGAAATCTTTTATCTTTTTTTTTTTTTTTTTTTTGTAGACGGAGTCTTGTCTGTGCGCCAGC 14138

QY 3153 ATGAGCAAGTGTGTCAACATAGGTCACTGACGCTCAACCTCTGAGCTCAAGGGATC 3212
D 14139 TGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAAGCTCTGCCTCCAGGTTACACCAATT 14198
QY 3213 TGTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACACGCTGGCTAA 3272
D 14199 CTCTGCTTCAAGCCTCCGAGTAGTGGGACTACAGGCGCCACCAACCATGCC--CTAA 14255
QY 3273 TTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTAGCTTGGCCAGGCTTGTCTTAAACT 3332
D 14256 TTTTCTGTACTTTTGTAGTAAGACAGGTTTACCATGTTAGCCAGATGCTGTGATCT 14315
QY 3333 CTGCGCTCAAGCAATCTCTCACTACCTTGGCATCCCAAGTGTGGGATTAAGGGGTGAG 3392
D 14316 CTTGACCTCATG--ATCCACTTGCCTCAGCTTCCCAAGTGTGGGATTAACAGTGTGAG 14373
QY 3393 CCACCATGTGGCGTACTTATTTCTTTTACATCCATCTTTCATAGATGTAAGATCCA 3452
D 14374 CCACTGCGCTGGCCCTTTTTTTTTTTTTTTCTTTTGAGA----- 14410
QY 3453 CAGAACAGGATTAAGCTATTTCTTCTCTTTTGTGAGACAGAGTCTCACTTCAT 3512
D 14411 -----CTGAGTCTCGTTGTGTCGCCAGGCTGGAGTGCA 14445
QY 3513 CACCTCAACCTCCGTTTCAAGTCACTCAACCTCTGCTCCCGGTTTCAAGYGAATCTCTCT 3572
D 14446 TGGTCCAATC-----TTGGCTCACTGCAACCTCTGCTCTCGGTTTCAACAGATCTCTCT 14500
QY 3573 GCTAAGCTCTGAGTAGCTGAATTAAGGCTGCACCAATGCTTGGCTAAATTTT 3632
D 14501 GCCTCAGACTCCCAAGTATCTGGGATTAACAGGCGCTGCCACCAACCTGGGCTAA--TTTT 14559
QY 3633 TGTATTTTAGCAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTGAC 3692
D 14560 TGTATTTTAGGAGAGATGGGTTTACCATGTTGCCAGACTGGTCTCAAACTCCCGAC 14619
QY 3693 CTCAGTGATCTCGCTCCCTCAGTCTCCCAAGTGTGGAAATPATAGGCTGAGTCACTG 3752
D 14620 CTCAGGTAAATCCACTGCTTGGCTCCCAAGTGTGGGATTAACAGGATGAGCCACCG 14679
QY 3753 TGGCTGGCGATTAAGTCTATTTTCTTTA-----TTGCTATATCCCGAGTCTAG 3803
D 14680 AGCTGGCGGAAATAAGATAATCTTAAACAATCATGGAGTGTCTAGTGTGCAGACAC 14739
QY 3804 AGCAGTCTGACATATAGTAGTGTCTCAATAATAATTGATGAATGCACAGCTAGATA 3863
D 14740 GGCACGTGAGGCTCTACATACATCGCTCCATGAACCTTTTCATAAACCAACCATCAGAA 14799
QY 3864 TAAACTTTCTTTTTTTTTTAAAAACAATCTTTGACAACCTTTGCAGAAATAAATACAATCT 3923
D 14800 GTGTGATTATATCATCTCTGTTTTATAGTAGAGAACACCCAGTCTTCAAGGGTAAAA 14859
QY 3924 TGCATTTCTGCTTT--TTCACTTATCAGCTTGTATGACTTTTTTCATATGCTCTCAACCTT 3982
D 14860 ATCACTCACCAGGTCACACAAGCACCAGGAGCCAGGACTTGAACCAAGATCAGTTTAT 14919
QY 3983 TATTGTTACTGTTTTTCTATTTTACTATTTTGTACTGCTGAATAATATGCTTAATTTGC 4042
D 14920 GCCAGGTTCAACCCCTTAAGTCAGTGATTTGATTCATGACTAGAGCAGCATATGTTG 14979
QY 4043 TTATACATCTCTCTGCTCCACTTTAGAAAGGCCAAAATTTACAAATCTGATGAAGCTATGA 4102
D 14980 TGGGAAAAGTACAAAACACCTATCAGCTGTGACATCCAGTTTTAGTTCTGACACACTG 15039
QY 4103 ACCCTCTCCCGAGAGAAATACACACACACACACTCA-----CACA 4146
D 15040 CACATTAATTTGTTTAAATAGCCATGATAAATGATGATGACTCATTTGTTGAGCATA 15099
QY 4147 CAGTTTTTTTATGTTTCACTAAGACAAGAACCTGCAATTAGAGATGTTTCTTC- 4205
D 15100 CGTTTTTTTGGAGTATCAATCTGATAACAGACCTCAGAGGAAAGTATTTATTTTC 15159
QY 4206 -----ATATTAATTAATAATAACTCAGTTGGGCACAGTGAATCAAGCCTGTGAACCA 4256

D 15160 TGACTTTTAGATGAAAAACAATCTCAGGGCCGAGCGGTGCTCATGCTGTAATCC 15219
QY 4257 CAGTACTTTTGGAGTCCCAAGTGGGTGGATCACTTTGAGTGAAGAAGTTTCGAGACACAGCT 4316
D 15220 CAGCACTTTTGGAGGCCAAGCAGGAGGATCCCTGAGGTGAGGAGTTTCGAGACACAGCT 15279
QY 4317 GGTCAATATGTTGAAACCCCTATCTCTACTTAAATAATACAAAAATTAGCTGGGTGTAGTAT 4376
D 15280 GGCCAAACATGGCAAAACCCCATCTCTACTTAAAAACACAAAAATTAGTTGGGTGTAGTGGC 15339
QY 4377 GCATGCTGTAGTCCAGCTACTCGGAGGCTTGAGGCAAGAGAATTTGCTTGAACCTGGGA 4436
D 15340 AGTGCCTGCACTGCCACCTACTTTGGAGGCTTAAGGCAGGAGAATCGCTTGAACCCAGGA 15399
QY 4437 GGCAGAGGTTGCAGTGAGCCGAGATCCCACTGCACCTCCAGCCTGGGCGCACACAGCCA 4496
D 15400 GCGGAGATTTGCAGTGAACCTGAGATCGTCCATTTGCATCTCCAGCCTGGGAGACAGACAA 15459
QY 4497 GACTCTATCTCAAAAAAATAAATAAATAAAGGATCGGAGAGAAAACAAAACTTAATA 4556
D 15460 GACTTCGTTCAAAACAACAATCTTAGAGAGATTGTTTGAACCTCACACAACACGTGAA 15519
QY 4557 AGATTCTCGAAGGTAA--GCAGAGATACGTAATTTATATGTAATTAAGTTTAAATGCAAT 4614
D 15520 ATGTGCTGATCCAAATTTGAGATGCTCTGCTCTGAAATATATACACAGATTTCAAAGACTTA 15579
QY 4615 TTAACGTGAATCTTATTTGTTTATTTTGGTTAT 4646
D 15580 GTATCAGAAAGAGAATTTAATAATTTCTTTTT 15611
RESULT 24
ACN44170/c
ID ACN44170 standard; DNA; 196686 BP.
XX
AC ACN44170;
DT 18-NOV-2004 (first entry)
XX
DE Human genomic sequence HCG39530.
XX
KW Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
OS Homo sapiens.
XX
PN WO2003073826-A2.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-US006235.
XX
PR 01-MAR-2002; 2002US-00087192.
XX
PA (SAGR-) SAGRES DISCOVERY.
XX
PI Morris DW;
XX
DR WPI; 2003-328604/31.
XX
PT Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
XX
PS Claim 1; SEQ ID NO 484; Opp; English.
XX
CC The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;

CC	(x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for									
CC	determining Carcinoma Associated (CA) gene copy number. In addition, the									
CC	CA genes are useful as DNA vaccines and the CAP are useful as markers of									
CC	carcinoma including lymphoma. The present sequence is one such CA coding									
CC	sequence. Note: This patent is an equivalent to basic patent									
CC	US2002182586A1, for which no sequence data was published									
XX										
SQ	Sequence 196686 BP; 53978 A; 42758 C; 43862 G; 55372 T; 0 U; 716 Other;									
Qy	Query Match	8.3%;	Score 414.2;	DB 11;	Length 196686;					
Db	Best Local Similarity	60.7%;	Pred. No. 2.8e-66;							
	Matches	869;	Conservative	1;	Mismatches 464;	Indels	97;	Gaps	8;	
Qy	3105	TTTTTTTGGTGGTTAGACAGG	GCTTCTGCTCTGTCACCCAGG	CATGAGCACAGTG	3164					
Db	98993	TTCAATTCATTTATTCATTCAG	ATGGGGTCTTGCTCTGTGTGCC	AGGCTGGAGTGAATG	98934					
Qy	3165	GTGCAACCATAGTCTCACTGC	AGCTCAACCTCCTGAGCTCA	AGGGATCTGCTGACCTCAG	3224					
Db	98933	GTGCAATCTCGGCTCACTGCA	ACCTCCACCTCAGGATTC	CAAGTGATCTCTGCTCCTCAG	98874					
Qy	3225	CTTCCCAAGTAGCTGGGACT	ACGAGCGTGCACCAACG	CGCTGGCTAAATTA	3284					
Db	98873	CTTCTCGAGTAACCTGGG	ATTACAGACACCTGCC	ACACACCCGGCTAA	98816					
Qy	3285	TTTTGTAGAGACTGGGCT	TTTACTACGTTGGCCAGG	CTTGCTTTAACTCTCGG	3344					
Db	98815	TTTAGTAAAGATGGAG	TTTCACCATGTTGGCCAG	CGTGGTCTCAAACTCTG	98756					
Qy	3345	CAATCTCTCACTTGGCAT	CCCAAGTGTGGGATTAC	AGGGGTGAGCCACCATG	3404					
Db	98755	GGATCCACCACCTTGG	CTCCCAAGTGTGGGATTAC	AGGATGAGCCACTG	98696					
Qy	3405	GCTACTTAATTTCTT	TACATTCCTTTCCAA	TAGAAATGAAGTCCAC	3464					
Db	98695	GCCATGTACATTTATA	ATTTGACTATATCT	CTCTTGGT-----	98644					
Qy	3465	TACTGCTATTCTTCT	CTCTTTTGTGAGACAG	AGTCTCACTTCATCA	3524					
Db	98643	TTTTTTTTTTTTTTTT	TTTTTTTTTTTGGAG	CAGAGTCTGCTCTG	98584					
Qy	3525	CGT-----	TCAGCTCACTGCAAC	CTCTGCTCTCCGG	3570					
Db	98583	AGTGCAGTGGCGG	ATCTCGCTCACTGCA	AGCTCCGCTCTCTG	98524					
Qy	3571	CTGCCTAAGCCTCT	CGAGTAGCTGGAATTA	CAAGCGTGCACCA	3630					
Db	98523	CTGCCCTCAGCCT	CCAGAGTAGCTGG	ACTACATGTGCC	98464					
Qy	3631	TTTTGTATTTTAC	GAGATGGGGTTTAC	CATGTTGCCAGG	3690					
Db	98463	TTTGTATTTTAA	TGGAGACGGGGTTT	ACCGTGTAGCC	98404					
Qy	3691	ACCTCAAGTGAT	CTGCTGCTCAGTCT	CCCAAAGTGTGGA	3750					
Db	98403	ACCTC--	GTGATCCACCAC	CTCAGCTCCCAA	98346					
Qy	3751	TGTGCTGGCCG	ATTAAGTCTATAT	TTTCTTTATTTG	3810					
Db	98345	TGGGCCCGG	CCACCACTCGT	CTCTTGATTTG	98291					
Qy	3811	TCCTGACAT	ATAGTAGGTGCT	CAATAAATAAT	3870					
Db	98290	-----	-----	-----	98283					
Qy	3871	TCCTTTTCT	TTTTTAAACA	CAATCTTGACA	3930					
Db	98282	TATATGTT	CTTACCATA	TCTCTAAT	98223					
Qy	3931	TGCTTTTCT	ACTTATAC	CTTTGATG	3990					
Db	98222	TATATACAT	ACATATAGT	GTGATATAT	98163					

Qy	3991	CTGTTTTTCTTACTATTATTTAGTCACTGAATAATATGCTTAAATTTGCTTATACAT	4050
Db	98162	ATATATTAACCAAGTCTTATTTATGTTATCATTCATTCGTTGAATTAACAATGTTTTTCA-	98104
Qy	4051	CCTCTGCTCCACTTTAGAGGCCAAAATTTCAAAATCTGATGAAAGCTATGAACCCCTCTC	4110
Db	98103	-----AAACCTATATAAAAGACCTTAAACAAGGTAAGGATGAGAGGAACCTTGAATTGC	98051
Qy	4111	CCAGAGAAATACACACACACACACTCACACAGTCTTTTAAATCTTTGCAAC	4170
Db	98050	CCAGATATAAATTTTGTCTCAAGTCTCTCACTTTGTTTTCATGTTTAAATCTCTCAATA	97991
Qy	4171	TAAGCAAGAAACCTGCAATTAGAGGATGTTTCTCATATTAATTAATAATAA--CTCA	4226
Db	97990	TATTTAACTATTTGGCAATTACAATAATTTTGTGTCACAAAAATAAGCTCCTCG	97931
Qy	4227	GTGGGCAAGTGAATCAAGCCTGTAAACACAGTACTTTTGAAGTCCAAAGTGGTGGAT	4286
Db	97930	GCTGGACACGGTGGCTCAGCCTGTAATCCAGCACCTTTGGGAGGCCGAGAGGTGGAT	97871
Qy	4287	CACTTGAGGTGAGAAGTTCGAGACCAAGCTGCTCAATATGTTGAACCTCTCTACTA	4346
Db	97870	CAC--CAGGTCAGGAGATGGAGACCATCTGCGCAACATGGTAAAACTCTGCTCTACTA	97813
Qy	4347	AAATACAAAAATTAGCTGGGTGTAGTGATGATGATGCTGTAGTCCAGCTACTCGGGAG	4406
Db	97812	CAATACAAAAATTAGCTGGGCTGTGGTGGCATGCGCTGTAGTCCAGCTACTCGGGAG	97753
Qy	4407	CTGAGCAAGAAATTTGTTGAACCTGGGAGCGACAGGTTTGCAGTGAGCCGAGATCCAC	4466
Db	97752	CTGAGGAGGAACTGCTTGAACCTGGGAGCGACAGCTTGCAGCGAGCTGAGATCAGC	97693
Qy	4467	CACCTCACTCCAGCTGGCGACACAGCGAGACTCTATCTCAAAAAATAA	4517
Db	97692	CACCTCACTCCAGCTGGGTGACAGCGAGACTCTATCTCAAAAAATAA	97642
RESULT 25			
ADP68568/c			
ID	ADP68568 standard; cDNA; 86000 BP.		
XX			
AC	ADP68568;		
DT	09-SEP-2004 (first entry)		
XX			
DE	Human PPAR-alpha cDNA.		
XX			
KW	cytostatic; gene therapy; PPAR-alpha;		
KW	peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator;		
KW	PPAR-alpha associated disorder; hyperproliferative disorder; human; gene;		
XX	ss.		
OS	Homo sapiens.		
XX			
PN	US2004115637-A1.		
XX			
PD	17-JUN-2004.		
XX			
PF	11-DEC-2002; 2002US-00317500.		
XX			
PR	11-DEC-2002; 2002US-00317500.		
XX			
PA	(ISIS-) ISIS PHARM INC.		
XX			
PI	Mckay R, Dobie KW;		
XX			
DR	WPI; 2004-449378/42.		
XX			
PT	New oligonucleotide compound that inhibits expression of PPAR-alpha,		
PT	useful for preparing a composition for treating hyperproliferative		
XX	disorders, e.g. cancer.		
PS	Claim 1; SEQ ID NO 4; 121pp; English.		

PT New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
XX cancers such as leukemia and lymphoma.

XX Claim 1; SEQ ID NO 500; 199pp; English.

XX The present invention relates to cancer associated sequences (ADO97025-
CC ADO98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic formate directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 215974 BP; 56601 A; 42897 C; 46516 G; 65586 T; 0 U; 4374 Other;

Query Match 8.3%; Score 413.6; DB 12; Length 215974;
Best Local Similarity 59.6%; Pred. No. 3.7e-66;
Matches 847; Conservative 0; Mismatches 529; Indels 46; Gaps 7;
QY 3110 TTTGTTGTTTGTAGACAGAGGCTTGTCTCTCACCAGGCTAGACACAGTGTGCA 3169
DB 4846 TGTCTTTTGTGAGACAGGCTCGCTCTGTGCCAGGCTGGAGTACAGTGGCACA 4787
QY 3170 ACCATAGTCACTGCGACCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGCCTCC 3229
DB 4786 ATCATGGCTCATTTGACGCTCAAACTCTGGGCTCAATGAGCTCAACCTCAGCCTCC 4727
QY 3230 CAAGTACGCTGGACTACGAGCTGCAACACCGCTGGCTAATTAATAAATTTTTTGG 3289
DB 4726 TAAGTAGCTGGAATCAGGACATACATCACCACTCTAGCTAATTTTGTATTTTTT--- 4670
QY 3290 TAGAGACTGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCCCTGGCTTCAAGCAATC 3349
DB 4669 -----GTCTCATGTTGTCAGGCTGGTCTTCAATTCCTAGGCTCAAGCAATC 4620
QY 3350 CTCTACTTGGCATCCAAAGTCTGGGATTAACGGGTGAGCCACCACTATGCGGCTAC 3409
DB 4619 ACTGCTCAAGCTCCCAAGTACTGGGATACAGACATGAGCCAGCACCCAGCTTG 4560
QY 3410 TTATTTCTTTACATTCATCTTTCCAAATAGAATGTAAAGATCCACAGAAAGGGATTACTG 3469
DB 4559 AAAGTGTCTTTTATTATTATTATTAATTTTTTTTTTTTTTTCAGATGAAG----- 4509
QY 3470 CCTATTTCTCTCTCTTTTGTAGACAGAGTCTCACTCATCATCACTCAACCTCCGTTTC 3529
DB 4508 -----TCTCGCTCTGTTGCCAGGTTCCGGGATTCCTGCTCAGCTCCGCTC 4462
QY 3530 AGCTCACTGCAACCTCTGCTCCCGGTTTCAAGYGATTTCTCTGCTCAAGCCCTCCTGAGT 3589
DB 4461 ACCGG---GCAACCTCTGCTCCAGGTTCCGGGATTCCTGCTCAGCTCCGAGT 4405
QY 3590 AGCTGGAATTTAAGCGTGCAACCATGTTGGCTTAATTTTTTGTATTTTATAGCAGAGA 3649
DB 4404 AGCTGGGATTTACAAGCATGCCACACGCGCCAGCTAA-TTTTGTAGTTTTAGTAGAGA 4346
QY 3650 TGGGTTTACCATGTTGCCAGGCTGCTCAAACTCCTGACCTCAAGTGATCTCGCTG 3709
DB 4345 TAGGCTTTTCATCATGTTGGCCAGGCTGGTCTTGAATCTCTGACCTCAGGTGATCCACCA 4286
QY 3710 CCTCAGTCTCCCAAGTCTGGGAATTTATAGGCGTGAGTCACTGTGCTGGCCGATTAAGT 3769
DB 4285 TCTCAGCTCCCAAGTCTGGGATTTACAGGCATGACCACCGACCTGGCCGGAAGATC 4226
QY 3770 TCTATTTTCTTTATGCTATATCCCGAGTCTAGAGAGTGTCTGACATATAGTAGGTGC 3829
DB 4225 TTTTAAAGTCTCTTGATCT---CTAACCTCGTATAGTGGCTGCTACTTAGTAGGCAC 4169
QY 3830 TCAATAAATAATGATGAATGACAGCTGATAGATAAATCTTCTTTTCTTTTAAATA 3889
DB 4168 T---TAACACATTTGGAGATGAAGATTAATTAACACATGGCAATTAATTAATCTCAGCTT 4112
QY 3890 CAAATCTTGACAACCTTTTGCAGATAAATAFACAAATCTTGCAATTTCTGCTTTTTCACCTTATCACC 3949

DB 4111 AAATGGCTTGCTCAAGCCACGACGCTGGTAGTGGCAGAGTTGGAATGCAAAACACAAAT 4052
QY 3950 TTGTTATGACTTTTTCATATATGCTCAAAACCTTTATTTGTTACTGTTTTTTCATTGTTACT 4009
DB 4051 TTGTTTGAATTCACAAATCTTTTGCCCTTTTCCACAAACAAAGGCCCTACATGTCCCTTTACA 3992
QY 4010 ATTTTGTAGTCACTGAATAATATGCGCTTAATTTGCTTTATACATCTCTCTGCTCCACTTTTACA 4069
DB 3991 TATTTTTCAGGTGATACATTAATCTTTCCAGCATTTGTGAC-TCTAGTGAAGCCCTAGATC 3933
QY 4070 AGGCCAAATTTTACAAATCTGATGAAGCTATGAACCTCTCTCCCCAGAGAAAATACACAC 4129
DB 3932 TCACTAATAGCAATGACCTCTTCTAGCTGTTTATTTATTGAGTGTATGATGTGCCAGGC 3873
QY 4130 ACACACACTCACACACAGTTTTTTTTTAAATGTTTGGCACTAAGACAAGAAACCTGCAT 4189
DB 3872 ATTGCAATTTAGCACTTCACACATATGATCTCATTTAATTTTTCACAACAATCCCATGAGAT 3813
QY 4190 TAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTAGTTGGGCACAGTCAAGCCT 4249
DB 3812 TGGCACTATTATATGGCTTTTAACAGAAAGAAACAGCCAGCATGTTGGCTCATGCCT 3753
QY 4250 GTAAACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTTGAGGTGAGAAAGTTGAGA 4309
DB 3752 ATAATCCTAGCACTTTTGGAGGCTGAGGTGGGTTCATCACCTGAGGTCAAGGAGTTCAAGA 3693
QY 4310 CAGGCTGGTCAATATGTTGAAACCTATCTCTACTTAAATAACAAAATTTAGCTGGGTG 4369
DB 3692 CCAACCTGCCCAACATAGTGAACCCCATCTCTACTTAAANAATACAAAATTTAGCCGGCA 3633
QY 4370 TAGTCATCATGCTCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAGAAATTTGCTTGA 4429
DB 3632 TGGTGGCGGTGCTCTGTTAATCCAGCTACTCGGAGGCTGAGACAGGAGAAATTTGCTTGA 3573
QY 4430 CTTGGGAGCAGAGGTTGTCAGTGAGCCGAGATCCCAACACTGCACTCCAGCTGGGCGAC 4489
DB 3572 CCAGGAGCGGAGGTTGCAGTGAGCAGAGATTGCACTGTTGCACTCCAGCTGGGAGAC 3513
QY 4490 ACAGGAGACTCTATCTCAAAAAAATAAATAAATAAATAA 4531
DB 3512 AGAGCAAGACTCCGCTCTCAAAAAAAGAACAGAGAGAAACAGA 3471

RESULT 27

AAL42369/c

ID AAL42369 standard; DNA; 13670 BP.

XX AAL42369;

AC AC

XX 28-JUN-2002 (first entry)

DT 28-JUN-2002 (first entry)

XX Human Guanine nucleotide binding protein gamma 7 (GNG7) gene sequence.

DE Human; gene; ds; guanine nucleotide binding protein gamma 7; G protein;

KW GNG7; novel polymorphic site; drug screening; gene therapy;

KW GNG7-related disease; pancreatic cancer; GNG7 haplotyping;

KW GNG7 genotyping.

OS Homo sapiens.

XX Key

XX replace(3900, T)

FT /tag= a

FT /note= "Single nucleotide polymorphism"

FT replace(3975, G)

FT /tag= b

FT /note= "Single nucleotide polymorphism"

FT 4005..9671

FT /tag= c

FT /product= "Guanine nucleotide binding protein gamma 7"

FT 4005..4085

FT /*tag= d

FT /number= 1


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Db          4496 CAAAT 4492
RESULT 28
ABAI6909
ID   ABAI6909 standard; DNA; 6519 BP.
XX
AC   ABAI6909;
XX
DT   23-JAN-2002 (first entry)
XX
DE   Human nervous system related polynucleotide SEQ ID NO 9240.
XX
KW   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
KW   immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnery;
KW   antiparkinsonian; antiskelting; antianemic; antiarthritic; cancer;
KW   antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW   antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
KW   antiparasitic; cardiant; immune disorder; cardiovascular disorder;
KW   neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
XX
OS   Homo sapiens.
XX
XX   WO200159063-A2.
XX
PD   16-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US0001334.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205151P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
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PR   20-OCT-2000; 2000US-0241826P.
PR   01-NOV-2000; 2000US-0242221P.
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PR   17-NOV-2000; 2000US-0249218P.
PR   17-NOV-2000; 2000US-0249244P.
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PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-541565/60.
XX
XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
PT useful for preventing, diagnosing and/or treating nervous system cancers
PT and metastases.
XX
XX Disclosure; SEQ ID NO 9240; 1701pp + Sequence Listing; English.
XX
XX The invention relates to novel genes (ABAI1004-ABAI21534) and proteins
CC (ABBI4678-ABBI18001) useful for preventing, treating or ameliorating
CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in
CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)
CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
CC; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
CC infectious diseases such as viral, bacterial, fungal and parasitic
CC infections. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 6519 BP; 1661 A; 1577 C; 1542 G; 1739 T; 0 U; 0 Other;
XX
XX Query Match 8.3%; Score 413.2; DB 5; Length 6519;
XX Best Local Similarity 59.8%; Pred. No. 2.6e-66;
XX Matches 865; Conservative 1; Mismatches 544; Indels 36; Gaps 9;
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QY 3082 TTCTAAGTGTGACAGTTTCGGGTTTTTTTTTTGTTGTTTGTAGACAGGCTTCGCTCT 3141
Db 4505 TTTTATGTTTTATTTTTTGGGTTTTTTTTTTTTTTTTTTTTTTTGGATGAGTCTCGCTCT 4564
QY 3142 GTCAACCCAGGATGAGACAGTGGTGCAACCATAGTGTCACTGAGGCTCAACCTCTCTGAG 3201
Db 4565 GTCAACCCAGGCTGGAGTGACGTGACGTGATCTCAGCTCACTGCAAGCTCCGTTTCCAGG 4624
QY 3202 CTCAAGGGATCTGCTGACCTCAGCTCCCAAGTAGCTGGAGCTACAGGCTGACACCA 3261
Db 4625 TTCACGCCATTTCTCTGCTCCAGCTCCCGAGTAGCTGGAGCTACAGGCTGCCACACCA 4684
QY 3262 CGCTTGCTTAATTAATAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCT 3321
Db 4685 TGCCCGGCTAATTTTTTTGTTATTTTTTAGTAGAGATGGGTTTCCACCATGTGGCCAGGAT 4744
QY 3322 TGTCTTAAACTCTGGCTTCAAGCAATCTCTTACCTTGGCATFCCCAAGAGTGTGGGATT 3381

Db 4745 GGTCTCCATCTCTGACCTC--GTGATCCACTCGCTTGGCTCCCAAGAGTGTGGGATT 4802
QY 3382 ACAGGGGTGAGCACCACCATGTGGGGTACTTATTTCTTTACATTCATCTTTCCAATAGAA 3441
Db 4803 ATGGGGGTGAGCACCACCGCACCAGGGGTTTTTTTCTGTTTTTTTTTTTTTTTTTTT 4862
QY 3442 TGTAAAGATCCACAGAAACAGGGATTACTGCTCTATTTCTTCTCTCTTTTGTAGACAGAG 3501
Db 4863 TTTTTTTTTTTTTTTTTTTTTTTTAAAGACAGAGTCTCGCTCTGCCAGGCTAGAGTGCAG 4922
QY 3502 TCTCACTTCATCACCTCA--ACCTCCGTTTCACTCACTCACTCACTCTGCTCCCGGGTTCA 3560
Db 4923 TGACACAATCTTTGGGCTCACTGCAACTCCCACTCCCTGCAACTCTGCTCCCGGGTTCA 4982
QY 3561 AGYGATTCTCCCTGCTTACGCTTCTGAGTGTGGAATTTACAAGGTGCACCACTGCT 3620
Db 4983 AGCAACCTCTCTGCTTACGCTTCTGAGTGTGGAATTTACAGGCGCTGCCACTGCACC 5042
QY 3621 TGGCTAAATTTTTTGTATTTTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGCT 3680
Db 5043 CAGCTAA--TTTTTGTATTTTTTAGTAGAGAGGGGTTTCTCATGTTGGTGGCTAGTCT 5101
QY 3681 CAAACTCTGACCTCAAGTGATCTGCTGCTCAGTCTCCCAAGGTCTGGAAATATAGG 3740
Db 5102 CAAACTCTGACCTCAGATGATCCATTGGCTTGGTGTCTCAAGGTCTGGGATTACAGG 5161
QY 3741 CGTGAGTCACTGCTGCTGGCCGATTTACTGCTCTATTTCTTTTATTTGCTATATCCCCAGATC 3800
Db 5162 CATGAGCCACACACTCAGCTGGT--TTAAGCATTTTTATGACTCACTCACTTTAAACC 5220
QY 3801 TAGAGCAGTGTCTGACATATAGTGTCTCAATAAATAATTTGATGAATGCACAGCTAG 3860
Db 5221 GCCCAACTCCCTGAGGTATGTTCTGTTAATAGTATCCCCACTTTACAAGTTAATTAAG 5280
QY 3861 APATAAATCTTTCTTTTCTTTTAAAAACAATTTGACAACCTTTGCAAGATAAATAACAA 3920
Db 5281 CCAGAAAG-----GTTAAGGACCTGCTGAGGCTGCACAGCAGTACTTGAA 5328
QY 3921 TCTTGATCTGCTTTTTCACCTTATCAGCTTGTATGACTTTTTCATATGCTCTCAACC 3980
Db 5329 CCTGGCTCTCGGCATTTCTTTAGCTGCTGTGTA-----GTGGCCCAAAATC 5376
QY 3981 TTTATTGTTACTGTTTTTTTCTTACTTATTTTACTGACTCACTGAATAATATGCTTAATTT 4040
Db 5377 AATGTTATTAGATTAGAAATTCAGGTATTGTTGAAATAGGCCAATTTAAGCTTTAATAA 5436
QY 4041 GCTTATACATCTCTGCTTCCACTTTTGAAGGCCAAATTTTACAATCTGATGAAAGCTAT 4100
Db 5437 TTTAAACCCAAATGTTGTTAAACATTTAGAATGTGCACCTTTAAATAATACACCAATTCGGG 5496
QY 4101 GA-ACCCTCTCCAGAGANAATACACACACACACACTCAGCTCAGCTCACTCACTCACT 4159
Db 5497 CACAGTGGCTCAGGCTGTGAATCCCAGCAGCTTTGGGAGGCCAAGGAGGAGTCACTCTG 5556
QY 4160 ATGTTTGAACCTAAAGCAAGAAACCTGCAATTAGAGAGTGTGTTGTTTCAATTAATTAATAA 4219
Db 5557 AGGTGAGGGTTTCAGACCACTCTGGCAACATGTTGAACCCCATCTCTATTATAAATA 5616
QY 4220 T----AATCAGTTGGGCACAGTGACTCAAGCTGTAAACCACTGTTTGAAGTGCAC 4275
Db 5617 TATAAATAATTAGCTGGCAGCGTGGCTCACCTGTAAATCCCAGCAGCTTTGGGAGGCTGA 5676
QY 4276 GGTGGGTGGATCAGTTGAGTGAAGTTCGAGACAGCTGCTCAATATGCTGAACCC 4335
Db 5677 CACGGGTGGATCA--TGAGGTGAGGATTCGGGATCCATCTCTGGCTAAACAGGCTGAACCC 5734
QY 4336 TATCTCTATAAATAACAAAAATTTAGCTGGGTGTAGTGTGATGATGATGCTGCTAGTCCCAGC 4395
Db 5735 TGTCTCTACCAAAATACAAAAATTTGGCGGCGTGGTGGCAGGTGACTGTGTAGTCCCAGC 5794
QY 4396 TACTCGGAGGCTGAGGCAAGAAATTCCTGAACTCTGGAGGAGGAGGTTCCAGTGAGC 4455

Db	5795	TACTCGGGAGGCTGAGCGACGAGAAATGCGCTGAACCTGGGAGCGGAGCTTGCGAGTGAGC	5854	PR	05-SEP-2000;	2000US-0229513P.
				PR	06-SEP-2000;	2000US-0230437P.
QY	4456	CGAGATCCCACTGCACTCCAGCCTGGCGGACACAGCGAGACTCTATCTCAAAAAAT	4515	PR	06-SEP-2000;	2000US-0230438P.
				PR	08-SEP-2000;	2000US-0231242P.
Db	5855	TGAGATCATGCCACTGCACCTTCAGCCTGGGTGACACAGCAAGACTCCATCTCAAAAAATA	5914	PR	08-SEP-2000;	2000US-0231243P.
				PR	08-SEP-2000;	2000US-0231244P.
QY	4516	AAATAA	4521	PR	08-SEP-2000;	2000US-0231413P.
				PR	08-SEP-2000;	2000US-0231414P.
Db	5915	AATAAA	5920	PR	08-SEP-2000;	2000US-0232080P.
				PR	08-SEP-2000;	2000US-0232081P.
				PR	12-SEP-2000;	2000US-0231968P.
RESULT 29				PR	14-SEP-2000;	2000US-0232397P.
AAK83897				PR	14-SEP-2000;	2000US-0232398P.
ID	AAK83897	standard; DNA; 17245 BP.		PR	14-SEP-2000;	2000US-0232399P.
XX				PR	14-SEP-2000;	2000US-0232400P.
AC	AAK83897;			PR	14-SEP-2000;	2000US-0232401P.
XX				PR	14-SEP-2000;	2000US-0233063P.
DT	07-NOV-2001	(first entry)		PR	14-SEP-2000;	2000US-0233064P.
XX				PR	14-SEP-2000;	2000US-0233065P.
DE		Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38709.		PR	21-SEP-2000;	2000US-0234223P.
XX				PR	21-SEP-2000;	2000US-0234224P.
KW		Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		PR	25-SEP-2000;	2000US-0234274P.
KW		cytostatic; gene therapy; vaccine; metastasis; ds.		PR	25-SEP-2000;	2000US-0234997P.
XX				PR	25-SEP-2000;	2000US-0234998P.
OS		Homo sapiens.		PR	26-SEP-2000;	2000US-0235484P.
XX				PR	27-SEP-2000;	2000US-0235834P.
PN				PR	27-SEP-2000;	2000US-0235836P.
XX				PR	29-SEP-2000;	2000US-0236327P.
XX				PR	29-SEP-2000;	2000US-0236367P.
PD				PR	29-SEP-2000;	2000US-0236368P.
XX				PR	29-SEP-2000;	2000US-0236369P.
				PR	29-SEP-2000;	2000US-0236370P.
				PR	02-OCT-2000;	2000US-0236802P.
				PR	02-OCT-2000;	2000US-0237037P.
				PR	02-OCT-2000;	2000US-0237038P.
				PR	02-OCT-2000;	2000US-0237039P.
				PR	02-OCT-2000;	2000US-0237040P.
XX				PR	13-OCT-2000;	2000US-0239935P.
				PR	13-OCT-2000;	2000US-0239937P.
				PR	20-OCT-2000;	2000US-0240960P.
				PR	20-OCT-2000;	2000US-0241221P.
				PR	20-OCT-2000;	2000US-0241785P.
				PR	20-OCT-2000;	2000US-0241786P.
				PR	20-OCT-2000;	2000US-0241787P.
				PR	20-OCT-2000;	2000US-0241808P.
				PR	20-OCT-2000;	2000US-0241809P.
				PR	20-OCT-2000;	2000US-0241828P.
				PR	01-NOV-2000;	2000US-0244617P.
				PR	08-NOV-2000;	2000US-0246474P.
				PR	08-NOV-2000;	2000US-0246475P.
				PR	08-NOV-2000;	2000US-0246476P.
				PR	08-NOV-2000;	2000US-0246477P.
				PR	08-NOV-2000;	2000US-0246478P.
				PR	08-NOV-2000;	2000US-0246523P.
				PR	08-NOV-2000;	2000US-0246524P.
				PR	08-NOV-2000;	2000US-0246525P.
				PR	08-NOV-2000;	2000US-0246526P.
				PR	08-NOV-2000;	2000US-0246527P.
				PR	08-NOV-2000;	2000US-0246528P.
				PR	08-NOV-2000;	2000US-0246532P.
				PR	08-NOV-2000;	2000US-0246609P.
				PR	08-NOV-2000;	2000US-0246610P.
				PR	08-NOV-2000;	2000US-0246611P.
				PR	08-NOV-2000;	2000US-0246613P.
				PR	17-NOV-2000;	2000US-0249207P.
				PR	17-NOV-2000;	2000US-0249208P.
				PR	17-NOV-2000;	2000US-0249209P.
				PR	17-NOV-2000;	2000US-0249210P.
				PR	17-NOV-2000;	2000US-0249211P.
				PR	17-NOV-2000;	2000US-0249212P.
				PR	17-NOV-2000;	2000US-0249213P.
				PR	17-NOV-2000;	2000US-0249214P.
				PR	17-NOV-2000;	2000US-0249215P.
				PR	17-NOV-2000;	2000US-0249216P.

17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483426/52.
DR
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 38709; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM81970 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 17245 BP; 4069 A; 4768 C; 4523 G; 3885 T; 0 U; 0 Other;
Query Match 8.2%; Score 408.8; DB 4; Length 17245;
Best Local Similarity 59.5%; Pred. No. 1.9e-65;
Matches 855; Conservative 1; Mismatches 533; Indels 47; Gaps 8;
3098 TTGGGTTTTTTTTTTTGTGTTTGTAGACAGGGCTTGTCTGTGCACCCAGGCAAGAG 3157
DB 8200 TTGGCTTTTTTTTTTTTTTTTTTTTGTAGATGGAGTCTGCTCTGTGCGCCAGGCTGGAG 8259
QY 3158 CACAGTGGTGCACCATAGTCTACTGAGCCTCAACTCTCTGAGTCAAGGATCTGCTG 3217
DB 8260 TGCAGGGGTGCATCTCTGGGCTCTACTCGAGCTCCACTCCCGGGTTTCAGCCCATCTCTCT 8319
QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGGTGCACCACACCGCTGGCTTAATAA 3277
DB 8320 GCTCAGCCTCCCGAGTAGCTGGGACTACAGGGGCCCCACACACACCGGCTTAATTTTT 8379
QY 3278 AAAAT-----TTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTGTGTCTTAAACTC 3333
DB 8380 GTTTTGTATTTTGTAGAGACGGGATTTTCCCGGTGTTTAAACACGAGCTGTCTTGAATC 8439

QY 3334 CTGGCTTCAAGCAATCTCTCTACCTTGGCATCCAAAGTGTGGGATTTACAGGGGTGAGC 3393
DB 8440 CTGACCTCAGGTGATCTGCCTGCTCGGCTCCCAAAGTGTGGGATTTACAGGCTGAGC 8499
QY 3394 CACANVTGGCGGTACTTATTTCTTTACATTCATCTTTTCCAATAGATGTAAGTCCAC 3453
DB 8500 CACCGCGCTGGCCTCTGAGTTTTCTGTGTTCTTTTCTTTTCTTTTGTGATGGA- 8558
QY 3454 AGAACAGGATTTACTGCGCTATTTTCTTCTTTTGTGAGACAGAGTCTCACATTATC 3513
DB 8559 -----GTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGT 8590
QY 3514 ACCTCAACCTCCGTTTCACTGCAACCTCTGCTCCCGGGTTTCAAGYATTTCTCTG 3573
DB 8591 GGCAGATC-----TTGCCCTCACTGCAAGCTCTGCCATCCAGGTTTCATGCGATTCTCCTG 8645
QY 3574 CCTAAGCCTCTGAGTAGCTGGAATTACAAGGGTGACACATGCTTGGCTTAATTTTTT 3633
DB 8646 CTTAGGCTCC- GAGTAGCTGGGACTACAGGTGGCCACCACTATATCCAGCTTAATTTTTT 8704
QY 3634 GTATTTTGTAGCAGAGATGGGGTTTTACCATGTGTCAGGCTGGTCTCAAACTCTGAC 3693
DB 8705 GTATTTTGTAGAGACGGGGTTTTACCATGTGTTAGTAGGATGGTCTCGATCTCTGAC 8764
QY 3694 TCAAGTGTCTGCTGCTCAGTCTCCCAAGTGTGGAATTTATAGGGCTGAGTCACTGT 3753
DB 8765 TC--GTGATCCGCTGCTCAGCCTCCCAAAGTGTGGGATTTACAGGCTGAGCAACGC 8822
QY 3754 GCCTGGCGGATTTACTGTCTATTTTCTTTTATGCTATATCCCAAGATCTAGAGCAGTGTCT 3813
DB 8823 GCCCGGCTCTTTTGTCTTTCTTTTGTG-----AGACAGAGTCTCACTGTGCTGCA 8878
QY 3814 GACATATAGTAGGTCTCAATAAATAATTGATGATGACAGCCTAGATATAAACTTTCT 3873
DB 8879 GGCTGGATACAGTGGGTGATCTCGGCTCACTGCAACCTCTGTCTCCGGGTTCAAAATGAT 8938
QY 3874 TTTTCTTTTAAACCAATCTTGCAAACTTTTGCAAGATAAATAACAATCTTGCATTTGCG 3933
DB 8939 TCTTCTGCTCAGCCTCAGCCTCCTGAGTAGTGGGACTACAGGCACGCACCAACACC 8998
QY 3934 TTTTCTACTATACCTTTGTATGACTTTTTCATAT-TGCCTCAAACTTTTATTTGTTACT 3992
DB 8999 CGGCTAAATTTTGTATTTTGTAGTAGATGGGATGCTCTGAGTTTATTTTAAAGAGACAG 9058
QY 3993 GTTTTCTTCAATTTTACTATTTTAGTCACTGATATATGGCTTAATTTGTTTATATACATCC 4052
DB 9059 GGTCTTGTCTGTCTACCTATGGTGGAGTGCGAGGTGCCACTGTAACTTCAAAATTCCTGG 9118
QY 4053 TCCTGCTCCACTTTAGAAGGCCAAATTTTCAAAATCTGATGAAAGCTATGAAACCTCTCCC 4112
DB 9119 GCTCATGTGATTTCTCTGCTGCTCAGCCTCCCAAAGCAGCTGAGATTATACGACGAGCCAC 9178
QY 4113 CAGAGAAATACACACACACACACACTCACACAGATTTTTTTTTTAATGTTTGGCAACTA 4172
DB 9179 TCACCCATCTTTGTTTTTAAATGAAATCATTTTTCTAAATGGCAATAGACTAAAAAAG 9238
QY 4173 AGACAAGAACTGCTATTTAGGAGATGTTTGTTCATATTAATTTAAAAATACTC-AGTTGG 4231
DB 9239 GAAAAAATAAGCAATTCACAATAGAAATGTTGGGAAAAAACAAGTGACAGCTCTCTGGCCA 9298
QY 4232 GCACAGTCACTCAAGCCTGTAAACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGATCACTT 4291
DB 9299 GCACAGTGGTTCACCTCTGTAATCCAGCAGCTTTTGGGAGGCCAAGCAGCGGATCACT 9358
QY 4292 GAGGTGAGAAGTTCCAGACCGCTGGTCAATATATGGTGAACCCCTATCTCTACTAAAAAT 4351
DB 9359 GAGGTGAGAAGTCCGAGACCGCTGGCCAAACACAGGTGAAACCCCGTCTCTACTAAAAAC 9418
QY 4352 AAAAAAATTTAGTGGGTGATGATGCTGTGTAGTCCCAAGCTACTCGGAGGCTGAG 4411
DB 9419 AAAAAAATTTAGCAGCTGTGGTGGGCACTGTAATCCCAAGTTTACTGAGGAGGCTGAG 9478

Db 98536 CTCAGTCTTACTATATAAATCAAAAAATTAGCTGGCATGATGGTGCATGCCCTGTGTATCCC 98595
QY 4393 AGCTACTCGGAGGCTGAGGCAAGAGAAATTGCTTTGAACCTGGGAGGACAGAGTTGTCAGTG 4452
Db 98596 AGTACTTGGGAGGCTGAGTGGAGGATCACTTGAGCCAGGACCCAGAGTTGTCAGTG 98655
QY 4453 AGCCGAGATCCCAACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAA 4512
Db 98656 AGCTGAGATCACACCCCTTCACTCCAGCCTGGGCAAGAGAGTGCAGACCCCTGTCTCAAAAC 98715
QY 4513 AATAAATAAATAAATAAAGATCGGAGAGAAACAA 4549
Db 98716 AAAAACAACAAAAACAGAAAGAAAGAAAAAGAA 98752

RESULT 31
ABD33272/c
ID ABD33272 standard; DNA; 227246 BP.
XX ABD33272;
XX 18-NOV-2004 (first entry)
XX Human cancer-associated (CA) gene HD07-047.
XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
KW ds; cancer; cytostatic.
XX Homo sapiens.
XX WO2004058146-A2.
XX 15-JUL-2004.
XX 15-DEC-2003; 2003WO-US040081.
XX 17-DEC-2002; 2002US-00322281.
XX (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Malandro MS;
XX WPI; 2004-499109/47.
XX Novel human cancer associated protein encoded within open reading frame
PT of cancer associated gene, useful as targets for diagnosing cancer.
XX Claim 16; SEQ ID NO 314; 182pp; English.
XX The invention relates to cancer-associated proteins (CAP) and the cancer-
CC associated (CA) nucleic acids encoding them. The invention also relates
CC to a method for treating cancers involving administering to a patient an
CC inhibitor of CAP, and a method of screening for anticancer activity in a
CC potential drug involving providing a cell that expresses a CA gene,
CC contacting a tissue sample derived from a cancer cell with an anticancer
CC drug candidate and monitoring the effect of the anticancer drug candidate
CC on expression of the CA gene. The CAP proteins are useful for detecting
CC cancer associated with expression of a CAP protein in a test cell sample
CC and for screening for a bioactive agent capable of modulating the
CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
CC cancer, involving determining the expression of a CA nucleic acid in a
CC tissue. This sequence represents a human CA gene of the invention. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 227246 BP; 57720 A; 53838 C; 54924 G; 60744 T; 0 U; 20 Other;

Query Match 8.1%; Score 405.8; DB 13; Length 227246;
Best Local Similarity 59.7%; Pred. No. 1e-64;
Matches 898; Conservative 1; Mismatches 558; Indels 48; Gaps 11;

QY 3082 TTGTAGTGGTGACAGTTTGGGTTTTTTTTTTTGTGTTTAGAGACAGGGTCTTGC-TC 3140

Db 140336 TGGTAATTGTAACTTTTTTTTTTTCTTTTCTTTTATTTTCTGAGACGGAGTTTGTCTTC 140277
QY 3141 TGTCAACCCAGGATCAGACACAGTGTGCAACCATAGTCTACTGCAGCCTCAACCTCCTCA 3200
Db 140276 TGTCAACCCAGGCTGAGTGCATATGTCATGCTTCTGCTCACTGCAACCTCTGCATCCCG 140217
QY 3201 GCTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTCGACACC 3260
Db 140216 GTTCAAGCAATTCTCTGCTCAGCCACCTGAGTATCTGGGATTACAGSCAGTGCACC 140157
QY 3261 AGCCTGGCTAATTAAAAAATTTTTTTGTAGAGACTGGTCTTACTAGTTGGCCAGCG 3320
Db 140156 ACACCTGGCTAATTTTGTGA--TTTAAAGTAGGACAGGGTTTCGCAATGTTGGCCAGC 140099
QY 3321 TTGCTCTTAACTCCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTGGGAT 3380
Db 140098 TGGTTTCAAACTCTGACCTCAGGTGATCCGCCCGCTCGGCTCCCAAGTGTGGGAT 140039
QY 3381 TACAGGGGTGAGCCACCATGTGCGGTACTTATTTCTTTTACATTCATCTTTTCCAATAGA 3440
Db 140038 TACAGCGGTGAGCCACACACTTGGCTACTTTTTTTGTTGTTTCTTTT----- 139988
QY 3441 ATGTAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTCTTTTGTGAGACAGA 3500
Db 139987 -----GAGATAAGGTCTCACTTTGTTGCCAGGCTGGAGTGCAGTG 139947
QY 3501 GTCTCACTTCATCACTCAACCTCCGTTCCAGCTCACTGCAACCTCTGCTCCCGGTTCA 3560
Db 139946 GTGTAATCTTGGCTCAGTAGCATGATCTTGGCTCACTGCAACCTCTGCAATCCAGGTTCA 139887
QY 3561 AGYGATTTCTCTGCTCCTAAGCCTCTCTGAGTAGCTGGAATTTACAAGCGTGCACCACCATGCT 3620
Db 139886 AGCAATTTCTCTGCTCAGCCACTGAGTATCTGGGATTTACAGSCAGTGCACCACACC 139827
QY 3621 TGGCTAAATTTTTGTATTTTTTAGCAGAGATGGGTTTTTACATGTTGCCAGCGTGGTCT 3680
Db 139826 TGGCTAA--TTTTTGTATTTTAAAGTAGGACAGGGTTTCGCAATGTTGGCCAGCTGGTTT 139768
QY 3681 CAAACTCTGACCTCAAGTGATCTGCTGCCCTCAGTCTCCCAAGTGTGGGAATTATAGG 3740
Db 139767 CAAACTCTGACCTCAGGTGATCCGCCCTCGGCTCCCAAGTGTGGGAATTACAGG 139708
QY 3741 CGTGAGTCACTGTGCTGGCCGA--TTACTGTCTATTTTCTTTTATTTGCTATATCCCCAGA 3798
Db 139707 CGTGAGCCACACACTTGGCCTACTTTTTTGTGTTTCTTTTGTAGATAAGTCTCAC 139648
QY 3799 TCTAGAGCAGTGTGACATATATAGTAG--GTGCTCAATAAATAATTAATGATGAATGCACAGCC 3857
Db 139647 TTTGTTGCCAGGCTGGAGTGCAGTGGTGTAGTCTTGGCTCAGTAGCATGATCTTGGCTC 139588
QY 3858 TAGATATAAACTTTCTTTTCTTTTAAACAATCTTGACAACCTTTTCAGAAATAAATA 3917
Db 139587 ACTGCAACCTCTGCTCCTGGGTTCAAGTAATTCCTCGCTCAGCCTCCAGAGTAGCTG 139528
QY 3918 CAATCT--TGCATTTGCTTTTTTCACTTATCACTTGTGTTATGACTTTTTTCATATTGCCCA 3976
Db 139527 GAATTACAGGCCCGCCACCATACCTAGATAATTTTATATATTTTAGTAGAGATTTTAC 139468
QY 3977 AACCTTTATGTTACTGTTTTTTTCAITGTTACTATTTTAGTCACTGAATAATATGGCTTA 4036
Db 139467 CATGTTGGCCAGGCTAGTCTCGACATCCGACCTCAGGTGATCGCCTGCTCAGCCTCCCA 139408
QY 4037 ATTTGCTTATACATCTCTCTGCTCCACTTTTAGAAGGCCAAATTTTCAAAATCTGATGAAAG 4096
Db 139407 AAATGCTGAGATTACAGCATGTGCCACCGCACCCAGCCTATGTTGATTTTTTTGAGGAAC 139348
QY 4097 CTATGAACCTCTCCCCAGAGAAA---TACACACACACACACACTCACACAGTTTTT 4153
Db 139347 CACCATGCTGTTGTTTCCACAGTGACTTCCACCATTTTACGTTCTCTACAGTGGTATGAA 139288
QY 4154 TTTTAAATGTTTGGCAACTAAGACAGAAACCTCGCATTAGAGGATGTTTGTTCATATTAA 4213

Db	139287	GGCTCCAATTTCCACATCCTCACCAACATTTATTATCTGTCTGTTTGGTTATAGTCCT	139228	PR	14-AUG-2000;	2000US-0225214P.
Qy	4214	TAAAAATACTCAGTTG-----GGCAGAGTCACTCAAGCCTGTAACACAGTACTTTG	4266	PR	14-AUG-2000;	2000US-0225266P.
Db	139227	AAGAAAGTGTATCTCAGGGGCCAGGTGCAGTGGCTCATGCCCTGTAATTCAGGAGTTTG	139168	PR	14-AUG-2000;	2000US-0225268P.
Qy	4267	GAAGTCCAAGTGGGTGGTCACTTGAGGTGAGAAGTTCGAGACCAAGCCTGGTCAATATG	4326	PR	14-AUG-2000;	2000US-0225447P.
Db	139167	GGAGGCCAAGGTGACACAGATCACTTTAGGTCAGAGTTGAGACCAAGCCTGGCCAACATG	139108	PR	14-AUG-2000;	2000US-0225757P.
Qy	4327	GTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTAGTGATGCATGCCTGT	4386	PR	14-AUG-2000;	2000US-0225758P.
Db	139107	GTGAACACGATCTCTACT-AAAATACAAAAATTAGCTGGGTGCGGGCAGGCACCTGT	139049	PR	14-AUG-2000;	2000US-0225759P.
Qy	4387	AGTCCCAAGTACTCGGAGGCTGAGCAAGAGAATTGCTTGAACCTGGGGAG-GCAGAGGT	4445	PR	18-AUG-2000;	2000US-0226279P.
Db	139048	AATCCCAAGTACTCGGAGGCTGAGGCAGAGAATTGCTTAAATCTGGGGGTGCGGAGGT	138989	PR	22-AUG-2000;	2000US-0226681P.
Qy	4446	TGCAGTGAGCCGAGATCCCAACCACTGCACCTCCAGCCTGGGCGACACAGCGAGACTCTATC	4505	PR	22-AUG-2000;	2000US-0226868P.
Db	138988	TGCAGTGAGCCAAGATCGCGCCACTGCCTCCAGCCTGGGAGACAGCAAGACTCCGTC	138929	PR	23-AUG-2000;	2000US-0227009P.
Qy	4506	TCAAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAACAAACTAATAAGATTCCCTG	4565	PR	30-AUG-2000;	2000US-0228924P.
Db	138928	TTGMAAAAAAAAAAAAAAAAAAGAGAGAAAAAGAAAAAGAAAGTGGTATCTCATTTAGTG	138869	PR	01-SEP-2000;	2000US-0229287P.
Qy	4566	AAGGT 4570		PR	01-SEP-2000;	2000US-0229343P.
Db	138868	ATGAT 138864		PR	01-SEP-2000;	2000US-0229344P.
RESULT 32				PR	01-SEP-2000;	2000US-0229345P.
AAK84027/c				PR	05-SEP-2000;	2000US-0229509P.
ID AAK84027 standard; DNA; 11872 BP.				PR	05-SEP-2000;	2000US-0229513P.
XX AAK84027;				PR	06-SEP-2000;	2000US-0230437P.
AC				PR	06-SEP-2000;	2000US-0230438P.
XX				PR	08-SEP-2000;	2000US-0231243P.
DT	07-NOV-2001 (first entry)			PR	08-SEP-2000;	2000US-0231244P.
XX				PR	08-SEP-2000;	2000US-0231413P.
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38839.			PR	08-SEP-2000;	2000US-0231414P.
XX				PR	08-SEP-2000;	2000US-0232080P.
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;			PR	12-SEP-2000;	2000US-0231968P.
KW	cytostatic; gene therapy; vaccine; metastasis; ds.			PR	14-SEP-2000;	2000US-0232397P.
XX				PR	14-SEP-2000;	2000US-0232398P.
XX	Homo sapiens.			PR	14-SEP-2000;	2000US-0232399P.
XX				PR	14-SEP-2000;	2000US-0232400P.
PN	WO200157182-A2.			PR	14-SEP-2000;	2000US-0232401P.
XX				PR	14-SEP-2000;	2000US-0233063P.
PD	09-AUG-2001.			PR	14-SEP-2000;	2000US-0233064P.
XX				PR	14-SEP-2000;	2000US-0233065P.
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Qy	1956	TGAGTCCCTGCGGGGGCGGGTGGGGCACACGCCAAAGGATCTCAGCAGGCATACAAAG	2015	CGC
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Qy	2308	TCATGCTGTAAATCCACAGCACTTTTGGAGGCGGAGCGGGCGGATCACTTGAGGTCAGGA	2367	CGC
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Qy	3199	GAGCTCAAGGATCTGTGTGACCTCAGGCTCCCAAGTAGCTGGGACTACGAGCGTGACCA	3258
Db	2662	GGGTTCAAGCCATTCTCTGCCTCAGCTCCCGAGTACCTGGGACTACAGGAGCCCGCCA	2603
Qy	3259	CCAGCCTCGCTAATTAATAAATTTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAG	3318
Db	2602	CCAGCTTGGCTAATTTTTTTTGTGTA-TTTTGTAGATGGGGTTTCAACCGTGTAGGCCAG	2544
Qy	3319	GCTTGTCTTAACTCCTGGCTTCAAGCAATCTCTACCTTGGCATCCCAAGTG-----	3373
Db	2543	GATGGTCTCGACTCTCTCTGACTC--GTGATCCACCGCTTTGGCTCCCAAGTGCTAAA	2486
Qy	3374	---CTGGGATTACAGGGGTGAGCCACCATGTGGGCTACTATTCTTTTACATTCATCT	3430
Db	2485	GTACTGGGATTACAGGCTGAGCCACGCGCCAGCCCTATTTTTTATTTATTTATTTT	2426
Qy	3431	TTCCAATAGAAATGAAGATCCACNAGACAGGATTAAGTCTATTTCTTCTCTTTCTTTT	3490
Db	2425	TCGAGATCAA-----GTCTCACTTTGTGCG	2401
Qy	3491	TTGAGACAGAGTCTCACTTTCATACCTTCAACCTCCGTTGAGCTCACTGCAACCTCTGCCT	3550
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Qy	3551	CCCGGGTTCAAGYGATTTCTCTGCTTAAGCTCTCTGATGAGTGGAAATTAAGAGCTGCA	3610
Db	2351	CCTGAGTTCAAGTGAATCTCTGCTCAGGCTCCCATGATGAGTGGGACTACAGGTGCGTG	2292
Qy	3611	CCACATGCTTGGCTAATTTTTTGTATTTTTAGCAGAGATGGGGTTTACCATGTTGGCC	3670
Db	2291	CCACCAAGCTAGTGTAA-TTTTGTGATTTTGTGTAGAGACAGAGTTTTCACCATGTTGGCC	2233
Qy	3671	AGGCTGTCTCAAACTCTGACCTTCAAGTGATCTGCTGCTCAGTCTCCCTCCCAAGTCTG	3730
Db	2232	AGGCTGGTCTCAAACTCTGACCTGAGGCAATCTGCCCGCTCAGCGCTCCCAAGTCTG	2173
Qy	3731	GAATTAAGGCGTGAGTCACTGTGCTTGGCGGATTAATCTGTCTATTT	3776
Db	2172	GGATTACAGGCGTGAGCAGTATGCTTGGCTGGCAATCTGTTTCTT	2127

RESULT 34
ADD.13556/0

ADL13556/C
ID ADL13556 standard; DNA: 95240 BP.

XX
AC ADL13556;

XX
DT 06-MAY-2004 (first entry)

XX DE Osteoarthritis-associated polymorphic nucleotide #88.

XX	ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy;
KW	joint space narrowing; osteophyte development; joint pain;
KW	osteoarthritis; SNP; single nucleotide polymorphism.
XX	
OS	Homo sapiens.
XX	
PN	W02003054166-A2.
XX	
PD	03-JUL-2003.
XX	
PF	19-DEC-2002; 2002WO-US041225.
XX	
PR	20-DEC-2001; 2001US-0342603P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
PI	Jones KA, Schafer A;
XX	
PI	WPI; 2003-559141/52.
XX	
PT	Determining susceptibility of an individual to joint space narrowing,
PT	osteoephyte development and/or joint pain comprises identifying whether
PT	the individual has at least one polymorphism in a polynucleotide encoding
PT	a protein.
XX	
PS	Disclosure; SEQ ID NO 88; 297bp; English.
XX	
CC	The invention relates to a method of determining susceptibility of an
CC	individual to joint space narrowing and/or osteophyte development and/or
CC	joint pain comprising identifying whether the individual has at least one
CC	polymorphism in a polynucleotide encoding at least one of the protein
CC	listed in the specification. The methods, composition and agent are
CC	useful for modulating the susceptibility of an individual to joint space
CC	narrowing and/or osteophyte development and/or joint pain that is
CC	associated with a disease, preferably osteoarthritis. The cell line and
CC	the non-human animal are useful for screening for an agent for diagnosing
CC	an individual having susceptibility to joint space narrowing and/or
CC	osteoephyte development and/or joint pain. This sequence corresponds to
CC	the polynucleotide encoding a protein listed in the specification. (Note:
CC	The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences).
XX	
SQ	Sequence 95240 BP; 23048 A; 23934 C; 24441 G; 23817 T; 0 U; 0 Other;
	Query Match 8.1%; Score 404; DB 10; Length 95240;
	Best Local Similarity 60.4%; Pred.No. 1.9e-64;
	Matches 897; Conservative 1; Mismatches 506; Indels 80; Gaps 11;
Qy	3099 TTGGGTTTTTTTTTGTGTGTTTATAGACAGAGGCTTCTCTGTCAACCCAGGCGATGAGC 3158
Db	12747 TTTATTATGTACTATTATTATTTTTCAGACAGAGTCTTCTCTGCCACCCAGGCTGGAGT 12688
Qy	3159 ACAGTGGTCAACCATAGGTCACTGACGCTCAACCTCTGAGCTCAAGGATCTGCTGA 3218
Db	12687 GCAGTGGTGTAAATCTCGGCTCACTGCAACCTCCACATCTGGGTTCAAGCGATTCTCCA 12628
Qy	3219 CCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACACACCGCTGGCTTAATAAAA 3278
Db	12627 CCTCAGCCTCTCGATAGCAGGAGATTACAGGCGCCCGCCAGACGCCGGTTAATTTTG 12568
Qy	3279 AAATTTTTTTGTATAGACTGGGCTTTACTACGTGTGGCCAGGCTTGCTTTAAACTCCTGGC 3338
Db	12567 TA--TTTTTGGTAGACACAGGGTGTGTGCCATGTGTGGCCAGGCTGTCTCAACACCTGAC 12510
Qy	3339 TTCAAGCAATCTCTTACCTTGGCATCCCAAGTCTGGGATTACAGGGGTGAGCCACCA 3398
Db	12509 CTAGGTGATTCACCTGCGCTTGGCCCTCCAAAGTGTGGGATTACAGGCTGAGCACCT 12450
Qy	3399 TGTGCGGCTACTTTATTTCATTTCATATTCATTTCCATATCTTTCCATAGAAATGTAAGATCCACAGAAC 3458
Db	12449 CGCGGGGCGCTCTTGACAATTTTTGATGATGAGCTTTCTGCAATCATTTGTTCTTATCTATTGT 12390

PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Baraah SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Disclosure; SEQ ID NO 32693; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 17173 BP; 4470 A; 4247 C; 4332 G; 4124 T; 0 U; 0 Other;
Query Match 8.1%; Score 403.8; DB 4; Length 17173;
Best Local Similarity 54.9%; Pred. No. 1.6e-64;
Matches 1336; Conservative 2; Mismatches 904; Indels 191; Gaps 20;
QY 2279 AAAATCGCTTTCAGGCGCGGGTGGCTCATGCTGTAATCCAGACCTTTGGGAGGC 2338
DB 13307 AAAATGAAGTCAAGCGCGGGTGGCTCAGCGCTGTAAATCCAGCACTTTGGGAGGC 13366
QY 2339 CGAGGCGGGCGGATCACTTCAGGTGAGGCTTCGAGCAGCGCTGGCCACATGGTGAAA 2398
DB 13367 TGAGGTGGGAGAGATAAAGTTCAGGTGAGGCTTCAGACAGCGCTGGCCACATGGCGAAA 13426
QY 2399 CCCTGTCTCTACTAAAAATACAAAAATTAGCGCGGACATGGTGGCGAGCGCTGTAAACCC 2458
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QY 2459 CAGTACTTGGGAGACTGAG-----TTGGAGGTTTCAGT 2492
DB 13486 CAGTACTCGCGCGGCTGAGGCGAGGAGAAATCACTTGAACCCAGGATGTGGAGGTTCGAGA 13545
QY 2493 GAGCAGAGGTGCTGCTACTGCTCCAGCGCTGGGTAAACAGCAACTCTGTCTCAAAAAA 2552
DB 13546 GAGCGGAGGCTTGTGCCACTTCAGCTTGGGTGGGTGACAGCAAGACTCTGTCTCAAAA 13605
QY 2553 AAAAAATGCTTCAATAAATATATGATAAAAAAGGACTTATATTTTTTCAAGCCATAGGATC 2612

DB 13606 AAAAAAGAAAGTCAGTTGCTCAAGGCCATTCACAACTCAACATT-----CACACTCGGGTC 13660
QY 2613 ATTTCTCTGTAAGCATCTTGGCGAAGTCAATCCCACTGTTCTCTGAGAGTGGCGAGGTGA 2672
DB 13661 TTTTGTATACCAACGCGCAGGCTGAAATGATCAAACTGTGTT--TTAGATGSGAAGAACTGA 13718
QY 2673 GGGCTGACCTATTGCTCTGCACTTACTCTATCTCAGCTGTCCCTCCCACTTTTCCAGGTG 2732
DB 13719 GGCATGGA--AGGGCAGTGTCTGCACAGTGTCTATGCTGGACTCACCTCGGGGAAC 13776
QY 2733 CTGCCAGACACATGACAACTGCTAYGACAGGCCAAGAGCTGSGACAGCTGTAATTTCT 2792
DB 13777 GAGGAGGGGATTGCTCTGTTG---GGACTGGAGGAGCTGATGGATTTAGAAGCTTGTGG 13832
QY 2793 GCTGGACAMMCGTACACCCACCACTATTCATCTGCTGCTGCTGCGCAATCACCTG 2852
DB 13833 GCAGGACACCGTCTCACAGCCTGGGCTGGGAGAGTAACACAGCCTCTGCAATTC----- 13888
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DB 13889 -----AAAAAGCTTAGCCCCAGTGAGACAAACAGCATCTACTTTCTCTACTGAGCTCCAG 13944
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DB 14056 -----GTGGGGTGCAGTGTAGAATAACAGATCTTTTA----- 14092
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DB 14413 -----CTGAGTCTGTTGTGTCGCCCGAGCTGGAGTGA 14446
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DB 14447 GTGGTCCAACTTT-----GGCTCAGTGCACAACTCTGCTCTCTGGGTTCAACAGATTCTCC 14501
QY 3572 TGCCTAAGCCTCCTGAGTAGCTGGAATTAACAAGCGTGCAACCACTGCTTGGCTAATTTT 3631
DB 14502 TGCTCAGACTCCCAAGTATCTGGGATTAACAGCGCTGCGCCACACACCTGGCTAA-TTT 14560
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Db 14621 CCTCAGGTAATCACCTGCTTGGCTCCCAAGTCTGGATTCAGGCATGAGCCACC 14680
Qy 3752 GTCCCTGGCGGATTAAGTCTATTTCTTTA-----TTGCTATATCCCCAGACTCA 3802
Db 14681 GAGCTGGCCGGAATAAGATAATCTTAAACAATCATGGAGTCTTAGCTAGTGCAGACA 14740
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Qy 3863 ATAACTTTCTTTCTTTTAAACAATCTTGACAATCTTGACAATTAATAACAATC 3922
Db 14801 GGTGTGATTAATATCTCTGTTTATAGTAGAACAACCCAGTCTTCAAGGGGTAAAA 14860
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Qy 4042 CTATATACATCTCTGCTCCACTTTAGAGGCCAAATTTTACAATCTGATGAAGCTATG 4101
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Qy 4206 -----ATATTAATTAATAAATACTCAGTTGGGCAAGTCAAGCTCTGAAC 4255
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Qy 4316 TGTCATAATGTTGAACCCCTATCTCTATAAATAACAAAATTAAGCTGGGTGTAGTGA 4375
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Qy 4436 AGCAGAGGTTGCGAGTGGCGGAGATCCCACTGCTCCAGCTCGGCGGAGCACACAGCG 4495
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Qy 4614 TTTAACCTGTAATCTTATTTTATTTTGTAT 4646
Db 15581 AGTATCAGAAAGAAATTTAATATTTCTTTT 15613

ID XX ABQ78991 standard; DNA; 23639 BP.
AC ABQ78991;
XX
DT 05-NOV-2002 (first entry)
XX Human phosphodiesterase genomic sequence.
XX
KW Human; phosphodiesterase; PDE; phosphoinositide-specific phospholipase C;
KW gene therapy; vaccine; protein therapy; inflammatory disease; asthma;
KW chronic obstructive pulmonary disease; rheumatoid arthritis; atopy;
KW chromosome 2; gene; ds; enzyme; SNP; single nucleotide polymorphism.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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FT 784..21639
FT /*tag= b
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FT /note= "Contains 14 introns"
FT exon 784..805
FT /*tag= c
FT /number= 1
FT intron 806..947
FT /*tag= d
FT /number= 1
FT exon 948..1106
FT /*tag= e
FT /number= 2
FT intron 1107..3651
FT /*tag= f
FT /number= 2
FT variation replace(1125,G)
FT /*tag= g
FT exon 3652..3880
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FT intron 3881..6538
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FT intron 6669..7713
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FT 17376..18667
FT /*tag= ah
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FT XX
FT PN US2002086810-A1.
FT XX
FT PD 04-JUL-2002.
FT XX
FT PF 20-DEC-2000; 2000US-00740043.
FT XX
FT PR 27-NOV-2000; 2000US-0252926P.
FT PR 04-DEC-2000; 2000US-0250497P.
FT XX
FT PA (GUEG/) GUEGLER K.
FT PA (BRAN/) BRANDON R C.
FT PA (DFRA/) DI FRANCESCO V.
FT PA (BEAS/) BEASLEY E M.
FT XX
FT PI Guegler K, Brandon RC, Di Francesco V, Beasley EM;
FT XX
FT DR WPI: 2002-635683/68.
FT DR P-PSDB; ABB99113.
FT XX
FT PT Novel isolated human phosphodiesterase peptide useful for diagnosing,
FT preventing and treating disorders characterized by aberrant expression of
FT the phosphodiesterase protein, and as immunogens to raise antibodies.
FT XX
FT PS Claim 4; Fig 3; 58pp; English.
FT XX
FT CC The invention relates to a novel human phosphodiesterase (PDE)

Query Match 8.1%; Score 403.6; DB 6; Length 23639;
Best Local Similarity 59.6%; Pred No. 1.8e-64;
Matches 882; Conservative 1; Mismatches 545; Indels 52; Gaps 10;

QY 3099 TTGGGTTTTTTTTTGTGTTTAGACACAGGGTCTGCTCTGTACCCAGGCATGAGC 3158
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Db 10144 GCAGTGGTGCAATCTCAGCTCACTGCAACCTCTGCTCTCCAGGTTCAAGCAATTCCTCG 10085

QY 3219 CCTCAGCTCCCAAGTAGCTGGGACTACGAGGCTGCACCACCGCCTGGCTTAATTAATA 3278
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Db 10084 TCTCAGCTCCCGAGTAAGTGGGATTACAGGCTCCTGCGCACCATACCCGGCTAATT-TTT 10026

QY 3279 AAATTTTTTGTAGAGACTGGGTCTTACTAGCTTGGCAGGGTGTGCTTTAAACTCCTGCG 3338
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QY 3600 ACAAGGTGCACACATGCTTGGCTAAATTTTGTATTTTATTTAGCAGATGGGTTTTA 3659
Db 9665 ACAAGGTGCACACATGCTTGGCTAA-TTTTTATATTTTATAGTAGACAGAGTTTTA 9607
QY 3660 CCATGTTGCCAGGCTGCTCAAACTCTCAAGTGTCTGCTGCTCAAGTCTCAGTCTC 3719
Db 9606 CCATGTTGCCAGGTTGGTCTGAACTCTGGCTCAGGTATCTGCC-----CGGTCTC 9552
QY 3720 CCAAAGTGTGGAATATAGGCTGAGTCACTGCTGCTGCGGATTTACTGTCTATTTTCT 3779
Db 9551 CCAAAGTGTGGAATTAGAGGCTGAGCCACTGCACTGCACTCAACCTCTACTCT--A 9494
QY 3780 TTATTGCTATATCCCGAGTCTAGACGAGTGTCTGACATATAGTAGTGTCTCAATAATA 3839
Db 9493 TTCTGAACACCCCAACAAATCTGAATAACAGATTTGTAATGTTTTCTGTTGACTTAAG 9434
QY 3840 ATTGATGAATGCACAGCTAGATATAAATCTTTCTTTCTTTTAAAAAATCTTGAC 3899
Db 9433 TTTTATGAGGCGAGTGTCTGTCTGATCTAGGCATTAATGATGCTGTGTGCTAGCAT 9374
QY 3900 AACTTTGAGAAATAATACTTGTGATTTCTGCTTTTTCACCTTATCACTTTGTTATGAC 3959
Db 9373 AGTCTCTGCACATATTAGGAATCAATAGCAATTCATTGAAGTAGTAATGAATG 9314
QY 3960 TTTTTCATATGCTCAACCTTTATTTGTTACTGTTTTTTCATTTGTTACTATTTTATGCA 4019
Db 9313 AATGAAAGGGAGTAAGAGTTTAGACCCAGAAATACCTTGTATCACTTGTCCAGCTCTCATTC 9254
QY 4020 CTGAATAATATGCTTAATTTGCTTATACATCTCTGCTCCACTTTTGAAGGCCAAAT 4079
Db 9253 ATCCCATCTTATCTCATTTCTCAGAGGAGGCCAACCTAAGATGATGATGCTGGGT 9194
QY 4080 TACAAATCTGATGAAAGCTATGAACCTCTCCCGAGAGAAATACACACACACACACAC 4139
Db 9193 TTGAATCTCAGTCTCTCTCATTTAGTGTGTGACTTTTGACAGAGTCAATGAATCTTTCTA 9134
QY 4140 TCACACACAGTTTTTTTTTAATGTTTGCACACTAAGACAGAAACCTGCAATTAGAGATGT 4199
Db 9133 AACCTCAGTTTTCTCTCTTTTATACAACTGATCTTAATAACAGGACCCATTTTCAACAGTCA 9074
QY 4200 TTGTTTCAATTAATAAATACTCAGTTGGGCACAGTGACTCAAGCTGTAAACACACAG 4259
Db 9073 TTGTTATTAGAAAGGTACGTAGATGCA---GGTACAGTGGCTCATGCTCTGATATCCAG 9017
QY 4260 TACTTTGGAGTCCAAGTGGGTGGATCACTTGAAGTGTGAAGTTCGAGACCAAGCTGTT 4319
Db 9016 CACTTTGGGAGTTGAGCGGGTGGATCACTTGAAGTTCGAGAGTTCGAGACCAAGCTGAC 8957
QY 4320 CAATATGGTGAACCCCTATCTCTACTAAATAACAAATAATAGCTGGGTGTAGTATGCA 4379
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QY 4380 TGCCTGTAGTCCAGCTACTCGGAGGCTGAGCAAGAGAAATGCTTGAACCTGGAGGC 4439
Db 8896 TGCCTGTAATCCAGCTACTCGGAGGCTAAGGCAGGAGAAATGCTTGAACCCGGAGGC 8837
QY 4440 AGAGGTTGAGTGAGCCGAGATCCACCACTGCATCTCAGCCTGGGCGA-CACAGGAGA 4498
Db 8836 AGAGGTTGTGTGGCCGAGATCGTGCCATTGCACTTCCAGTCTGGGCAATAAGAGCAAA 8777
QY 4499 CTCTATCTCAAAAAATAATAATAAATAAAGATCGG 4538
Db 8776 CTCTGTCTCAAAAAACAAAAAATAGAAAAAGGAAAGG 8737
RESULT 37
AAS26670/c
ID AAS26670 standard; DNA; 14176 BP.
XX
AC AAS26670;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1644.
XX
KW Human; immunosuppressive; antiarthritic; ds; antirheumatic; cytostatic;
KW cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW antibacterial; virucide; fungicide; ophthalmological; vulnery;
KW secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW cerebral ischaemia; angiogenesis; nervous system disorder;
KW Alzheimer's disease; infection; ocular disorder; corneal infection;
KW wound healing; epithelial cell proliferation; skin ageing; food additive;
KW preservative; antiproliferative.
XX
OS Homo sapiens.
XX
PN WO200155322-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US0001341.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
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PR 02-MAR-2000; 2000US-0186350P.
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PR 30-AUG-2000; 2000US-0228924P.
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PR 02-OCT-2000; 2000US-0236802P.
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PR 08-NOV-2000; 2000US-0246613P.

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PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0256719P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-488783/53.
DR
XX
PT New nucleic acid molecules encoding 461 human secreted proteins for
PT diagnosing, preventing, treating or ameliorating medical conditions and
PT used as food additives or preservatives.
XX
PS Disclosure; SEQ ID NO 1644; 980pp; English.
XX
CC The invention relates to isolated nucleic acid molecules and their
CC encoded secreted proteins. The nucleic acids and proteins are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC in diagnosing a pathological condition or susceptibility to a
CC pathological condition. Antibodies to the proteins can also be used in
CC alleviating symptoms associated with the disorders and in diagnostic
CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
CC (ELISA). Disorders which are diagnosed or treated include autoimmune
CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC nervous system disorders e.g. Alzheimer's disease, infections caused by
CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC and many other disorders listed in the specification. The polypeptides
CC can also be used to aid wound healing and epithelial cell proliferation,
CC to prevent skin aging due to sunburn, to maintain organs tissues,
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present
CC sequence is a genomic DNA encoding a partial novel secreted protein of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format

Query Match 8.0%; Score 400.4; DB 4; Length 14176;
Best Local Similarity 60.5%; Pred. No. 6.6e-64;

	Matches	-859;	Conservative	1;	Mismatches	477;	Indels	83;	Gaps	9
Qy	3104	TTTTTTTTTTGTTGTTT	TAGACACAGGGTCTT	CTCTGTCACCCAGGCATGACACAGT	3163					
Db	4608	TTGACTCTTTTGT	TTTTTTT	TGAGATGGAGTCT	CTCGTGTGTGGCCAGGCTGGAGTGCAGT	4549				
Qy	3164	GGTGCAACCATAGT	CTACTGACGCGCTCAA	CCTCTCTGAGCTCAAGGGATCTGCTGACCTCA	3223					
Db	4548	GGGCAATCTTGGCT	CTACTGCAACCTCTG	CGCTCTTGGGTTCAAGCAATTTCTCTG-CCTCA	4490					
Qy	3224	GCCTCCCAAGTAGCT	TGGGACTAC-GAGCGTGCACACACACCGCTGGCTGAATTA	AAAAAAT	3282					
Db	4489	GCCTCTGGAGTAGCT	GTGTATACAGGGCACCCACCA	CCATGCCAGCTAATTTTTTGA--	4432					
Qy	3283	TTTTTTGTAGACAT	TGGGTCTTACTACGT	TGGCCAGCGCTGTCTTAAACTCCTGGCTCA	3342					
Db	4431	TTTTTTAGTAGAT	TGGGTTTTCACTGTCTTGGT	CAGGCTGGTCTTGAATTCCTGACCTC-4373						
Qy	3343	AGCAATCCTCTAC	TTGGCATCCCAAGTCTGGGATACAGGGGTGAGCCACCATGTG	3402						
Db	4372	-GTGATCCACCCAC	CTCGGCTCCCAAAGTCTCGGATACAGCGCTGAGCCACCTGCAC	4314						
Qy	3403	CGGCTACTTATTTCT	TTTACATTCCATCTTTCCATAGAA	TGTAAGATCCACAGAACAGGG	3462					
Db	4313	CGGCGCTTTTTTTTT	-----	-----	4298					
Qy	3463	ATTACTGCCTATTTTCT	TTCTTTCTTTTTTGAGACAGAGTCTCACTTCATCACCTCAACC	3522						
Db	4297	-----	TTTTTTTTTGAGATGGAGTCT	TGCTGTGCCAGGCTGGAGTGCATGGCG	4247					
Qy	3523	TCCGTTGAGCTCA	CTGCAACCTCTGCGCTCCGGGTTCAAGVGATTCCTGCGCTAAGCCT	3582						
Db	4246	CAGTCTCGGCTCACT	TGCAACCTCAGCCTCTCGGGTTCAAGGGAATTCCTCGCTCAGCCT	4187						
Qy	3583	CCTGAGTAGCTGGAA	TACAGCGTGACACACCATGCTTGCTGAATTTTGTGATATTTTA	3642						
Db	4186	CCTGAGTAGCTGGGAT	TACAGGCGCCGCCACCATGCCAGCTAATTTTGTATTTTTTAG	4127						
Qy	3643	GCAGAGATGGGGTTT	TACCATGTGTGCCCAGGCTGGTCTCAAACCTCTGACCTCAAGTGAT	3702						
Db	4126	TAGAGATGTGGTTT	TACCAATGTTGGCCAGGCTGGTTTCGAACTCCTGACCTCAGGTGAT	4067						
Qy	3703	CTGCTCGCTCAGTCT	CCCCAAGTCTGGAAATTAAGCGGTGAGTCACTGTGCGCTGGCGG	3762						
Db	4066	CTGCCCGCTCGGCT	CTCCATGCTGCGGATTAACAGGTGTGAGCCACACGCGCCGCGCT	4007						
Qy	3763	ATTACTGTCTATTTT	CTTTATTTGCTATATCCCGAGTCTAGACAGGTCTGACATATAG	3822						
Db	4006	TTTGACTTC-----	TTAAATAATGGGCACTCTTTCGAGGAGTAGGACAGTACCT-----	3960						
Qy	3823	TAGTGTCTCAATAA	TAAATGATGAATGCACAGCCTAGATATAA	CTTTCTTTTTCTTTT	3882					
Db	3959	TATTTGGCTTTAAT	TTTGCACCTTCTCTGATGATTTAGTGATGTTT	CAGCAATTTTTTTCATGT	3900					
Qy	3883	TTTAAAAA	CAATCTTTGCAGAAATAAATCA	ATCTTGCATTTCTGCTTTTTTCACT	3942					
Db	3899	TTGTTGGTCA	TTTGTATATAATTTTGAGAACTGCTCCATGTCATTTTGGCCTACTTTTT	3840						
Qy	3943	TATCACCTTGTAT	GTACATTTTTCATATTTGCCCTCAAA	CCTTTATTTGTACTGTTTTTTTCAT	4002					
Db	3839	GATGGGATTTTTTTT	CTTCTGTGACTTG-----	TTAGAGTTACTTTGTAGATTCT	3790					
Qy	4003	TGTTACTATTTT	TAGTCACTGAATAATATGGCTTA	TTTGTCTTATACATCCTCCTGCTCCA	4062					
Db	3789	GGATATTAGT	CCTTTGCTGATGATAGTTTGGAAAATATTTTCTGCCATCTCTGTGGATGA	3730						
Qy	4063	CTTTAGAGGCGCAA	ATTTTACAAATCTGTATGAAGAGCTATGA	ACCCCTCTCCCCAGAGAAATA	4122					
Db	3729	GTCCTTGCTCTTT	TCGTGAGAAAATTC	CAAAAGTTTGTGTTTACATCTCTGTGGCATCA	3670					
Qy	4123	CACACACACACAC	ATCTCAACACAGTTTTTTTTTTTAA	TGTTTGCACATAAGACAGAAA	4182					
Db	3669	AGTACACACACAC	ATCCACCTCTGTACTCCCGTTATCATCATAGTTTTTC-ATCTGATGAAC	3611						

RESULT 38

ABX74019/c

ID ABX74019 standard; DNA; 14176 BP.

XX
XX

AC ABX74019;

XXXXXX

DT 18-MAR-2003 (first entry)

XX

XX

Human; gene; ds; neural disorder; immune system disorder; renal disorder;
KW

KW muscular disorder; respiratory disease; reproductive disorder; ..

KW gastrointestinal disorder; pulmonary disorder; cardiovascular disorder;

hyperproliferative disorder; inflammatory disease; allergic reaction;

blood related disorder; cancer; immunosuppressive; antiinflammatory;
KW

cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; immunostatic; antineoplastic

kw naemostatic; antiarteriosclerotic.
vv

Page	Page
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US Homo sapiens.
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17-JAN-2001: 2001US-00764864.

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PK DD

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PK DD

PK PR

PK PR

Db 165366 TTGTTGGTCATTTGTATATATTTTGGAGAACTGTCATGTCATTTTGGCCTACTTTT 165307
Qy 3943 TATCACCTGTTATGACTTTTTCATATGCTCAAAACCTTTATTTGTTACTGTTTTCAT 4002
Db 165306 GATGGGATTTTTTTTCTTGTGACTTG-----TTAGATTACTTTGTAGATTCT 165257
Qy 4003 TGTACTATTTTGTACTCAATATATGCTTAATTTGGCTTATATCATCTCTGCTCCA 4062
Db 165256 GGATATTAGTCCTTGTCTGATGATGTTTGGCAATATTTTCTGCCATCTGTGGATGA 165197
Qy 4063 CTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATA 4122
Db 165196 GTCTGTCTCTTTCGTCAGAAATTCCAAAGTTGTTGTTTACATTCCTGTTGGCATCA 165137
Qy 4123 CACACACACACACACTCACACAGTTTTTTTTTAAGTTTGGCAACTAAGACAAGAAA 4182
Db 165136 AGTACACACACACATCCACCTCTGTTACTCCCGTTACATCATAGTTTC-ATCTGATGAAC 165078
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Qy 4363 CTGGGTGTAGTGATGATGCTCTAGTCCAGCTACTCCGGAGGCTGAGGCAAGAGAAAT 4422
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Qy 4483 GGGCGACAGCAGAGACTCTATCTCAAAAAATAAATAAA 4522
Db 164777 GGGCGACAGCAAGAACCCCATCTCAAAAAATAAATAA 164738

RESULT 42
ADB96919/c
ID ADB96919 standard; DNA; 177531 BP.
XX AC ADB96919;
XX DT
XX DT 04-DEC-2003 (first entry)
XX DE Human MDR1 related DNA sequence SEQ ID NO:660.
XX
XX irinotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; Cyp3A5; MRP1; MDR1;
KW TOP1; ds.
XX
XX Homo sapiens.
XX
XX WO2003013537-A2.
XX
XX 20-FEB-2003.
XX
XX 23-JUL-2002; 2002WO-EP008218.
XX
XX 23-JUL-2001; 2001EP-00117608.
XX 24-MAY-2002; 2002EP-00011710.
XX
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
XX
XX Heinrich G, Kerb R;

XX WPI; 2003-268145/26.
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
XX Disclosure; SEQ ID NO 660; 130pp; English.
XX
CC The invention relates to the novel use of irinotecan or its derivative
CC for the preparation of pharmaceutical compositions for treating
CC colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
CC malignant glioma in a subject having a genome with a variant allele which
CC comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition
CC of the invention has cycostatic activity. The invention is useful for the
CC preparation of pharmaceutical compositions for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject (preferably human, more preferably African or Asian)
CC or a mouse. The present sequence is used in the exemplification of the
CC invention.
XX
SQ Sequence 177531 BP; 51602 A; 39077 C; 38304 G; 48548 T; 0 U; 0 Other;

Query Match 8.0%; Score 400.4; DB 10; Length 177531;
Best Local Similarity 60.5%; Pred. No. 9.5e-64;
Matches 859; Conservative 1; Mismatches 477; Indels 83; Gaps 9;

Qy 3104 TTTTTTTTTTGTGTTTGTAGAGACAGGGTCTTGTCTGTCAACCAGGAGTACAGCAGT 3163
Db 166075 TTGACTTCTTTGTTTTTTTGTAGATGGAGTCTCGCTGTGTGCCAGGCTGGAGTGCAGT 166016
Qy 3164 GGTGCAACCATAGTCTCAGGAGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCA 3223
Db 166015 GGGCAATCTTGGCTCAGTCAACCTCTGCTCTTGGGTTCGAAGCAATTTCTCTG-CTCA 165957
Qy 3224 GCCTCCCAAGTAGCTGGGACTAC-GAGGGTGCACCAACCAAGCTGGCTGTGCTAATAAATAA 3282
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Qy 3343 AGCAATCTCTTACCTTCCATCCCAAGTCTGGGATTACAGGGGTGAGCCACCATGTG 3402
Db 165839 -GTGATCCACCACCTCGCTTCCCAAGTCTGGGATTACAGGGGTGAGCCACCTGCAC 165781
Qy 3403 CGGCTACTTATTTCTTTTACATTTCCATCTTTCCATAGAATGTAGATCCACAGAACAGGG 3462
Db 165780 CGGGCTTTTTTTTTT----- 165765
Qy 3463 ATTACTGCTATTCTTCTCTCTTTTGTGAGACAGAGTCTCACTTCACTCACTCAACC 3522
Db 165764 -----TTTTTTTTTGAGATGGAGTCTTGTCTGTCCAGGCTGGAGTCAATGGCG 165714
Qy 3523 TCCGTTAGCTCAGTCAACCTCTGCTCCGGGTTCAAGYATTCTCTGCTGCTAAGCCT 3582
Db 165713 CAGTCTCGGCTCACTGCAACCTCAGCTTCTGGGTTCAAGGATTTCTCTGCTCAGCCT 165654
Qy 3583 CCTGAGTAGCTGGAAATTACAAGCGTGCACCACTGCTTGGCTAATTTTTTGTATTATTFA 3642
Db 165653 CCTGAGTAGCTGGGATTACAGGCGCCGCCACCATGCTCCAGCTAATTTTGTATTATTAG 165594
Qy 3643 GCAGAGATGGGGTTTTTACATGTTGCCAGGCTGTCTCAAACTCTGACCTCAAGTGT 3702
Db 165593 TAGAGATGGGGTTTCAACATGTTGGCCAGGCTGTTCGAACTCTGACCTCAGGTGTAT 165534
Qy 3703 CTGCTGCTCAGTCTCCAAAGTCTGAAATTATAGGCGTGAAGTCACTGTGCTGGCGCG 3762
Db 165533 CTGCCCCGCTCGGCTCCCATAGTCTGGGATTACAGGTGTGAGCCACCAAGCCGCGCT 165474
Qy 3763 ATTACTGTCTATTTTCTTTTATTTGCTATATCCCAAGATCTAGAGCAGTGTCTGACATATAG 3822

Db 165473 TTGACTTC-----TTAATAATGCCATCTTTCGAGGAGTAAGCAGTACCT----- 165427
Qy 3823 TAGGTGCTCAATAAATAATGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3882
Db 165426 TATTGGGCTTTAATTGACCTTCCTGATGATAGTATGATTCAGCATTTTTCATGT 165367
Qy 3883 TTTTAAACAATCTTGCACACTTTGCGAGAAATAACAATCTTGCATCTGCTTTTTCAC 3942
Db 165366 TTGTTGGTCATTGTATATATTATTTGAGAACTGTCTCAATGCTATTTGCTTACTTTT 165307
Qy 3943 TATCACCTGTTTATGACTTTTTCATATGCTCAAAACCTTTATGTTACTGTTTTCAT 4002
Db 165306 GATGGGATTTTTTTTCTGTTGACTTG-----TTAGAGTTACTTGTAGATTCT 165257
Qy 4003 TGTACTATTATTAGTCACTGAATAATGCTTAATTTGCTTATACATCTCTGCTCCA 4062
Db 165256 GGATATTAGTCTTGTCTGATGATGATTTTGGAAATATTTTCTGCATCTGTGATGA 165197
Qy 4063 CTTTAGAAGGCCAAATTTTCAAACTGTATGAAAGCTATGAACCTCTCTCCCGAGAGAA 4122
Db 165196 GTCTTGCTCTTTTCGTCAGAAATTCAAAAGTTTGTGTTTACATTCCTGTTGGCATCA 165137
Qy 4123 CACACACACACACACTACACACAGTTTTTTTTTAAATGTTTGAACCTTAAGCAAGAAA 4182
Db 165136 AGTACACACACACATCCACTCTGTTACTCCCGTTACATCATAGTTTC-ATCTGATGAAC 165078
Qy 4183 CTTGCATTAGAGGATGTTGTTTCATATTAAATAAATACTCAGTTGGGCACAGTACT 4242
Db 165077 ATTTTATGACAGTTTATTTTTCCTTTATAAAGAACTGATGGGCGGACGCGTGGCT 165018
Qy 4243 CAAGCCTGTAACACACAGTACTTTGGAAGTCCAAAGTGGGTGGATCACTTGAGTGAGAAG 4302
Db 165017 TAAACCTGTAATCCAGCCTTTTGGGAGGCTGAGGCGGTGGATCACCCAAAGTCAGGAG 164958
Qy 4303 TTCGAGACAGCCTGTTCAATATGTTGAACCCCTATCTCTACTATAAAATACAAAATTAG 4362
Db 164957 TTTGAGACAGCCTGGCCACATGCGCAAAACCCCATCTCTACTTAAACATACAAAATTAG 164898
Qy 4363 CTGGGTGATGATGATGATGCTGCTAGTCCAGCTACTCCGGAGGCTGAGGCAAGAAAT 4422
Db 164897 CTGGGTGATGATGATGATGCTGCTAGTCCAGCTACTCCGGAGGCTGAGGCAAGAAAT 164838
Qy 4423 GCTTGAACCTGGGAGGCGAGGTTGAGTGGAGCCGAGATCCCACTGCACTCCAGCCT 4482
Db 164837 ACTTGAACCCAGGAGGCGAGGTTGAGTGGAGCCGAGATCGCATCATTTGCACTCTAGCCT 164778
Qy 4483 GGGCGACACGCGAGACTCTATCTCAAAAATAAATAA 4522
Db 164777 GGGCGACAGCAAGACCCCATCTCAAAAATAAATAA 164738

RESULT 43
ADB92110/c
ID ADB92110 standard; DNA; 177531 BP.
XX
AC ADB92110;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human MDR1 related DNA sequence SEQ ID NO:660.
XX
DE itirnotecan; colorectal cancer; cervical cancer; gastric cancer;
KW lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
KW multidrug resistance 1; MDR1; cytostatic; human; UGT1A1; MRP1; TOP1; ds.
XX
OS Homo sapiens.
XX
PN WO2003013535-A2.
XX
PD 20-FEB-2003.
XX
PF 23-JUL-2002; 2002WO-BP008220.

PR 23-JUL-2001; 2001EP-00117608.
PR 24-MAY-2002; 2002EP-00011710.
XX (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
PA
PI Heinrich G, Kerb R;
XX WPI; 2003-342400/32.
XX
DR
XX
XX New use of irinotecan for preparation of pharmaceutical compositions for
PT treating cancer in subject having genome with variant allele comprising
PT multidrug resistance 1 polynucleotide.
XX
PS Disclosure; SEQ ID NO 660; 104pp; English.
XX
CC The invention relates to a novel use of irinotecan or its derivative for
CC the preparation of a pharmaceutical composition for treating colorectal,
CC cervical, gastric, lung, ovarian or pancreatic cancer, or malignant
CC glioma in a subject having a genome with a variant allele which comprises
CC a multidrug resistance 1 (MDR1) polynucleotide. A composition of the
CC invention has cytostatic activity. The present sequence is used in the
CC exemplification of the invention.

XX Sequence 177531 BP; 51602 A; 39077 C; 38304 G; 48548 T; 0 U; 0 Other;
Qy 3104 TTTTGTGTTGTTTGTAGACAGGGTCTTGTCTGTACCCAGGCGATGAGCACGT 3163
Db 166075 TTGACTTCTTTGTTTGTAGATGGAGTCTCGCTGTGTTGCCAGGCTGGAGTGCAGT 166016
Qy 3164 GGTGCAACATAGGTCTGACGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCA 3223
Db 166015 GCGCAATCTTGGCTCAGTGCACCTCTGCTTCTGGGTTCGAAGCAATTTCTCTG-CCTCA 165957
Qy 3224 GCCTCCCAAGTAGCTGGGACTAC-GAGGCTGCACCAACCAACGCTGGCTAATTTAAAAAAT 3282
Db 165956 GCCTCTGAGTAGTCTGTGATACAGGGCCACCAACCATGCCAGCTAATTTTGTGTA-- 165899
Qy 3283 TTTTGTGAGAGCTGGGTCTTACTAGCTTGCCAGGCTTGTCTTAAACTCTGGCTTCA 3342
Db 165898 TTTTGTGAGAGTGGGTCTTCACTGTCTGCTGAGGCTGGTCTTGAATTCCTGACCTC- 165840
Qy 3343 AGCAATCTCTACTCTGGCATCCCAAGTGTGGGATACAGGGGTGAGCCACCATGTG 3402
Db 165839 -GTGATCCACCCACCTCGGCTTCCCAAGTTCCTGGATTTACAGGCGTGAGCCCTGCAC 165781
Qy 3403 CGGCTACTTATTTCTTTACATTTCCATCTTTCCAATAGATGTAAGATCCACAGAACAGGG 3462
Db 165780 CCGGCTTTTCTTTT----- 165765
Qy 3463 ATTTACTGCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACC 3522
Db 165764 -----TTTTTTTGTAGATGGAGTCTTCTGTTGCCAGGCTGGAGTGCATGGCG 165714
Qy 3523 TCCGTTGAGCTCACTGCAACCTCTGCTCCCGGTTTCAAGYATTTCTCTGCTCAAGCCT 3582
Db 165713 CAGTCTCGGCTCACTGCAACCTCAGCCTCTCGGTTTCAAGCGATTTCTCTGCTCAGCCT 165654
Qy 3583 CTTGAGTAGTGGAAATTACAAGCTGCACCACTGCTTGGCTAATTTTCTGATTTTTPA 3642
Db 165653 CTTGAGTAGTGGGATTTACAGGCGCCGCCACCATGCCAGCTAATTTTGTATTTTAG 165594
Qy 3643 GCAGAGATGGGTTTACATGTTGCCAGGCTGTCTCAAACTCTGACCTCAAGTGTAT 3702
Db 165593 TAGAGATGGGGTTTCAACCATGTTGCCAGGCTGGTTCGAACTCTGACCTCAGTGTAT 165534
Qy 3703 CTGCTGCTCAGTCTCCCAAGTGTGGAATATTAGGGCTGAGTCACTGTGCTGGCG 3762
Db 165533 CTGCCCGCTCTCGGCTCTCCCATAGTCTGGGATTCAGGTTGTAGGCCACCAACCGCGCCT 165474

Db 165713 CAGTCTCGGCTCACTCAACCTCAGCCTCTCTGGTTCAAGCGATTCTCTGCTCAGCCT 165654
QY 3583 CCTGAGTAGTGAATATACAGCGTGCAACCATGCTTGGCTTAATTTTGTATTTTAA 3642
Db 165653 CCTGAGTAGTGGGATATACAGGCGCGCCGACCATGCCAGCTAAATTTGTATTTTAA 165594
QY 3643 GCAGAGATGGGTTTTACCATGTTGCCAGCTGGTCTCAAACTCTGACCTCAAGTGAT 3702
Db 165593 TAGAGATGGGTTTACCATGTTGGCAGCGTGGTTTGAACCTCTGACCTCAGTGAT 165534
QY 3703 CTGCTGCTCAGTCTCCCAAGTGTGGAATATAGGGGTGAGTCACTGTGCTGGCCG 3762
Db 165533 CTGCCGCTCGCCTCCCATAGTGTGGATACAGGTGTGAGCCACACGCGCGCCT 165474
QY 3763 ATTACTGTCTATTTCTTTATGCTATATCCCGAGATCTAGAGCAGTGTGACATATAG 3822
Db 165473 TTTGACTTC-----TTAATAATGCCATTCTTGAGGAGTAAGCAGTACCT----- 165427
QY 3823 TAGGTGCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3882
Db 165426 TATTGTGGCTTTAATTGACCTCTCTGATGATTAGTGAATGTTTCAGCATTTTTTTCATGT 165367
QY 3883 TTTAAACCAATCTTGCAAACTTTGAGAAATAACAATCTTGCAATCTGCTTTTTCAC 3942
Db 165366 TTCTGTGCTATTTGTATATATTTTGGAGAACTGTCTCATGTCTATTTGGCTACTTTT 165307
QY 3943 TATCACTTGTATGACTTTTTCATATTTGCTCAAACTTTATTTGTTACTGTTTTCAT 4002
Db 165306 GATGGGATTTTTTTTTTCTTTGACTTG-----TTAGATTACTTGTAGATTCT 165257
QY 4003 TGTACTATTTAGTCACTGAATAATATGCTTAATTTGCTTATACATCTCTCTGCTCA 4062
Db 165256 GGATATTAGTCTTGTCTATGCTAGTTTGGAAATATTTTCTGCAATCTCTGTGATGA 165197
QY 4063 CTTTAGAAGGCCAAATTTTCAAACTCTGATGAAGTATGAACCTCTCCCGAGAGAAATA 4122
Db 165196 GTCTGTCTTTTCGTGAGAAATTTCCAAAGTTTGTGTTTACATCTCTGTTGGCATCA 165137
QY 4123 CACACACACACACTCACACAGTTTTTTTTAATGTTTGAACCTTAAGCAAGAA 4182
Db 165136 AGTACACACACATCCACCTCTGTACTCCCGTTTACATCATAGTTTC-ATCTGATGAAC 165078
QY 4183 CTGTCATTAGAGGATGTTTCTTATTAATAAATAACTCAGTTGGCAGTGACT 4242
Db 165077 ATTTTATGACAGTTTATTTTCTTTTATAAAGAACTGATGGCGCAGCGTGGCT 165018
QY 4243 CAAGCCTGTAACCAACAGTACTTTTGAAGTCCAAAGTGGGTGGATCACTTTGAGTGAGAAG 4302
Db 165017 TAAACCTGTAATCCAGCCTTTTGGAGGCTGAGCGGGTGGATCACCCAAAGTCAGGAG 164958
QY 4303 TTCGAGACAGCCTGGTCAATATGGTGAAACCTTATCTCTACTATAAATAACAAATTAG 4362
Db 164957 TTTGAGACAGCCTGGCCAACTGGCAAAACCCCATCTCTACTATAAATACAAATTAG 164898
QY 4363 CTGGGTGATGATGATGCTCTAGTCCAGCTACTCCGGAGGCTGAGCAGAGAAAT 4422
Db 164897 CTGGGTGATGATGATGCTCTAGTCTCTAGTCTCTAGTCTCTAGAGGCTGAGCAGAGAAATC 164838
QY 4423 GCTTGAACCTGGGAGGAGAGTTGAGTGGAGCGGAGATCCCACTGCTCTCCAGCCT 4482
Db 164837 ACTTGAACCCAGGAGGAGAGTTGAGTGGAGCGGAGATCGCATCTTGCACCTTAGCCT 164778
QY 4483 GGGCGACAGCAGAGACTCTATCTCAAAAAATAAATAA 4522
Db 164777 GGGCGACAGAGCAAGACCCCATCTCAAAAAATAAATAA 164738

RESULT 45
ACN45166
ID ACN45166 standard; DNA; 87687 BP.
XX
AC ACN45166;

XX 18-NOV-2004 (first entry)
DT Human genomic sequence hCG37872.
XX Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
XX Homo sapiens.
OS WO2003073826-A2.
XX 12-SEP-2003.
XX 28-FEB-2003; 2003WO-US006235.
XX 01-MAR-2002; 2002US-00087192.
XX (SAGR-) SAGRES DISCOVERY.
XX Morris DW;
XX WPI; 2003-328604/31.
XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
XX Claim 1; SEQ ID NO 1978; Opp; English.
XX The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
XX
SQ Sequence 87687 BP; 23583 A; 17049 C; 18231 G; 28170 T; 0 U; 654 Other;

Query Match 8.0%; Score 399; DB 11; Length 87687;
Best Local Similarity 60.1%; Pred. No. 1.6e-63;
Matches 900; Conservative 1; Mismatches 511; Indels 85; Gaps 11;

QY 3111 TTGTTTGTGTTTGTAGAGACAGGGTCTTGTCTCTCACCAGGCATGAGCACAGTGGTGCAA 3170
Db 5754 TTTTGTGTTTGTGAGACAGTCTCGCTCTGTCAACCAGGCTGGAGTGCAGTGGCGCA 5813
QY 3171 CCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGA-TCTGCTGACCTCAGCCTCC 3229
Db 5814 TCTTGCTCACTGCAAGCTCTGCTCTCTGGGTTACGCCATTTCTCTGTGCTCAGCCTCC 5873
QY 3230 CAAGTAGCTGGGACTACAGAGGTGCACACAGCCTGGCTAATTAATAAATTTTGTG 3289
Db 5874 CGAGTAGCTGGGACTACAGGTGCCGCCACCATGCTGGCTAATTTTGTGTTTGTAG 5933
QY 3290 TAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAACTCTGGCTTCAAGCAATC 3349
Db 5934 TAGAGACTGGGTCTTACT--GTTAGCCAGGATAGTCTCGATCCCTGAC--CTTGTGATC 5989
QY 3350 CTCCTACCTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGCGGCTAC 3409
Db 5990 TGCCCGCCTCAGCCTCCCAAGTGTGGGATTTACAGGCGTGGCCACTGCGTCTGCTT 6049
QY 3410 TTATTTCTTTACATCTTTCATAGTATGAATGTAAAGTCCACAGACAGGATTA--C 3467
Db 6050 ACCTTTATACATATGATAGAAATGTATAGGAGGCTTTTAGGTAAGAGACTGGCAATTAGTT 6109

CC the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published pct sequences

CC from WIPO at http://wipo.int/pub/published_pct_sequences

XX
SQ Sequence 6131 BP; 1422 A; 1665 C; 1561 G; 1483 T; 0 U; 0 Other;

Query Match	8.0%	Score 398.4;	DB 4;	Length 6131;
Best Local Similarity	54.0%;	Pred. No. 1.4e-63;		
Matches 1259;	Conservative	3;	Mismatches 894;	
			Indels 176;	Gaps 15;

Best local similarity	54.0%	Pred	No	14e-63
Best local similarity	54.0%	Pred	No	14e-63

Matches 1259; Conservative 3; Mismatches 894; Indels 176; Gaps 15;

Qy 2287 TTTCAGGCAGCGCGGTGGCTCATGCCGTGTAATCCACAGCACTTTGGAGGCCGAGCGG 2346

DB 789 TTTTAGGCCAGGCACGGTGGCTTATGCTTGTAATCTTAGCACTTTGGGAGGCTGAGGCGG 848

Qy	2347	GCGGATCACTTGGAGTTCAGGAGCCAGCCCTGGCCCAACATGGTGAATACCCCTGTCT
Dp	849	GCGGGTCATTGTGGTCAGGAGTTTGGACGAGCCCTGACTAACATGGTGAATACCCCTGTCT

2407 CTACTAAAAATACAAAATTAGCCGGACATGTTGGCGAGCGCTTAACCCAGTACT 2466

Db	909	CTACTGAAATACAGAAAATTAGCCAGGGTGCTGGCGGGCGTCTGTATAATCCCAGTACT	968
Qv:	2457	TCCCCACACACACATTCCTCCACCTCCTTTCACTCACACCAATC--CTGCCTC	2506

QY
240 / TGGGAGCTTGAGTGGACGAGAAATCCCTTGAACCCGAGGGGTGCAGTTGCAGTCAGCTGAG 1028

Dbb

QY 2507 TCACTGCTGCAGCGCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAATGCTTTCA 2566

DB	1029	ATTGCAAACTCCAGCCCTGGGGGACAGAGCCGAGATGCCGTCCTTTTAAAAA	108
QV	2567	ATAAATATATGATAAAAGGACTTATATTTTTTCAAGCATAGGATCATTTCTCCTGAAGC	2626

Db 1089 AGTAGCAGAAAACTGGGAGGTTGAGGGTGTTCCATTGGTAGCCCGAGAGCTGGGTCC 1148

Qy	2627	ATCTTGGCGAAGTGCATCCCCACCTGTTCTTGAGAGTGGGGCAGGTGAGGGCTGACCTATTG	2686
Dh	1149	AGCTTAGGAGAGCGTCAACCCCGGGC-----CTGCTGGCCCTCCGAGCGTCCCTCCCTCTCTCT	1204

QY 2687 CTCTGCACCTTACTCCTATCTCAGTGTCCCTCCCACTTTCCAGGTGCTGCCAGACACATG 2746

Db 1205 CTCTCCCGTCTTCCTCGCTGGGAAAGCAGCAGACATTCACGGCTGTGGAGGGATGGG 1264

Db 1265 GGAGGCCAGAGCCAGGGACGTCCAGGCAGCTGTGTTCACTGGGCATCAGCCCTGAGGA 1324

QY 2802 MCGGTACACCCACACCTATTTCATACTCGTGTCTGGCTCGGCAATCACTGTAGCAGTAG 2861

QY 2862 GTTTATCCCTTCCTTGACCTATGAATCTTAGTTGGTTCTCAGTAGGCCGGGGGAAATAA 2921

Db 1385 GGCAATGTATCCAGGCACATTCTACTTCCAATTTAAAAACCTATGGGAAGCCAACGATCG 1444

Db 1445 GAACGAAACCTTGGCTGTGCTTCAACGCTGGAAGGTATAAAGCGCGCTCAGTGTCTCTCTG 1504

QY 2979 TAATCCTCAGAACAACTATGGGATAGGTACAATTATCCTCCTACTTAACAGATAAGAAA 3038

1505	GTGAGACGGGGGCGTCCTCCGAAATCCAGGTAGCACCTAAAGATCTAGTATACACCTCCCTAAATAGGA	1506	
1506	CTGAGGC-----TCAGAAGGCTGAGCTATTGGCCCCAAGATCACACAGC	3081	
QY	3039	CTGAGGC-----TCAGAAGGCTGAGCTATTGGCCCCAAGATCACACAGC	3081

Db
1565 GCTAAGCAGCTGGGAATGCAGAAAAAGCAATAAGTGTATGCCCCGGCGTGGGCTCTC 1624

QY
 3082
 TTGTAAAG-----TGGTGACAGATTGGGGTTTTTTTTTTTGTGTGTGTATTAGACACAGGGTCTT
 1625 CTGTGTGCACNTTCTGTGCACATTTCTATTTTTTTTTTTTTTTTTTTTTTTGATGTGGAGTCTC
 pb

QY 3137 GCTCTGTACCCAGGCATGAGCAGTGGTGCAACCATAGGTCACTGCAGCTCAACCTC 3196

Db 1685 GCCTGTGTCACCCAGGCTGGAATGCAGTGGTCTGATTTTCAGCTCACGGCAACCTCTGCTTT 1744

Db	2743	GGCTCATGCTGTAATCCAGCACTTTGGAGGCTGAGGCGGATCA--TGAGGTTG	2800
Qy	4299	GAAGTTTCGAGACCAAGCTGCTCAATATGTTGAACCTTACTCTACTAAATACAAAA	4358
Db	2801	GGAGTTTCGAGACCAAGCTGGCTAACATGATGAAACCCAGTCTCTACTAAATACAAAGA	2860
Qy	4359	TTAGCTGGGTGATGATGATGCATGCCCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAG	4418
Db	2861	TTAGCCAGGTTGGGGTGCATGCCCTGTAGTCCAGCTACTCAGGAGGCTGAGGCAAGGAG	2920
Qy	4419	AATTGCTTGAACCTCGGAGGACAGAGTTGCAGTGAGCCGAGATCCCAACCTGCATCCA	4478
Db	2921	AATTGCTTGAACCTCGGAGGACAGAGTTGCAGTGAGCCGAGATTTGCCACTGCACTCCA	2980
Qy	4479	GCTGGGCGACACAGCGAGCTTACTCTCAAAAAATAATAAATAAATAA	4530
Db	2981	GCCTTGGCGACAGCAAGAACTCCATCTTTGAAAAAAAATAAAAAATAAAGAA	3032
RESULT 49			
AAK69784			
ID	AAK69784 standard; DNA; 6131 BP.		
XX	AAK69784;		
AC	AC		
XX	XX		
DT	06-NOV-2001 (first entry)		
XX	XX		
DE	Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24596.		
XX	XX		
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;		
KW	cytostatic; gene therapy; vaccine; metastasis; ds.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
PN	WO200157182-A2.		
XX	XX		
PD	09-AUG-2001.		
XX	XX		
PF	17-JAN-2001; 2001WO-US001354.		
XX	XX		
PR	31-JAN-2000; 2000US-0179065P.		
PR	04-FEB-2000; 2000US-0180628P.		
PR	24-FEB-2000; 2000US-0184664P.		
PR	02-MAR-2000; 2000US-0186350P.		
PR	16-MAR-2000; 2000US-0189874P.		
PR	17-MAR-2000; 2000US-0190076P.		
PR	18-APR-2000; 2000US-0198123P.		
PR	19-MAY-2000; 2000US-0205515P.		
PR	07-JUN-2000; 2000US-0209467P.		
PR	28-JUN-2000; 2000US-0214886P.		
PR	30-JUN-2000; 2000US-0215135P.		
PR	07-JUL-2000; 2000US-0216847P.		
PR	07-JUL-2000; 2000US-0216880P.		
PR	11-JUL-2000; 2000US-0217487P.		
PR	11-JUL-2000; 2000US-0217496P.		
PR	14-JUL-2000; 2000US-0218290P.		
PR	26-JUL-2000; 2000US-0220363P.		
PR	26-JUL-2000; 2000US-0220364P.		
PR	14-AUG-2000; 2000US-0224518P.		
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PR	14-AUG-2000; 2000US-0225759P.		
PR	18-AUG-2000; 2000US-0226279P.		
PR	22-AUG-2000; 2000US-0226681P.		

PR	22-AUG-2000; 2000US-0226688P.
PR	22-AUG-2000; 2000US-0227182P.
PR	23-AUG-2000; 2000US-0227009P.
PR	30-AUG-2000; 2000US-0228924P.
PR	01-SEP-2000; 2000US-0229287P.
PR	01-SEP-2000; 2000US-0229343P.
PR	01-SEP-2000; 2000US-0229344P.
PR	01-SEP-2000; 2000US-0229345P.
PR	05-SEP-2000; 2000US-0229509P.
PR	05-SEP-2000; 2000US-0229513P.
PR	06-SEP-2000; 2000US-0230437P.
PR	06-SEP-2000; 2000US-0230438P.
PR	08-SEP-2000; 2000US-0231242P.
PR	08-SEP-2000; 2000US-0231243P.
PR	08-SEP-2000; 2000US-0231244P.
PR	08-SEP-2000; 2000US-0231413P.
PR	08-SEP-2000; 2000US-0231414P.
PR	08-SEP-2000; 2000US-0232080P.
PR	12-SEP-2000; 2000US-0232081P.
PR	14-SEP-2000; 2000US-0232397P.
PR	14-SEP-2000; 2000US-0232398P.
PR	14-SEP-2000; 2000US-0232399P.
PR	14-SEP-2000; 2000US-0232400P.
PR	14-SEP-2000; 2000US-0232401P.
PR	14-SEP-2000; 2000US-0233063P.
PR	14-SEP-2000; 2000US-0233064P.
PR	14-SEP-2000; 2000US-0233065P.
PR	21-SEP-2000; 2000US-0234223P.
PR	21-SEP-2000; 2000US-0234274P.
PR	25-SEP-2000; 2000US-0234997P.
PR	25-SEP-2000; 2000US-0234998P.
PR	26-SEP-2000; 2000US-0235484P.
PR	27-SEP-2000; 2000US-0235834P.
PR	27-SEP-2000; 2000US-0235836P.
PR	29-SEP-2000; 2000US-0236327P.
PR	29-SEP-2000; 2000US-0236367P.
PR	29-SEP-2000; 2000US-0236368P.
PR	29-SEP-2000; 2000US-0236369P.
PR	29-SEP-2000; 2000US-0236370P.
PR	02-OCT-2000; 2000US-0236802P.
PR	02-OCT-2000; 2000US-0237037P.
PR	02-OCT-2000; 2000US-0237038P.
PR	02-OCT-2000; 2000US-0237039P.
PR	13-OCT-2000; 2000US-0237040P.
PR	13-OCT-2000; 2000US-0239335P.
PR	13-OCT-2000; 2000US-0239337P.
PR	20-OCT-2000; 2000US-0240960P.
PR	20-OCT-2000; 2000US-0241221P.
PR	20-OCT-2000; 2000US-0241785P.
PR	20-OCT-2000; 2000US-0241786P.
PR	20-OCT-2000; 2000US-0241787P.
PR	20-OCT-2000; 2000US-0241808P.
PR	20-OCT-2000; 2000US-0241809P.
PR	01-NOV-2000; 2000US-0244617P.
PR	08-NOV-2000; 2000US-0246474P.
PR	08-NOV-2000; 2000US-0246475P.
PR	08-NOV-2000; 2000US-0246476P.
PR	08-NOV-2000; 2000US-0246477P.
PR	08-NOV-2000; 2000US-0246478P.
PR	08-NOV-2000; 2000US-0246523P.
PR	08-NOV-2000; 2000US-0246524P.
PR	08-NOV-2000; 2000US-0246525P.
PR	08-NOV-2000; 2000US-0246528P.
PR	08-NOV-2000; 2000US-0246527P.
PR	08-NOV-2000; 2000US-0246528P.
PR	08-NOV-2000; 2000US-0246532P.
PR	08-NOV-2000; 2000US-0246609P.
PR	08-NOV-2000; 2000US-0246610P.
PR	08-NOV-2000; 2000US-0246611P.
PR	08-NOV-2000; 2000US-0246613P.
PR	17-NOV-2000; 2000US-0249207P.

QY 3437 TAGAATGTAAGATCCACAGAAAGGAGTACTGCCTATTCTTCCTTTCTTTTGGAGA 3496
Db 1981 -----TTATTTATTTTGGACGGAGTCTTGCTCT 2013
QY 3497 CAGAGTCTCATTATCATCACTCAACCTCGGTTCCAGCTCACTGCAACCTCTGCTCCCGGG 3556
Db 2014 ATCGCCAGGCTGGAGTGCAGTGGCAAACTCTCAGCTCACTGCAAGCTCCGCTCCCGGG 2073
QY 3557 TTCAAGVGATTTCTCCCTAGCCTTAAGCTTCCAGTAGCTGGAATTACAAAGGTCGACACCA 3616
Db 2074 TTCACGCCATTTCTCCCTGAGCTCCCAAGTAGCTGAGCTACAGGCGCCACACCA 2133
QY 3617 TGCTTGCTTAATTTTTTGTA-----TTTTAGCAGAGATGGGGTTTT 3658
Db 2134 TGCCACAGTAATTTTTCTTTTTTTCTTTTTTTTTTTTTTTAGAGCGGGTTTC 2193
QY 3659 ACCATGTTGCCAGGCTGGTCTCAAACTCTGACCTCAAGTAGTATGCTGCTGCTCAGTCT 3718
Db 2194 ATGGTGTAGCCCAAGATGGTCTCGATCTCTGACCTCA--TGATCGCGCGCTTGCGCT 2251
QY 3719 CCCAAGTCTGGAATTATAGGCTGAGTCACTGCTGCGCGATTACTGTCTATTTC 3778
Db 2252 CCCAAGTCTGGGATTTAGCGGATGAGCCTGTCGCCGCGCTCCCCACATTTTTTAAG 2311
QY 3779 TTTATTGTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAT 3838
Db 2312 TCCATGG-----CCAGATCTTCTCCTGACTCTCTGTGATC----- 2350
QY 3839 AATTGATGAATGCACAGCCTAGATATAAATTTCTTTTCTTTTCTTTTAAACAACTTGA 3898
Db 2351 -----AGATCGTGGAGGGGTTTGCTTCTCCCAAAAGGCTTGT 2390
QY 3899 CAACTTTGAGATAAATAAATCAATCTTGCATTCTGCTTTTCACTTATCACTTGTATGA 3958
Db 2391 TTAGCGCCAG-----CACCTCACTCTTGACTTTGTTTCCCAAAATCTGTTATGG 2442
QY 3959 CTTTTTCATATTGCTCAAACTTTATTGTTACTGTTTTTTCATTGTTACTATTATTAGTC 4018
Db 2443 AGCTGTGCGTCCGAGTCTCGGAAATCAGCAGCTGTGGGAAGCGGGGGTGTGTGTC 2502
QY 4019 ACTGAATAATATGGCTTAATTGCTTATACATCCTCTGCTCACTTTTAAAGGCGCAAT 4078
Db 2503 CAGCGCTGTGCTGGGCCAGTACTGCGGCTGGTGGGCGCGCCCGCACTGCGCCTGA 2562
QY 4079 TTACAAATCTGATGAAGCTATGAA-----CCCTCTCCCGAGAGAAATACACACACA 4132
Db 2563 TTCTCAGCAGAAAGGAGGAGGAGGAAACAAGCTGACCCAGAGAGCCAGGCCATAGCAGG 2622
QY 4133 CACACACTCACACACAGTTTTTTTTTTTAAATGTTTGAACAAAGAAACCTGCATTAG 4192
Db 2623 GGCTGAGGATGCTGTGTAATGCTGCTGGGAGAAAGATGGCAGAAATTCACATAGAG 2682
QY 4193 AGAATGTTGTTCAATTAATTAATAAATA-----ACTGATGGGCAAGT 4238
Db 2683 TCTATGAGACAGGGAAGAATCAATAAAATAAAGAAAGGAGGCGCGGCAAGCGCGT 2742
QY 4239 GACTCAAGCTGTAACACAGTACTTTGGAAGTCCAGGTGGTGGTCACTTGAGGTGA 4298
Db 2743 GGCTCATGCTGTAATCCAGCACTTTGGAGGCTGAGGAGCGGATCA--TGAGGTG 2800
QY 4299 GAAGTTTCGAGACCGCTTGCTCAATATGTTGAAACCTTATCTCTACTAAAAATACAAAAA 4358
Db 2801 GGAGTTTCGAGACCGCTGGCTAACATGATGAACCCAGTCTCTACTAAAAATACAAAGA 2860
QY 4359 TTAGCTGGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4418
Db 2861 TTAGCCAGGTGTGGGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 2920
QY 4419 AATTGCTTGAACCTGGGAGCAGAGTTGAGTGAGCCGAGATCCCAACCACTGCACTCA 4478
Db 2921 AATTGCTTGAACCTGGGAGCAGAGTTGAGTGAGCCGAGATTTGTGCCACTGCACTCCA 2980

QY 4479 GCCTGGGCGACACAGCAGACTCTATCTCAAAAAATAAAATAAAATAAAATAA 4530
Db 2981 GCCTTGGCGACAGACCAAGACTCCATCTTTGAAAAATAAAATAAAAGAA 3032
RESULT 50
ABL64403/c
ID ABL64403 standard; DNA; 167343 BP.
XX ABL64403;
AC ABL64403;
XX
DT 15-MAY-2002 (first entry)
XX
Stomach cancer related gene sequence SEQ ID NO:2740.
XX
Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
gene; ds.
XX
Homo sapiens.
OS
XX WO200194629-A2.
PN
XX 13-DEC-2001.
PD
XX 30-MAY-2001; 2001WO-US010838.
PF
XX 05-JUN-2000; 2000US-0209473P.
XX 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
XX (AVAL-) AVALON PHARM.

PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX Claim 1; SEQ ID NO 2740; 44pp; English.
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms's
CC tumour
XX
SQ Sequence 167343 BP; 49550 A; 37098 C; 35753 G; 44929 T; 0 U; 13 Other;

Query Match 8.08; Score 398.4; DB 6; Length 167343;
Best Local Similarity 60.1%; Pred. No. 2.2e-63;
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;
QY 3098 TTTGGGTTTTTTTGTGTTAGAGACAGGGTCTTCTGTGACGCCAGGCATGAG 3157
DB 147653 TTTTTTTTTAATTAATTTTGTGAGACGGAGCTTGTCTGTCACTAGGCTGGAG 147594
QY 3158 CACAGTGGTCAACCATAGTGTCTAGCAGCCTCAACCTCTGTAGCTCAAGGGATCTGTG 3217
DB 147593 TGCAGTGGCAACATCTTGGCTCACTGCAGCCTCCGCTCCGGGTGAAAGCGATTCTCCT 147534
QY 3218 ACCTCAGCCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACCAACCGCTGGCTAATTAA 3277
DB 147533 GCCTCTGCCCTGCCAGTAGTTGGATTACAGGTGTGTGTACCAACGCCAGCTAAATTTT 147474
QY 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTGTGGCCAGGCTTGTCTTAAACTCCTGG 3337
DB 147473 TGTAT-TTTTGTAGAGACGGAGTTTACCACATGTTGGCTAGGCTAGTCTTGAACCTCTGA 147415
QY 3338 CTTCAAGCAATCTCCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACC 3397
DB 147414 CCTCAGGTGATATGCCACCTTGGCCTCCCAAGTGTGGGATTACAGGCATGAGCCACT 147355
QY 3398 ATGTGGG-CTACTTATTTCTTTACATCCATCTTTCCAATAGAAATGAATGCCACAGA 3456
DB 147354 GTGCCTGGCCTAATTTTATTTTATGTTTGTGTTTTTGTGTTTTTTTTTTTTTTTGA 147295
QY 3457 ACAGGGATTACTGCCTATTTTCTTCTCTTCTTTTGTGAGACAGAGTCTCACTTTCATCACC 3516
DB 147294 GACCGACTCTCTCTGTTGCTAGGCTGGAGTGCAGTGTCAAGATCTCTGCTCACTCTC 147235
QY 3517 TCAACC-----TCGGTTCAGCTCACTGCAACCTCTGCTCCGGGTTCAAGYATTTCTCT 3572
DB 147234 TCCTCGCAACCTCTCAAGATTTTCGCAACCTCTGCTCTCTGAGTTTCAAGCGATTCTTGT 147175
QY 3573 GCCTAAGCCCTCTGAGTAGCTGGAATTAAGAAGGTGCACACCATCTTTGGCTAATTTTTT 3632
DB 147174 GCTTCAACCTCTGGAGTAGGTGAGATTACAGGTGTGTGTCACCATGCTGGCTTAA-TTTT 147116
QY 3633 TGTATTTTTTAGCAGAGATGGGTTTTTACCATTGTGCCCCAGGCTGGTCTCAAACTCCTGTAC 3692

DB 147115 TGTGTTTTTTAGTAGAGATGGGGTTTTACCATGTTGGCCAGGCTGGTCTTTGAACTCCTGAC 147056
QY 3693 CTCAAAGTGAATCTGCCCTCAGTCTCCCAAGTCTCTGGAATTTATAGGCGTAGTCACTG 3752
DB 147055 CTCAGGTGTGC-ACCTGCTTTTGGCTCCCAAGTCTGGGATTACAGGCATGAGCCTCCA 146997
QY 3753 TGCCCTGGCGGA-----TTACTGTCTATTTTCTTTTATTGCTATATATATATATATATAT 3800
DB 146996 TGCCAGGCCCATAGCTCCTATTTTAAATTGTACCTGTAAATGTTGGCTGCCCTTTAATC 146937
QY 3801 TAGACAGTGTCTGCATATATAGTAGTGTCTCAATAAATAAATTGAATGACAGCCTAG 3860
DB 146936 AAACCTCACCCCATGTTAATGCATCAGTCACTAAACTAGGATAAAGTAGGAGTTACTGAA 146877
QY 3861 ATATAAATCTTCTTTTCTTTTCTTTTAAACAATCTTGACAACCTTTTGCGAGAATAATA--- 3917
DB 146876 ATGCTGCTTTTCCACTGGCACCACCTTTGTGAGGAAAGGAAACCCCTAGAAAAATAACATTG 146817
QY 3918 ---CAATCTTGCATCTCTGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3973
DB 146816 TGGGCATGATTTCTTTATCGTACGGTGAATTCAGCCTTGCAGTGATTTTTTTCGAGATGA 146757
QY 3974 TCAAACTTTTATTTTGTACTGTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4033
DB 146756 ACAGAATTTAAAGTGTAGAACTCATTTTGGGAGGCTAAAGCAGGTAAGTCTTGAGCCC 146697
QY 4034 TTAATTTGCTTTATACATCTCTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4093
DB 146696 AGGAGTTTGTAGACA-AGGCTGGGTAACATAATAGAACCCCTGTCTCTCAAAACAAAACAA 146638
QY 4094 AAGCTATGAACCTCTCTCCCGAGAGAAATACACACACACACACACACACACACACAGTTT 4153
DB 146637 AAACCTATGTTCTCTCCGCTTTTCCCAACATTTAACTTTTACATACACAGTTGATGTTTCA 146578
QY 4154 TTTTAAATTTTGTCACTTAAGACAAGAAACCTGTCAATTAGAGGATGTTTGTTCATA----- 4208
DB 146577 TCCCTTAAG-TAGCAAAGAGGAGATGGAGTTTGTGAAAGTGTGTAATTTGTGATACTGTT 146519
QY 4209 -----TTAATTTAAATAATCACTCAGTTGGGCACAGTCACTCAAGCCTGTAAACCACAG 4259
DB 146518 TGCTTTTCCCTTGAATATGTTTCTTGGCCAGGAGCGTTTGTGTCACGCTGTGTAATCCAG 146459
QY 4260 TACTTTTGAAGTCCAAAGTGGTGGATCACTTTGAGTGCAGAAAGTTTCGAGACCAGCCTGCT 4319
DB 146458 CAGTTTGGAGCCCAAGTGGTGGATCACTGAGTGCAGAGATCGAGACCATCTCTGCG 146399
QY 4320 CAATATGTGAAACCTATCTCTACTAAAAATAC-AAAAAATAGCTGGGTGTAGTGATG 4377
DB 146398 TAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAAATTTAGCCGGCATGGTGGTG 146339
QY 4378 CATGCTGTAGTCCAGCTACTCGGAGGCTGAGCAAGAGATTTGCTTGAACCTGGGAG 4437
DB 146338 GGCACCTATAGTCCAGCTACTCTCGGAGGCTGAGCAGGAGATGGCATATGAACACAGAG 146279
QY 4438 GCAGAGTTTGCAGTGCAGCCGAGATCCCACTCAGCTCCAGCCTGGGCGACACACAGCCAG 4497
DB 146278 GCGAGCTTGCAGTGCAGCCGAGATCGTCCACTGCAGTCCAGTCTGGGCAACCGAGCGAG 146219
QY 4498 ACTCTATCTC 4507
DB 146218 ACTCCTTCTC 146209

RESULT 51
ABL67239/c
ID ABL67239 standard; DNA; 167343 BP.
XX
AC ABL67239;
XX
DT 15-MAY-2002 (first entry)
XX
DE Thyroid cancer related gene sequence SEQ ID NO:5576.
XX

KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; CC
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; CC
KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma; CC
KW gene; ds. CC

XX OS Homo sapiens. CC
XX PN WO200194629-A2. CC
XX PD 13-DEC-2001. CC
XX PF 30-MAY-2001; 2001WO-US010838. CC

XX PR 05-JUN-2000; 2000US-0209473P. CC
PR 05-JUN-2000; 2000US-0209531P. CC
PR 18-SEP-2000; 2000US-0233133P. CC
PR 18-SEP-2000; 2000US-0233617P. CC
PR 20-SEP-2000; 2000US-0234009P. CC
PR 20-SEP-2000; 2000US-0234034P. CC
PR 22-SEP-2000; 2000US-0234052P. CC
PR 22-SEP-2000; 2000US-0234509P. CC
PR 22-SEP-2000; 2000US-0234567P. CC
PR 25-SEP-2000; 2000US-0234923P. CC
PR 25-SEP-2000; 2000US-0234924P. CC
PR 25-SEP-2000; 2000US-0235077P. CC
PR 25-SEP-2000; 2000US-0235134P. CC
PR 25-SEP-2000; 2000US-0235144P. CC
PR 25-SEP-2000; 2000US-0235280P. CC
PR 26-SEP-2000; 2000US-0235637P. CC
PR 26-SEP-2000; 2000US-0235638P. CC
PR 27-SEP-2000; 2000US-0235711P. CC
PR 27-SEP-2000; 2000US-0235720P. CC
PR 27-SEP-2000; 2000US-0235840P. CC
PR 27-SEP-2000; 2000US-0235863P. CC
PR 28-SEP-2000; 2000US-0236028P. CC
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PR 28-SEP-2000; 2000US-0236034P. CC
PR 28-SEP-2000; 2000US-0236109P. CC
PR 28-SEP-2000; 2000US-0236111P. CC
PR 29-SEP-2000; 2000US-0236842P. CC
PR 29-SEP-2000; 2000US-0236891P. CC
PR 02-OCT-2000; 2000US-0237172P. CC
PR 02-OCT-2000; 2000US-0237173P. CC
PR 02-OCT-2000; 2000US-0237278P. CC
PR 02-OCT-2000; 2000US-0237294P. CC
PR 02-OCT-2000; 2000US-0237295P. CC
PR 02-OCT-2000; 2000US-0237316P. CC
PR 03-OCT-2000; 2000US-0237425P. CC
PR 03-OCT-2000; 2000US-0237598P. CC
PR 03-OCT-2000; 2000US-0237604P. CC
PR 03-OCT-2000; 2000US-0237606P. CC
PR 03-OCT-2000; 2000US-0237608P. CC
PR 01-NOV-2000; 2000US-0244867P. CC
PR 01-NOV-2000; 2000US-0245084P. CC

XX (AVAL-) AVALON PHARM. CC
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S; CC
XX Soppet DR, Weaver Z; CC
XX WPI; 2002-188264/24. CC

XX Screening for anti-neoplastic agent involves exposing cells to a chemical CC
PT agent to be tested for anti-neoplastic activity, and determining a change CC
PT in expression of a gene of a signature gene set. CC

XX Claim 1; SEQ ID NO 5576; 44pp; English. CC
XX The present invention describes a method (M1) for screening for an anti- CC
CC neoplastic agent. The method involves exposing cells to a chemical agent CC
CC to be tested for anti-neoplastic activity, determining a change in CC
CC expression of at least one gene (I) of a signature gene set, where (I)

CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664 CC
CC to ABL70110), or is at least 95% identical to (S), where a change in CC
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic CC
CC activity and can be used in gene therapy. M1 can be used for screening an CC
CC anti-neoplastic agent, and can be used for producing a product which is CC
CC the data collected with respect to the anti-neoplastic agent as a result CC
CC of M1, and the data is sufficient to convey the chemical structure and/or CC
CC properties of the agent. M1 can be used in the treatment of cancer such CC
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, CC
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell CC
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous CC
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms' CC
CC tumour CC
XX Sequence 167343 BP; 49550 A; 37098 C; 35753 G; 44929 T; 0 U; 13 Other;

Query Match 8.0%; Score 398.4; DB 6; Length 167343; CC
Best Local Similarity 60.1%; Pred. No. 2.2e-63; CC
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11; CC

QY 3098 TTTGGGTTTTTTTTTGTGTTGTTTGTAGACAGAGGCTTGTCTCTCACCCAGGCATGAG 3157 CC
DB 147653 TTTTGTAAATTAATTAATTAATTTTGTAGACGGAGCTTGTCTCTCACCTAGGCTGGAG 147594 CC
QY 3158 CACAGTGGTGCACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGATCTGCTG 3217 CC
DB 147593 TGCAGTGGCACAATCTTGGCTCAGTCAGCCTCCGCTCCCGGTTGAAGCGATTTCTCCT 147534 CC
QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTAGAGCGCTGCACACCGCCTGGCTGCTTAATAA 3277 CC
DB 147533 GCCTCTGCCTGCCAGTAGTTGGGATTACAGGTGTGTGTACACGCCAGCGATAATTTT 147474 CC
QY 3278 AAAATTTTTTGTACAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCCTCG 3337 CC
DB 147473 TGTG-TTTTGTAGTAGACGGAGTTTCCATGTTGGTAGGCTAGTCTTGAATCTCTGA 147415 CC
QY 3338 TTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACC 3397 CC
DB 147414 CCTCAGGTGATATGCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACT 147355 CC
QY 3398 ATGTGCGG-CTACTTATTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 3456 CC
DB 147354 GTGCCTGGCCTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 147295 CC
QY 3457 ACAGGGATTACTGCCTATTTTCTCTTCTTTTGTAGACAGAGTCTCACATTCATCAC 3516 CC
DB 147294 GACCGACTCTCTCTGTGCTGCTAGGCTGGAGTCAGATCTCTGCTCACTCTC 147235 CC
QY 3517 TCAACC---TCGGTTCAGCTCACTGCACACCTCTGCTCCCGGTTCAAGYATTTCTCT 3572 CC
DB 147234 TCCTCGCAACCTCTCAAGATTTCGGCAACCTCTGCTCTGAGTTCAAGCGATTTCTT 147175 CC
QY 3573 GCCTAAGCCTCTGAGTAGCTGGAAATTACAGCGTGCACACCATGCTTGGCTAATTTT 3632 CC
DB 147174 GCTTCAACCTCTGGAGTAGTGGAGATTACAGGTGTGTGCCACCATGCTCTGGGTAA-TTTT 147116 CC
QY 3633 TGTATTTTGTAGCAGAGATGGGGTTTTTACCATGTTCCCGAGGCTGCTCTCAAACTCCTGAC 3692 CC
DB 147115 TGTGTTTTTGTAGTAGAGATGGGGTTTTTACCATGTTGGCAGGCTGCTTGTAACTCTCTGAC 147056 CC
QY 3693 CTCAAGTAGTCTGCCTGCTCAGTCTCCCAAGTGTCTGGAATTTATAGGCGTAGTCAGTG 3752 CC
DB 147055 CTCAGTGGTC-ACCTGCTTTTCGCTCCCAAGTGTGGGATTACAGGCATGAGCTCCA 146997 CC
QY 3753 TGCCTGGCGGA-----TTACTGTCTATTTTCTTTTATTTGCTATATATCCAGATC 3800 CC
DB 146996 TGCCCGAGCCCATAGCTCTCTATTTTAAATTTGTAACCTGTAATTTGGCTGCCCTTTAATC 146937 CC
QY 3801 TAGACAGTGTCTGACATATAGTAGTGCTCAATAAATAATTTGATGAATGCACAGCTAG 3860 CC
DB 146936 AAACCTACCCCATGTTAATGATCAGTCACTAACTAGATGAAGGTAGGATTTACTGNA 146877 CC
QY 3861 ATATAAACTTTCTTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTTGCAATAAATA --- 3917 CC

Qy	2287	TTTCAGGCCAGGCGCGGTGCGCTCATGCTGTAAATCCAGCACTTTGGAGGCCGAGGCCG	2346
Db	130818	TTTTAGGCCAGGCAAGCGGTGGCTTATGCTGTAAATCCTAGCACTTTGGAGGCTGAGGCCG	130877
Qy	2347	GCGATCACATTGAGGTCAGAGTTTCAGACACGAGCTGSCCAACATGGTGAACCCCTGCT	2406
Db	130878	GCGGTCACATTGCTCAGGAGTTTGAGACCAAGCTGACTAACATGGTGAACCTCGCT	130937
Qy	2407	CTACTAAAAAATACAAAAATTTAGCCGGACATGGTGGCAGGCGCTGTAAACCCAGCTACT	2466
Db	130938	CTACTGAAATACAGAAAAATTTAGCCAGGGTGCTGGCGGCGCTGTGTAATCCAGCTACT	130997
Qy	2467	TGGGAGACTGAGTTGGAGGTTTCAGTGAGCCCAAG-----GTCGTG	2506
Db	130998	TGGGAGGCTCAGGCAGGAGAAATCCCTTTGAACCCGAGGGGTGGAGGTTGCAGTGAGCTGAG	131057

QY	2507	TCACTGCTGTCCAGCCTGGGTAAACAGACAACTCTGTCTCAAAAAAATAATGCTTTCA	2566	QY	3557	TTCAAGYGATTCTCTGCTAAGCCTCTGAGTAGCTGGAATTAACAAGCGTGACACCA	3616
Db	131058	ATTGCAAACTCCAGCTTGGGGACAGCGAGATGCGGTCTTTAAAAAATAAATAA	131117	Db	132103	TTACAGCCATTCTCTGCTCAGCCTCCAAGTAGCTGGACTACAGGCGCCACCA	132162
QY	2567	ATAAATATATGATAAAGGACTTATATTTTTTCAAGCCATAGGATCATTTCTCTGAAGC	2626	QY	3617	TGCTTGGCTAAATTTTTTGTATA-----TTTTTAGCAGATGGGGTTTT	3658
Db	131118	AGTAGCAAAAAACTGGAGGTTGAGGTGTTCATTTGGTAGCCACAGAGCTGGGTTCC	131177	Db	132163	TGCCCAGCTAAATTTTTTCTTTTTTTTTTTTTTTTTTTTAGTAGAGCGGGTTTC	132222
QY	2627	ATCTTGGGAGTCATCCACCTGTTCTGAGAGTGGGAGGTGAGGCTGACCTATTG	2686	QY	3659	ACCATTTTGGCCAGGCTGGTCTCAAACTCTGACCTCAAGTGATCTGCTGCTCAGTCT	3718
Db	131178	AGCTAGAGAGGTCAACCCCGGCC-----CTGCTGCCCTGCCAGCGTCCCTCTCTTCT	131233	Db	132223	ATGGTGTTAGCAAGATGCTCTGATCTCTGACCTCA--TGATCCGCGGCTTGGGCT	132280
QY	2687	CTCTGCACTTACTCTCTATCTCACTGTCCCTCCACTTTTCCAGGTGCTGCGACACATG	2746	QY	3719	CCCAAAGTCTGGAATATTAGCGTGAAGTCACTGTGCTGSCCGATTAAGTCTATTTC	3778
Db	131234	CTCTCCCGTCTCTCTGCGTGGAAAGACGACACATTTCTCAGGCTGTGGAGGATGG	131293	Db	132281	CCCAAAGTCTGGGATTTACAGGCATGAGCCACTGTGCGCGGCTCCCCACATTTT	132340
QY	2747	ACAACTGCTAYGACCAAG-----CCAAAGACTGGSACAGCTGPAATTTCTGCTGGACAM	2801	QY	3779	TTTTTGTCTATATCCCCAGATCTAGAGCAGTGTCTGACATATATAGTAGTGTCTCAATAAT	3838
Db	131294	GGAGGCCACAGGCCAGGGAGCTCCAGGAGCTGTGTTCAGTGGGCATCAGCCCTGAGGA	131353	Db	132341	TCCATGG-----CCAGATCTTCTCCTGACTCTCTGTGATC-----	132379
QY	2802	MCGGTACACCCACCACTATTATCATCTGCTGCTCTGCTCGGCAATCACCTGTAGAGTAG	2861	QY	3839	AATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTTCTTTTTTAAAAACAATCTTGA	3898
Db	131354	CTCCGGTGGGGGTCTCTGCATTTGGGTTTCTCTTGTGCTTCAGAAACCCGATGAA	131413	Db	132380	-----AGATCGTGGAGGGGTTTGTCTTCTCCCAAAAGGCTTGT	132419
QY	2862	GTTTATCCCTTCTTGACCTATCAATTTCTAGTTGGTTCTCAGTAGGCCGGGGAAATAA	2921	QY	3899	CAACTTTGCAGAAATAATACAATCTTGCAATCTGCTTTTTTTCATTTATCACCTTGTATGA	3958
Db	131414	GGCAATGTATCAGGCACATTTACTTCCATTTTAAACCTATGGAAGCCAACGATCG	131473	Db	132420	TTAGCGCCAG-----CACCTCACTCTTGACTTTGTTTCCCAAAATCTTGTATGG	132471
QY	2922	TAGTAAACAAGCCATGATTT-----AGTGTAAATTTTCTTGGTCTGGGAGTGTCTCCTT	2978	QY	3959	CTTTTTCAATTTGCTCAAACTTTATTTGTTACTGTTTTTCTGTTTTTCACTATTATTTAGTC	4018
Db	131474	GAACGAAACTTGGCTGTGCTTACCCTGGAAGGTATAAGCGCGCTCAGTTGTCTCCTG	131533	Db	132472	AGCTGTGCTCGCGCAGTCTCGGGAATCAGCAGCTGTGGGAAGCGGGGTGTGTGTGC	132531
QY	2979	TATCTCTCAGAACAACTATGGATAGGTAGTACAATTTACTCTACTTTAACAGATAAGAAA	3038	QY	4019	ACTGAATAATATGGCTTAATTTGCTTATACATCTCTGCTCCACTTTTAGAAGGCCAAAT	4078
Db	131534	GAAGACGGGCGTCTTCGAAACAGAGTAGCACCAAAAGTCTAGTTACACCTTAAATAGGA	131593	Db	132532	CAGCCCTGTCTGCGGCCAGTGACTGCGGGCTGTGGGGCGCCCGCCACTGCGCTGA	132591
QY	3039	CTCAGGC-----TCAGAAGGCTGAGCTATTTTGCCCAAGATCACACAGC	3081	QY	4079	TTACAAAATCTGATGAAAGCTATGAA-----CCCTCTCCCCAGAGAAATACACACACA	4132
Db	131594	GCTAAGCAGCTGGAAATGCNAAAAACCAACATAAGTATGTGCCCGGGTGGCTCTC	131653	Db	132592	TTCTCTCAGAGAAGCGCAGGAGGAACAAAGCTGACCCAGAGAGCCAGGCATAGCAGG	132651
QY	3082	TTGTAAG-----TGGTGACAGTTGGGTTTTTTTTTTGTTGTTTGTAGACAGAGGTCTT	3136	QY	4133	CACACACTCACACACAGTTTTTTTTTAAATGTTTGTGCAACTAAGACAAGAAACCTGATAG	4192
Db	131654	CTGTGTGCACTTTCCTGCCACATTTCTATTTTTTTTTTTTTTTTTTTTGTAGATGAGTCTC	131713	Db	132652	GGCTGAGGATGCTCTGTGTAATGGATGCCCTGGGAGAAAAGATGGCAGAAATTCACATGAG	132711
QY	3137	GCTCTGTACCCAGGATGAGCAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTC	3196	QY	4193	AGGATGTTTGTTCATATTAATTTAAAAATA-----ACTCAGTTGGGCACAGT	4238
Db	131714	GCTCTGTACCCAGGCTGGAAATGCATGGTGTCTGATTTCAAGCTCACGGCAACCTCTGCTTT	131773	Db	132712	TCTATGACAGGGAAGAATCAATAAATAAGAAAGGGCGGGCAGCGCGGT	132771
QY	3197	CTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGAC	3256	QY	4239	GACTCAAGCCTGTAAACCAAGTACTTTGGAAAGTCCAAGTGGGTGGGTGATCACTTTGAGGTGA	4298
Db	131774	CCAGGTTACGCGATTTCTCTGCTCAGTCTCCGAGTAGCTGGGATTTACAGGCACCTGC	131833	Db	132772	GGCTCATGCTGTAATCCAGCACITTTGGAGGCTTGGAGGCTGAGGCGGATCA--TGAGGTTG	132829
QY	3257	CACCAAGCCTGGTAAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTAGTTGGCC	3316	QY	4299	GAAGTTTCAGAGCACCGCTGGTCAATATATGTTGAAACCTTATCTCTACTAAAAATACAAAA	4358
Db	131834	CACCATGCCAGCAATCTTTTGTATTTTAGTAGAAACAGGATTTTGCATTTGGGCT	131893	Db	132830	GGAGTTCAGAGCACCGCTGGCTGATGATGATGAAACCCAGTCTCTACTAAAAATACAAAGA	132889
QY	3317	AGGCTTGTCTTAACTCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTG	3376	QY	4359	TTAGCTGGGTGTAGTGATGCTGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAG	4418
Db	131894	AGGCTGGTTTCGAACCTCCTGACCTCAAGTGATCCACAGCCTTGGGCTCCCAAGTGCTA	131953	Db	132890	TTAGCCAGGTGTGGGGGTGCATGCTGTATGTTCCAGTACTCTCAGGAGGCTGAGGCGAGG	132949
QY	3377	GGATTACAGGGGTGAGCCACCATGTGCGGTACTTATTTCTTATCATTTCCATCTTTCCAA	3436	QY	4419	AATTGCTTTGAACTCTGGGAGGAGGTTGCAAGTACGAGCGAGATCCCACTGCACTCCA	4478
Db	131954	GGATTACATGCGTGAGACACCATGCCCCCTGGCTCTCTCCCAATTTATTTATTTAT- ---	132009	Db	132950	AATTGCTTTGAACTCTGGGAGGAGGTTTGCAGTGGCGAGATTTGTCACCTGCACTCCA	133009
QY	3437	TAGAAATGATAGATCCACAGAACAGGGAATTACTGCCATTTTCTCTTTTCTTTTGTAGA	3496	QY	4479	GCCTGGGCGACACACCGGAGACTCTATCTCAAAAAAATAAATAAATAAATAA	4530
Db	132010	-----TATTTATTTATTTTGTAGACGGAGTCTTGTCTCT	132042	Db	133010	GCTTTGGCGACAGACAGACTCCATCTTTGAAAAAATAAATAAATAAATAA	133061
QY	3497	CAGAGTCTCACTTATCATCACTCAACCTCCGTTGAGCTCACTGCAACCTCTGCTCCCGG	3556				
Db	132043	ATCGCCAGGCTGGAGTGCAGTGGCAAAATCTCAGCTCACTGCAAGCTCGGCTCCCGG	132102				

RESULT 53

ABN97454

ID ABN97454 standard; DNA; 76798 BP.

XX

[illegible]

13454	Db	CTTTGCAATGCTCATGATGATATATATCATATATTTTTTATTTTTTTTGAGACGAGCTCTCACT	13511
3509	Qy	TCATCACCTCAACCTCCGGTTCA-----GCTCACTGCGAACCTCTGCTCCTCG	3554
13514	Db	CAATTGCCACGCGCTGGCGTGCAATGGCAGCATCTTGGCTCACTGCAACCTCCGCTCTCTG	13573
3555	Qy	GGTTCAAGYGATTTCTCTGCGCTTAAGCCTCTGAGTGTGGAAATTACAAGGGTGCACAC	3614
13574	Db	GGTTCAAGCGATCTCTCCACCTCAGCCTCCCAAGTAGCTAGAAATTACAGGCACCTGCCAT	13633
3615	Qy	CATGCTTGCTAAATTTTTTTTGATTTTTTACGACAGATGGGTTTTACCATGTTGCCAGGC	3674
13634	Db	CATGCTTGCTAAATTTTT--GTAATTTTTGTAGAGACAGGGTTTACCATTGTGGCCAGGC	13691
3675	Qy	TGCTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCCTCAGTCTCCCCAAAGTGCTGGAAT	3734
13692	Db	TGGTCTTGAACCTCTGACCTCAGGTGATCTCCCATCTCGGCTCTCCAAAGTGTGGGAT	13751
3735	Qy	TATAGCGTGAGTCACTGTGCGCTGGCCGATTACTGTCTATTTTTCTTTTATTTGCTATATCCC	3794
13752	Db	TGTAGGCATGAGCCACCATGCGCGGCTCATGATGTATCTTGTGTGCGACAGATTATGA	13811
3795	Qy	CAGATCTAGACGAGTCTCGACATATAGTAGGTCTCAATAAATAAATTGATGAATGCAC-	3853
13812	Db	TAAAGAAGAGCAGAGATTGAATTCGATATAAACCCCCCAAGAAAGGGCTTGCACATT	13871
3854	Qy	-----AGCCTAGATATAAATCTTCTTTTTCTTTTTTAAAAACAATCTTGACAA	3901
13872	Db	CCTGTGTCAAGTAGCCAGGATGAGGCTGTTCTCTTCTAAGCTAATCAGGAGTGGCT	13931
3902	Qy	CTTTGCGAATAAATACAATCTTGCAATCTCTCTTTTTCACCTTATCACCTGTTATGACTT	3961
13932	Db	GGTGTCCAGGTTTAGTTGGTTTTCAGTTTATCTTTGGTTTCAAATATCTTGAATGTGAGAT	13991
3962	Qy	TTTTCATATTGCTCTAAACCTTTATTGTTACTGTGTTTTTTCATTGTTTACTATTTTACTCACT	4021
13992	Db	CAGGTCACTAGTCTAGCTAGCATGGCTTTTGGAAATCTAATCACCACATCAAGTGTGCT	14051
4022	Qy	GAATAATATGGCTTAATTTGCT-----TATACATCTCTCTCTCCACTTTAGA	4069
14052	Db	GTAAGATCTCTGTCTTTTTCATCCCTGCCCCAGTTCCCAACTGTCTCTCAGTCAGAAA	14111
4070	Qy	AGGCCAAATTTTCAAAATCTGATGAAGATGATGAACCTCTCCCCAG-----AGA	4118
14112	Db	AGCCCATGCTGTGCAGTCTTTCTCCAGCTGCTTGGGCCCCAAGGAAATGAATAATTGA	14171
4119	Qy	AATACACACACACACACACTCACACAGTTTTTTTTTAAATGTTGCACTAAGACAA	4178
14172	Db	ATGAAGTAGTCTCATCTAGGAACGGCTTATGCCCTCTGGAATTTAGTTCAATTTAGTCAA	14231
4179	Qy	GAACCTGCTATTAGAGGATGTTTGT-----C	4205
14232	Db	GTGCTGTCGATAGAAGTATAAAGTGAGCCACATAGTAAATTTTAAATTTCTAGTAGGC	14291
4206	Qy	ATATTAAATTAATAAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGTACTTT	4265
14292	Db	ACATTTAAAAAGTAAAAAAGAGTCCAGGCACAGTGGCTCATGCCAATAATCCTAGCACTTT	14351
4266	Qy	GGAAGTCCAAGTGGGTGGATCACTTAGGTGAGAAAGTTTCAGAGACCAGCTTGGTCAATAT	4325
14352	Db	GGAGGCCAAG-CAGTGGATCACCTGAGTCAGGAGTTCGAGAGCCAGCCTGGTCAACAT	14410
4326	Qy	GGTGAACCTTACTCTACTAAAAATACAAAAATTTAGCTGGGTGTAGTGATGCATGCCCTG	4385
14411	Db	GGGGAAACCTTGCTCTCTACTAAACCAAAAAATTTAGCCAGGCTTGGTGGCTGTGGCTA	14470
4386	Qy	TAGTCCCACTACTCGGAGGCTGAGGCAAGAGAAATTGCTTTGAACCTGGGAGGAGGTT	4445
14471	Db	TAATCCACCTACTCAGGATGCTGAGGCAGGAGAAATGCTTTGAACCCAGGGGGCAAGTT	14530
4446	Qy	TGCAGTGAGCCGAGATCCCACTGCACTCCAGCCTGGGCGACACACGGAGACTCTATC	4505
14531	Db	GGCAGTGTGCCAGATGGTGGCACTTCACTCCAGCTGGGTGACAGAGCTGAACATGTC	14590

Db 2821 TCCAGCCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAATAAATAATAA 2876

RESULT 56
ADP74371

ID ADP74371 standard; DNA; 19300 BP.
XX XX
XX ADP74371;
DT XX
26-AUG-2004 (first entry)
DE Human X chromosome nucleotides 469701-489000.
XX XX
KW Human; ds; antisense; NRF; NF-kappaB repressing factor;
KW nuclear factor kappaB; immune response; inflammatory response;
KW oncogenesis; apoptosis; cell cycle; differentiation; cell migration;
KW chromosome Xq24-25.
XX XX
Homo sapiens.
OS XX
US2004110156-A1.
PN XX
10-JUN-2004.
PD XX
10-DEC-2002; 2002US-00317271.
PF XX
10-DEC-2002; 2002US-00317271.
PR XX
(ISIS-) ISIS PHARM INC.
PA XX
Dobie KW;
PI XX
WPI; 2004-440344/41.
DR XX
New antisense oligonucleotides for modulating NF-kappaB repressing factor
PT expression, useful for diagnosing, preventing or treating diseases or
PT conditions involving an immune response.
XX XX
Claim 1; SEQ ID NO 4; 61pp; English.
PS XX
The invention relates to a compound 8-80 nucleobases in length targeted
CC to a nucleic acid molecule encoding NF-kappaB repressing factor (NRF). NF
CC -kappaB (nuclear factor kappaB) is involved in such cellular processes as
CC the immune response, inflammatory response, oncogenesis, apoptosis, cell
CC cycle, differentiation and cell migration. The compound (an antisense
CC oligonucleotide) specifically hybridises with the nucleic acid molecule
CC encoding NRF (which appears as ADP74371 and comprises nucleotides 469701-
CC 489000 of the X chromosome containing the NRF gene at Xq24-25) and
CC inhibits the expression of NRF. Also included are inhibiting the
CC expression of NRF in cells or tissues, screening for a modulator of NRF,
CC a diagnostic method for identifying a disease state, a kit or assay
CC device comprising the above compound, and treating an animal having a
CC disease or condition associated with NRF. The antisense oligonucleotide
CC is useful for inhibiting the expression of NRF in cells or tissues to
CC prevent or treat diseases associated with aberrant NRF expression, such
CC as diseases or conditions involving an immune response. In addition, the
CC compound is used for diagnostics, prophylaxis, or as research reagents or
CC kits. The present sequence comprises nucleotides 469701-489000 of the X
CC chromosome containing the NRF gene at Xq24-25, and is a target for the
CC antisense oligonucleotides.

XX SQ Sequence 19300 BP; 4979 A; 4025 C; 4288 G; 6008 T; 0 U; 0 Other;

Query Match 7.9%; Score 394.6; DB 12; Length 19300;
Best Local Similarity 60.1%; Pred. No. 8e-63;
Matches 908; Conservative 1; Mismatches 520; Indels 82; Gaps 12;

QY 3099 TTGGTTTTTTTGTGTGTTTAGACACAGGGCTTGCTC-TGTACCACGAGCATGAG 3157
Db 8747 TTTTTTTTTTTTTTTTTTTTTTTTGTAGATGGAGTTTCACTCTTTGTTGCCAGGCTGAA 8806

QY 3158 CACAGTGGTGAACCATAGGTCACTGCAGCGCTCAACCTCTAGCTCAAGGATTCCTGCT 3217

9882 TTCTATCAAGCAGCAATCTTCATAGGAGCCCTTTTTTTTTTTTTTTTTTAAGAGACCGT 9941
4223 CTGAGTTGGCAGAGTACTCAAGCCTGTAAACACAGTACTTTGGAGTCCAAAGTGGGT 4282
9942 CTCAGCGGGTGCAGTTGGCTCACACCTGTAACTTAGCACTTTGGGAGGCTGAGGCAGGT 10001
4283 GGATCACTTCAGGTGAGAAGTTCGAGACCAAGCTGTCAATATGGTGAACCCCTATCTCT 4342
10002 GGATTACCTGAGTCAAGGTTCAAGTCAGCTGGCCAACTGGCAAAACCCCTGTCTCT 10061
4343 ACT-AAAAATACAAAATTAGCTGGGTGTAGTGATGTCATGCCCTGTAGTCCCACTACTCG 4401
10062 ACTAAAAAATACAAAATTAGCCAGCGGTGGTGGCGCATGCTGTAAATCCAGCTACTTG 10121
4402 GGAGGCTGAGCAAGAAATTGCTTGAACCTGGGAGGAGAGTTTCAGTGAGCCAGAT 4461
10122 GSAGGCTGAGGCGAGGAAGTGTGAAACCCGGGAGGTGGAGGTTGCAAGTGAGCTGATAT 10181
4462 CCACCACTGCACCTCCAGCCTGGCGACACAGCGAGACTCTATCTCAAAAAAATAATAA 4521
10182 TGTGCCACTGCATCCAGCCTGGGACACAGCAAGACTCCCTCTCAAAAAAATAATAA 10241
4522 ATAAATAAAG 4532
10242 AAAAAAAG 10252

RESULT 57
ADE84033
ID ADE84033 standard; DNA; 9289 BP.
XX AC ADE84033;
XX DE 29-JAN-2004 (first entry)
XX DE 5' regulatory region of human gene RBL2.
XX de; lymphoid cell proliferative disorder; methylation;
KW methylated CpG dinucleotide; single nucleotide polymorphism; SNP;
KW diffuse large B-cell lymphoma; mantle cell lymphoma;
KW chronic lymphocytic leukemia; small lymphocytic lymphoma;
KW follicular lymphoma; diagnosis; prognosis.
XX Homo sapiens.
XX OS
XX PN WO2003044226-A2.
XX PD 30-MAY-2003.
XX 25-NOV-2002; 2002WO-EP013265.
XX 23-NOV-2001; 2001DE-01057491.
XX 28-DEC-2001; 2001DE-01064501.
XX (EPIG-) EPIGENOMICS AG.
XX Burger M, Caldwell C, Genc B, Becker E, Maier S, Nimmrich I;
XX WPI; 2003-457621/43.
XX
XX Detecting and differentiating between lymphoid cell proliferative
XX disorders comprises contacting a target nucleic acid with at least one
XX reagent that distinguishes between methylated and non-methylated CpG
XX dinucleotides.
XX
XX Disclosure; SEQ ID NO 29; 449pp; English.
XX
XX The invention relates to a method of detecting and differentiating
XX between lymphoid cell proliferative disorders associated with at least
XX one gene and/or their regulatory regions in a subject by contacting a
XX target nucleic acid in a biological sample obtained from the subject with
XX at least one reagent or series of reagents that distinguish between
XX methylated and non-methylated CpG dinucleotides within the target nucleic

CC acid. The genes and/or their regulatory regions are preferably selected
CC from MDR1, CSNK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYO1, CDH3,
CC MYO11, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2a, CDKN2B, FOS,
CC GSK3beta, ESRI, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic
CC acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences
CC of the genes are useful for detecting the methylation state of all the
CC CpG dinucleotides within one or more the sequences, or their complements,
CC for determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs), and for differentiating at least two of the medical
CC conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma,
CC chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular
CC lymphoma. They are also useful for detecting of a predisposition to,
CC differentiation between subclasses, diagnosis, prognosis, treating and/or
CC monitoring of lymphoid cell proliferative disorder. This sequence
CC represents the 5' and/or regulatory region from one of the above
CC mentioned genes.
XX
XX Sequence 9289 BP; 2515 A; 1963 C; 2097 G; 2714 T; 0 U; 0 Other;
SQ
Query Match 7.9%; Score 392.4; DB 10; Length 9289;
Best Local Similarity 57.9%; Pred. No. 1.8e-62;
Matches 832; Conservative 1; Mismatches 532; Indels 71; Gaps 5;
QY 3094 ACAGTTTGGGTTTTTTTTTTTGTGTTTAGAGACAGGGTCTTGCTCTGTCACCCAGGCA 3153
DB 2360 ACACCTATTATTATTATTAATTTATTTATTTAGATGGAGTTGCTCTGCGCCAGGCT 2419
QY 3154 TGAGCACAGTGGTGCAACCATAGTGCTACTGACGCTCAACCTCTTGAGCTCAAGGATCT 3213
DB 2420 GGAGTGCAAGTGCATGATCCAGCTAACTGCAGTCTTTGGCTCTCTGGGTTCCAGCAATTC 2479
QY 3214 GCTGACCTCAGCTCCCAAGTAGCTGGGACTACGAGCTGCACACCGCTGCTGCTAAT 3273
DB 2480 TCCTGCCTCAGCTCTCAGTAGCTGGGATTTACTGGCACCGACCACTCTCTGGCTAAT 2539
QY 3274 TAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTC 3333
DB 2540 TTTTGTGA-TTTTGTAGTAGAATGGGTTTACATATGTTGCCAGGCTGGTCTTAAACTC 2598
QY 3334 CTGGCTTCAAGCAATCTCTTACCTTGGCATCCCAAGAGTCTGGGATTTACAGGGGTGAGC 3393
DB 2599 CTAACCTTAAGTGATCTGCCGCTTGGCTCTCCCAAGTGTAGGATTTACAGCGCTGAGC 2658
QY 3394 CACCATGTGGGCTACTTATTTTACATTTCCATCTTTTCCAAATAGATGAATCCAC 3453
DB 2659 CACCGCGCTTGCCTTATTTATTTA
QY 3454 AGAACAGGGATTTACTGCTTATTTCTCTCTTTTGTAGACAGAGTCTCAGCTTCACTC 3513
DB 2686 -----TTATTTTTTTGAGACAGGGTCTCTGTGCCC 2716
QY 3514 ACCTCAACCTCGTTTACGCTCACTGCAACCTCTGCTCCGGGTTCAAGYGATTTCTCTG 3573
DB 2717 AAGCTGTAGTGGCATGGTCAAGTTTCACTGCAAGCTCTCCCGAGGCTTAGCGGTTCTCCCA 2776
QY 3574 CCTAAGCTCTCTGAGTAGCTGGAATTAAGAAGTGCACACCATGCTCTGGCTAAATTTTTT 3633
DB 2777 CCTCAGTCTCCCAAGTAGTAGATTACAGGGGTGTACACCACTCTGGGTAA-TTTTT 2835
QY 3634 GTATTTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTGACC 3693
DB 2836 CTATTTTTTTGAGACAGAGGTTTTCATATGTGCGCCAGGCTGGTCTCGAACTCTGTGAC 2895
QY 3694 TCAAGTGATCTGCCCTGCTCAGCTCTCCCAAGTGTGGAATTTATAGGCGTGAGTCACTGT 3753
DB 2896 TCAAGCAGTCTCTCCCACTTGACCTCCCAAGTGTGGAATTTACAGGTGTGTACCAAC 2955
QY 3754 GCCTGCGGATTTACTGCTCTATTTCTTTTATTTCTAT-ATCCCCAGATCTAGAGCACT 3809
DB 2956 GTCCAGGCTATATATCTTAAGATACCTTTAAACCAATTTGTGTTCAACTCTGTTTGGCCC 3015
QY 3810 GTCTGACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGCCTAGATATAAACT 3869

Db 3016 CATAGTCACCTTGAGACTCATCACTTAGCCAACTCCAAAAGCATTGCTGATTACTGTGAA 3075
Qy 3870 TTCCTTTTCTTTTAAACAATCTTGACAACCTTTGAGAGTAATAACAATCTTGCATT 3929
Db 3076 TTTTACTAAGGTTTCTTAAGAGGTTCCATTGTCTCAAAATTTGTTCCCGAAATATCCCTG 3135
Qy 3930 CTGCTTTTTCACCT--TATCACCTTCCTTATGACTTTTTCATATGCTCAAAACCTTTATT 3986
Db 3136 TTACCTGTCTACTGATTTTCTCTATCTTCAGAGTTCCATTTCCTGCTCCGCTGT 3195
Qy 3987 GTTACTGTTTTTCACTGTTTACTATTTTATGTCACCTGAATAATATGCTTTAAATTTGCTTAT 4046
Db 3196 CATTATACCTTCCATAAGCCCTACTTTTGTGCCAGCACTTTTCCCTCTGTCAGTTTACA 3255
Qy 4047 ACATCTCTCTGCTCCACTTTAGAGGCCAAATTTACAATCTGATGAAGCTTATGAACCC 4106
Db 3256 TATCCCAACCAAGCAAAACAAAATAGCAAAACAGTAATCCCTCTGAATCCCTCAAAATTGC 3315
Qy 4107 TCTCCCCAGAGAAATACACACACACACACACTCACACAGATTTTTTTTTTAAATGTTTG 4166
Db 3316 TCAATCTCAGATGCTCTCTCAATCTGGAATAATGTTTTATATCAAGCCCATTTATAATC 3375
Qy 4167 CAACTAAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAAATTAATAAATACTCA 4226
Db 3376 AAGGATTGGCAATTTAAAAAATTAATAAAGAGGAGAATTTGGAATAAAAAATGAATTG 3435
Qy 4227 GTTGGCAGAGTCACTCAAGCCTGTAAACACAGTACTTTTGGAGTCCAAGTGGGTGGAT 4286
Db 3436 GCTGGCAGCGTGGCTCAGCCCTGTAAATCCAGAACTTTTGGAGGCCGAGGTGGGTGGAT 3495
Qy 4287 CACTTGAGGTGAGAAGTTCGAGACCACTGGTCAATATGTTGAAACCTTACTCTACTA 4346
Db 3496 CACTTGAGGTGAGAGTTTGAGACCACTGGTCCCAACATGGTGAACCTGCTGTACTG 3555
Qy 4347 AAAATACAAAAATTAGCTGGGTGTAGTGATGATGCTGTAGTCCAGCTACTCCGGAGG 4406
Db 3556 AAAATACAAAAATTAGCTGGGTGGTGGCGACACCTGTAAATCCAGATACTCAGAGG 3615
Qy 4407 CTGAGCAGAGAAATGCTTGAACCTGGGAGGAGAGTTGCAGTGAGCGGAGATCCAC 4466
Db 3616 CTGAGCAGAGAAATCGCTTGAACCCAGGAGCGAGGTTGCAGTGAGCGGAGATCGTC 3675
Qy 4467 CACTGCACTCCAGCCTGGCGACACAGCAGACTCTATCTCAAAAAATAAATAAA 4522
Db 3676 CACTACACTCCAGCCTGGCGACAGAGCCAGACTCTGTCTCAAAAAAATAAATAAA 3731

RESULT 58
ID AAS00624
XX AAS00624 standard; DNA; 36221 BP.
AC AAS00624;
XX
XX 07-SRP-2001 (first entry)
DT Human death-associated protein 6 (DAXX) gene.
XX
DE
XX Death-associated protein 6; DAXX; polymorphism; haplotype pair; human;
KW immune disorder; autoimmune disease; population diversity; ds;
KW paternity testing; anthropological lineage; forensic application.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH variation replace(26869,G)
FT /*tag= a
FT variation replace(26870,T)
FT /*tag= b
FT variation replace(27145,A)
FT /*tag= c
FT variation replace(27239,G)
FT /*tag= d

FT variation replace(27620,T)
FT /*tag= e
FT variation replace(27788,G)
FT /*tag= f
FT variation replace(27806,T)
FT /*tag= g
FT variation replace(27816,T)
FT /*tag= h
FT variation replace(27869,T)
FT /*tag= i
FT variation replace(27905,A)
FT /*tag= j
FT variation replace(27916,C)
FT /*tag= k
FT variation replace(28194,T)
FT /*tag= l
FT variation replace(28339,T)
FT /*tag= m
FT variation replace(28470,C)
FT /*tag= n
FT variation replace(29010,T)
FT /*tag= o
FT variation replace(30235,T)
FT /*tag= p
FT variation replace(30665,A)
FT /*tag= q
FT variation replace(30666,T)
FT /*tag= r
FT variation replace(30752,T)
FT /*tag= s
FT variation replace(31916,T)
FT /*tag= t
WO200125245-A2.
XX 12-APR-2001.
XX
XX 05-OCT-2000; 2000WO-US027487.
XX
XX 06-OCT-1999; 99US-0157909P.
XX
XX (GENA-) GENAISSANCE PHARM INC.
XX
XX Chew A, Choi JY, Denton RR, Nandabalan K, Stephens JC;
XX WPI; 2001-308220/32.
XX
XX New human death-associated protein 6 (DAXX) gene variants comprising 19
XX polymorphic sites useful in studying the effect of variation on the
XX biological activity of DAXX and in developing drugs targeting the
XX protein.
XX
XX Claim 1; Fig 1; 97pp; English.
XX
XX The sequence represents a DNA encoding human death-associated protein 6
XX (DAXX). This gene may comprise one or more polymorphisms at specific
XX nucleotide positions to form one of nineteen possible polymorphic
XX variants. Associations between a trait and a genotype or a haplotype of
XX the DAXX gene can be identified by comparing the frequency of the
XX genotype or haplotype in a population exhibiting the trait with that of a
XX reference population. A higher frequency in the trait population
XX indicates an association. Methods involving genotyping or haplotyping of
XX the DAXX gene of an individual can lead to prediction of haplotype pairs
XX for the DAXX gene of related individuals, and may be useful in studying
XX the expression and biological function of DAXX, as well as in developing
XX drugs targeting this protein. Polymorphic variants of DAXX are useful in
XX studying the effect of the variation on the biological activity of DAXX
XX as well as on the binding affinity of candidate drugs targeting DAXX for
XX the treatment of autoimmune diseases and other immune disorders.
XX Polymorphism is also useful for studying population diversity.
XX Anthropological lineage, paternity testing, forensic applications, and
XX for identifying associations between the DAXX genetic variation and a
XX trait such as level of drug response or susceptibility to disease. DAXX

CC proteins may be used to measure binding affinities of one or more
CC candidate drugs targeting the DAXX protein

XX	Seq	Sequence	36221 BP; 8897 A; 8473 C; 9437 G; 9414 T; 0 U; 0 Other; 10; Matches 857; Conservative 1; Mismatches 551; Indels 37; Gaps 10;
QY	Query Match	7.8%; Score 391.8; DB 4; Length 36221;	
DB	Best Local Similarity	59.3%; Pred. No. 2.9e-62;	
QY	3109	TTTTGTTGTTTGTAGAGACAGGGTCTTGCTCTGTCAACCAGGCATGACACAGTGGTC	3168
DB	13286	TGTTTTTGTGTTTGTAGATGGAGTTGGCTCTGTCAAGCAGGCTGGAGTGCAGTGGTGT	13345
QY	3169	AACCATAGTCACTGAGCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCNC	3228
DB	13346	GATCTTAGTCACTGCAACCTCTCTCTGGGTCAAGTATTCCTCGCTCAGCCCTC	13405
QY	3229	CCAAGTAGCTGGGACTACGAGCGTGCACCAACGCTGGCTAAATTAATAAAATTTTTT	3288
DB	13406	CTCATTTAGCTGGGACTACAGGCGGTGCCACGCCAGCTAAATTTTGTGA--TTTTTA	13463
QY	3289	GTAGAGACTGGGCTTACTACGTTGGCAGGCTTGCTTAACTCTGGCTTCAAGCAAT	3348
DB	13464	GTAGAGATGGGGTTTCAACATGTTGGCCAGGCTGTCTCGATCCCTTGACCTC--GTGAT	13521
QY	3349	CCCTCTACCTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGGCT-	3407
DB	13522	CCGCTCGCTCGGCGCTCCCAAGTGTGAGATTTACAGGGGTGAGCCACCGTGCCTAGT	13581
QY	3408	--ACTTATTTTTCATCTTCATCTTTTCCAATAGAAATGTAAGATCCACAGACAGGGAT	3465
DB	13582	ACAGTTTTTATTTACAATGTCAATATTTATATAAGACACAGATCTGTACACTCTTTT	13641
QY	3466	ACTGCGCTATTTCTCTTTTGTGAGACAGATCTCACTTTCATCACTCAACCTCC	3525
DB	13642	TTTTTTCTGAGATGGAGTCTCGCTCTGTTGCCAGGCTGGAATGCAGTGG-----TATGA	13696
QY	3526	GTTCACTCACTCAACCTCTGCTCCCGGTTCAAGYGATTCCTGCTTAAGCCTCT	3585
DB	13697	TATCGGCTACTGCAACACCGCTCCAGGTTCAAGCAATCTTGCTCTCAGCCTCCC	13756
QY	3586	GACTAGCTGGAATTACAAGCGTGCACCACTGCTTGGCTAAATTTTGTATTTTATAGCA	3645
DB	13757	GAGTAGCTGGATTACAGGCATACGCCACCACTGCCAGCTAA--TTTTTGTATTTTAGTA	13815
QY	3646	GAGATGGGTTTACCATGTGGCCAGGCTGCTCAAACTCTGACCTCAAGTATCTG	3705
DB	13816	CAGACAGGGTTTCACTATGTTAGCCAGGCTGGTCTTGAATCTCTGACCTC--GTTATCCA	13873
QY	3706	CTGCTCTCAGTCTCCCAAGTGTGGAAATTTATAGGCGTGAGTCACCTGCTGGCGGAT	3765
DB	13874	CTGCTCTGCGCTCCCAAGTACTGGATTTACAGGTGAGCCATGTCACCAAGCGGAT	13933
QY	3766	ACTGCTATTTCTTTTATTTGCTATATCCCAGATCTAGACAGTGTCTGACATATA----	3821
DB	13934	TGTTATACTCTTTGCGAGTTATTTAAATCAACAGGAAATAAATTAGATGCCAAATAAAA	13993
QY	3822	-----GTAGGTCTCAATAATAATTTGATGATGACAGCCTAGATATAAAC	3868
DB	13994	TATATACAAAATGGSCATAAATTTTCCAAAATGTTTTTAAGGAGCATGCAACGAAGAAA	14053
QY	3869	TTTTTTTTTTTTTTTTTAAACAATCTTGACAACCTTTGCAGAAATAATACAATCTTGCAT	3928
DB	14054	TGTGAAGACTGATAGACTAAATCTAGTGTGCTCTTATATCCNAGCAAGAGAGATCCTG	14113
QY	3929	TCGCTTTTTCATTAATCACTTTGTTATGACTTTTTTATATTGCCTCAAACTTTATTGT	3988
DB	14114	CCTGGAGCCCCACATTTTCAGAGGCCCCACATATATAAATGTTAAAGAAATAAATTTGG	14173
QY	3989	TACTGTTTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATAC	4048
DB	14174	AAGCAATATATGGGTGTATCTGTGTACTGAAGATCTGGTCAATTTCTAGCACAGTGTA-	14232

QY	4049	ATCCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAGACTATGAACCCCTC	4108
DB	14233	TGAGTTATCTATGCTGTGTAAACAATTAACCCAAAACCCGGTGGCTCAAAACAACACAC	14292
QY	4109	TCCCAGAGAAATACACACACACACACACACTCAACACAGTTTTTTTTTAATGTTTGA	4168
DB	14293	TGTTATCTGATGGCTTCTGTGGGGAGAAATCTGGGAACAGCTTAGCTGGATCCTCTGCT	14352
QY	4169	ACTAAGAC---AAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAAATACTC	4225
DB	14353	TCGGAGGCTCTCATAGACTGCAGTCTATGATTTGCTGTGATCTCATCTGGAAGCTCAG	14412
QY	4226	AGTTGGGCACAGTACTCAAGCTCTAACCACAGTACTTTTGGAACTCCAAGTGGGTGA	4285
DB	14413	GGCGGGCTCAGTGGCTCATGATGTAATCCAGGACATTTTGGAGGCTGAGGCAGGTGA	14472
QY	4286	TCACTTGAAGTGAAGTTTCAGACACAGCCTGGTCAATATATGGTGAACCCCTATCTACT	4345
DB	14473	TCACCTGAGGTCAGGATTCAGACACAGCCTGGCCCACTGGTGAACCCGGTTTCTACT	14532
QY	4346	AAAAATACAAAAATTTAGCTGGGTGATGATGCATGCTGTAGTCCAGCTACTCGGGAG	4405
DB	14533	AAAAATACAGAAATTTAGCTGGGTGTTTGGCGGCACCTGTAAATCCAGCTACTTTGGGAG	14592
QY	4406	GCTGAGGCAAGAGAAATTCCTTGAACCTGGGAGCAGAGTTGTCAGTGAAGCCAGATCCCA	4465
DB	14593	GCTGAGGCAAGAGAAATCAATTGAACCTGGAGGTGGAGTTGCAATGAGCGAGATAGCA	14652
QY	4466	CCACTGCACTCCAGCCTGGGCGACACAGCGAGCTCTATCTCAAAAAATAAATAAATAA	4525
DB	14653	-CATTGCACTCTAGCCTGGGTGACGAGCAAGACTCTGTCTCAAAAAATAAATAAATAA	14711
QY	4526	AATAAA 4531	
DB	14712	AATAAA 14717	
RESULT 59			
ID	AAD58279	standard; DNA; 226475 BP.	
XX	AC	AAD58279;	
XX	DT	20-NOV-2003 (first entry)	
XX	DE	Human tumour suppressor gene, Lmt reverse complement DNA.	
XX	KW	Tumour suppressor gene; Lmt; cancer; therapy; cytostatic; human; ds.	
OS	OS	Homo sapiens.	
PN	PN	WO2003066869-A1.	
XX	PD	14-AUG-2003.	
XX	PF	07-FEB-2003; 2003WO-AU000126.	
XX	PR	07-FEB-2002; 2002AU-00000371.	
XX	PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.	
XX	PI	Cook WD, Mccaw BJ;	
XX	DR	WPI; 2003-646311/61.	
XX	PT	New nucleic acid molecule, useful for screening a subject for the	
XX	PT	presence of an aberration in a gene encoding an LMT.	
XX	PS	Claim 10; Page 233-299; 373pp; English.	
XX	CC	The invention relates to novel tumour suppressor gene, referred to as	
XX	CC	Lmt. The invention also relates to the field of cancer therapy and cancer	
XX	CC	diagnostics. The nucleic acid molecule is useful for screening a subject	

CC for the presence of an aberration in a gene encoding an LMT. The present
XX sequence is human Lmt reverse complement DNA
SQ Sequence 226475 BP; 61024 A; 41761 C; 40916 G; 57494 T; 0 U; 25280 Other;

Query Match 7.8%; Score 391.4; DB 9; Length 226475;
Best Local Similarity 58.9%; Pred. No. 4.5e-62;
Matches 853; Conservative 1; Mismatches 557; Indels 38; Gaps 9;

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QY 3094 ACAGTTTGGGTTTTTTTTTTTGGTCTTTAGACAGGGTCTTGCTCTCACCAGGCA 3153
D 3236 ACAATGTTAGGTAATAATTTTTTTTTTTGGATGGAGTCTGCTCTCACCAGGCT 73295
QY 3154 TGAGCACAGTGGTGAACCATAGTCACTGACGCTCAACCTCCTGAGCTCAAGGATCT 3213
D 73296 GGAGTGCAGTGGTGCACCTCGCTCACTGCAACCTCTGCTCTGGGTTACAGTGATTC 73355
QY 3214 GCTGACCTCAGCCTCCCAAGTACAGTGGGACTAGAGCGGTGCACCAACGCTGGCTAAT 3273
D 73356 TCCTGCTCAGCCTCCGAGTAGCTGGATGT-----GCCAGCTAAT 73397
QY 3274 TAAAAAATTTTTTTAGAGACTGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTC 3333
D 73398 TTTTTTGTATTTTAGTAGAGATGGGGTTTCAACCGTTTAGCTAGGATGGTCTCGATCTC 73457
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D 73458 CTGACCTCTG--ATCCGCTGCTTGGCTCCCAAAGTCTGGGATTACAGGTGAGC 73515
QY 3394 CACCATGTGGGCTACTTATTTCTTACATTCATCTTTTCCAATGAATGTAAGATCCAC 3453
D 73516 CACCGCCCCAGGCAATGTAGTAAATTTTAAACCACTATGCTCAATTTCTTATCTT 73575
QY 3454 AGNACAGGAGTACTGCCTATTTCTTCTCTCTTTTGTAGACAGAGTCTCACITCATC 3513
D 73576 TTTTTTTTTTTTGGAGATGGAGTCTCGCTGCTCTGCTCTGTTGC--CCGGGCTGGAGT 73633
QY 3514 ACCTCAACCTCCGTTTCCAGTCACTGCAACCTCTGCTCCCGGTTTCAAGYGATTTCTCTG 3573
D 73634 GCAGTTGTGTGATCTCGGCTCACTGCAAACTCTGCTCCAGGTTTCATGCCATTTCTCTG 73693
QY 3574 CTTAGCCTCTGAGTGTGGAATTTACAAGCGTGCACCACTGCTTGGCTTAATTTTTT 3633
D 73694 CTTAGCCTCTGAGTGTGGAATTTACAAGCGTGCACCACTGCTTGGCTTAATTTTTT 73753
QY 3634 GTATTTTACAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCTGACC 3693
D 73754 GTATTTTACAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCGATCTCTGACC 73813
QY 3694 TCAAGTGTATCTGCTCCCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGAAGTCACTGT 3753
D 73814 T--TGTGCTCCGCCACCTCGGCTCCCAAGTGTGGAATTTACAGGCGTGAAGTCCGT 73871
QY 3754 GCTGCGCAGTACTCTCTATTTTCTTATGCTATATATATATATATATATATATATATATAT 3813
D 73872 GCGCGGCC--CTCAATTTCTTATCTTTAAATAGATATAATAATATATATATATATATAT 73930
QY 3814 GACATATAGTGTGCTCAATAATTTGATGAATGCACAGCCTAGATATAAATTTCT 3873
D 73931 GATAAAGGGCTCAATFACTATAATTTATGTAAGATTTAAACCTTAATTCCTGGCAGATGT 73990
QY 3874 TTTTCTTTTTTAAAAAATCTTGCAAACTTTGCAATAAATAAATAAATAAATAAATAAATAA 3933
D 73991 AAATGCTCAATAATGATAGTATTTATATATATATATATATATATATATATATATATAT 74050
QY 3934 TTTTTCATATACCTGTATGACTTTTTCATATATGCTC---AAACCTTTATTTGTTA 3990
D 74051 CCCATGATGCTGAATCAGTACACGGCAATTTCCAGGAGCTCTCTGACCTTTCTCTAT 74110
QY 3991 CTGTTTTTTCATTTGTTACTATTTTAGTCACTGATATAATATGCTTAATTTGCTTATACAT 4050
D 74111 GTGCATTTCTATATGTTAATATGTAATAACCTACTTGTAGTGTCAAAACCTGTTTTTTTTTC 74170
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QY 4051 CCTCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAAC---CCT 4107
D 74171 CATCTTAAGACATTTTAAATATTTGATAGAGTATCTGTAAACTATATACAAACTTACTT 74230
QY 4108 CTCCCAGAGAAATACACACACACACACACACTCACACAGTGTTTTTTTTAAATGTTGC 4167
D 74231 GACTTCTCTAAAAAAGATGATAGTGAACATCAGTCACCTTTTGTGTTATCAACTCTGTTCA 74290
QY 4168 RACTAAGACAAGAACCTGCTATTTAGAGGATGTTTCTTCATA---TTAATTTAAAAATAAC 4223
D 74291 ACATTTGCTACTCTCTCATTTTCTTTGGACCATAGTAGATACCTTTAAAGAACAAAAAGA 74350
QY 4224 TCAGTTGGGCACAGTGACTCAAGCCTGTAACACACAGTACTTTTGAAGTCCAAAGTGGGTG 4283
D 74351 CATGCCAGTGCAGTGGCTCAGCCTGTAACTCTAGCACTTTTGGAGGCCAAGGCGGCG 74410
QY 4284 GATCACTTGAGTGAAGTTTCGAGACCAAGCTGTGTCATATGTTGGTGAACCCCTATCTCTA 4343
D 74411 GATCACTTGAGTGGGAGTTTCGAGACCAAGCTGTGAGCAACCGTGGAGAAACCCCTCTCTA 74470
QY 4344 CTAAAAATAC---AAAAATTTAGCTGGTGTAGTGATGCTGCTAGTCCCGACTACTC 4400
D 74471 CTAAAAACACAAAAAATTTAGCTGGCATGTTGGCATGCTGTATATCCCGACTACTC 74530
QY 4401 GGGAGGCTGAGCAAGAGAAATTTGCTTTGAACCTGGGAGGCAGAGTTGCAGTGAGCGGAG 4460
D 74531 CGGAGGCTGAGCGAGAGATTCGCTTTGAACCTGGGAGGCAGAGTTTGTGTCAGCTGAGA 74590
QY 4461 TCCCACTGCTGCTTCCAGCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATA 4520
D 74591 TCCCACTTGCATCTCCAGCTTAGGCAACAAAGCGAAACTCCGTTCAAAACAAAAAGA 74650
QY 4521 AATAAANTA 4529
D 74651 AAAAAAGA 74659

RESULT 60
ABL62905
ID ABL62905 standard; DNA; 15000 BP.
XX
AC ABL62905;
DT
DT 15-MAY-2002 (first entry)
XX
DE Breast cancer related gene sequence SEQ ID NO:1242.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
XX gene; ds.
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 22-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
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QY 3464 TTACTGCTATTTTCTTCTTTCTTTTGGAGACAGAGTCTCACTTCATCATCACTCAACCT 3523
 Db 10784 TTTTCTTTTCTTTTCTTTGAGACAGTTCACCTCTGTTGCCAGGCTGGAGTGAATGGCGT 10843
 QY 3524 CCCTTCAGCTCACTGCAACCTCTGCTCCGGGTTCAAGYGATTCCTGCTGCTCAAGCCTC 3583
 Db 10844 GATCTCAGTTCACTGACGCTCCCTCTCTGGGTTCAAGTGATTCCTGCTGCTCAGCCTC 10903
 QY 3584 CTGAGTAGCTGGAAATACAGCGCTGACCAACCATGCTTGGCTAAATTTTGTATTTTAG 3643
 Db 10904 CTGAGTAGCTGGGAATACAGGCATGTACCACCAATCCAGCTAA--TTTGTATTTTAG 10961
 QY 3644 CAGAGATGGGGTTTACCATGTTGCCAGGCTGCTCAAACTCCTGACTCAAGTGATC 3703
 Db 10962 TAGAGACGGAGTTTCTTCACTGTTGGTCAAGCTGCTTGAATCTCTGACTCAGTGATC 11021
 QY 3704 TGCTGCTCAGTCTCCCAAGTGTGGAATATAGCGGTGAGTCACTGTGCTGGCCGA 3763
 Db 11022 CACCTACCTCAGCTCCCAAGTGTGGAATACAGGTGTAGCCACACGCGCGCCAA 11081
 QY 3764 TTA-----CTGCTATTTTCTTTATTTGCTAT 3789
 Db 11082 CTATTCATTTTGTGCGAGATTTTGTGTTTGTGTTTGTGTTTAAATTTCTTCTTC 11141
 QY 3790 ATCCCGAGATCTAGACAGTGTCTGACATATAGTGTCTCAATAAATAATTTGATGAAT 3849
 Db 11142 TTAGGAGCTGAAGACTATTCAGAGAGTTCAGAAAGGCAAAATGGAAGTAATGGCT 11201
 QY 3850 GCACAGCTAGATATAAATTTCT-----TTTTCTTTTTTAAACAATC 3894
 Db 11202 TCCACTCTTTCTCTTAAAGGAACCTACTAAATACAGTGTCTGGGTATTTTCTTAAAGTTT 11261
 QY 3895 TTGACAACTTTGAGAAATAAATAAATCTTGCAATCTGCTTTTCACTTATCACCTTGT 3954
 Db 11262 TTAATAAATAAATAAATTTTGTGCAATTTGTTTCACTTGGTAAATTTGGAGGTCACTCATC 11321
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 Db 11322 AGTATATTTATCTTTGCAATGTTTCTAGGAGTTATGTTGGTTTACATTTGTAAGAACTT 11381
 QY 4015 AGTCACTGAATAATATGGCTTAATTTGCTTTATACATCCTCCTGCTCCACTTTTGAAGGCC 4074
 Db 11382 TAGAAAAATACATTTAGCCAGTTCTGTAAACATGTAATTTGATAGTTTGTAGCTGACA 11441
 QY 4075 AAATTTACAAATCTGATGAAGCTATGAACCC---TCTCCCCAGAGAAATACACACAC 4131
 Db 11442 TAAAGCAGTGTGTCAGTCCCTTTATATGTACCTATTTGTGTAGGTACAACCTGGTCCCTGGC 11501
 QY 4132 ACACACACTCACACAGTTTCTTTTAAATGTTTGGCACTTAAGACAAGAAACCTGCA--- 4188
 Db 11502 TTATGAAGTTTGACCTGATTTTTCGACTTTACATGGTGTATACCATCTTTGAGCA 11561
 QY 4189 -TTAGAGGATGTTTGTTCATTAATTAATAA-----TAACTCAGTTGGGCACAGTGA 4240
 Db 11562 CTCACAGTTGTTTCTTTTCTTTCTTTTAAGACACAGGCTCTTGGCTGGGAGAGTGG 11621
 QY 4241 CTCAAGCCTGTAAACACAGTACTTTTGGAACTCAAGGTGGGTGGATCACTTGAGGTGAGA 4300
 Db 11622 CTCACGCTGTAAATCCCAACACTTTGAGAGGCCAGGGTGGC--GGATCACTTTGAGCTCAGG 11680
 QY 4301 AGTTGAGACAGCCTGGTCAATATGTTGAAACCTTATCTTACTAAATAACAAAAAT 4360
 Db 11681 GGTTTGAGAACAGCCTGGGCAACATAGTGAGACCTTGTCTCTTAAATAACACA--AAAAAT 11739
 QY 4361 AGCTGGGTGTAGTGTGATGATGCTGCTGTAGTCCCACTACTCGGAGGCTGAGGCAAGAGAA 4420
 Db 11740 AGCTGTGTAGTGGCAGCAGCCTGTGTTCCAGGTACTCAGGAGGCTGAGGTGGGAGAG 11799
 QY 4421 TTGCTTGAACCTGGGAGGCAAGGTTGCACTGAGCCGAGATCCCAACCACTGCACTCCAGC 4480
 Db 11800 TAACTTGAGCCTTAGGAGGTGGAGGTACAGTGGGCCACAGTGCATGCCACTTACACTCTAGC 11859

QY 4481 CTGGSCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAG 4532
 Db 11860 CTGGGTGACAGAGTAAGACCCCATCTCAAAAAATAAATAAATAAAG 11911

Search completed: May 12, 2006, 07:27:57
 Job time : 1975 secs

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OM nucleic - nucleic search, using sw model

Run on: May 12, 2006, 07:28:08 ; Search time 12140 Seconds
(without alignments)
19273.657 Million cell updates/sec

Title: SEQ1-4500-9500-7328G
Perfect score: 4997.8
Sequence: 1 ctgtgcatctcagttctttt.....tttgaccagcctggacaa 5001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 150 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

10: gb_est10:*

11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	520.2	10.4	599	5	BU785306
2	505.4	10.1	507	5	BU785040
3	349	7.0	349	9	AQ017732
4	344.2	6.9	4087	4	BC024593
5	341	6.8	3990	4	HSM803026
6	337.2	6.7	15970	9	AQ839852
7	334	6.7	347	1	AL708471
8	315.8	6.3	897	6	CD557847
9	311	6.2	3095	4	CR858326
10	309.8	6.2	3775	4	CR627381
11	308	6.2	891	5	BU174155
12	307.2	6.1	5797	4	CR749233
13	307	6.1	1654	4	CR591354
14	306.6	6.1	777	8	DR761502
15	306.6	6.1	832	5	BU180590
16	305.2	6.1	935	5	BU838401
17	303.2	6.1	910	5	BQ722917
18	301.8	6.0	627	6	CD702127
19	301.2	6.0	1805	4	CR860521
20	301.2	6.0	1863	4	CR599842
21	300.6	6.0	946	5	BQ958903
22	300	6.0	820	5	BU568843

C 96	269.8	5.4	1036	3	BQ070834	AGENCOURT
C 97	269.6	5.4	763	8	CX871744	HESCA_60
C 98	269.9	5.4	5155	4	BX648923	Homo sapi
C 99	268.8	5.4	753	1	AL691690	DKFZp313B
C 100	268.8	5.4	823	9	BZ608535	WHACA90TR
C 101	268.8	5.4	1108	3	BM065595	AGENCOURT
C 102	268.6	5.4	3179	4	AL832834	Homo sapi
C 103	268.4	5.4	923	6	DS18127	AGENCOURT
C 104	268.4	5.4	8488	4	CR933654	Homo sapi
C 105	268	5.4	704	5	BU677563	UI-CF-ECO
C 106	267.8	5.4	586	1	AL701696	DKFZp68D
C 107	267.8	5.4	697	5	BU930659	AGENCOURT
C 108	267.8	5.4	3146	4	BC036603	Homo sapi
C 109	267.8	5.4	6181	4	AL832201	Homo sapi
C 110	267.4	5.4	613	6	CD709038	EST25565
C 111	267.4	5.4	646	10	AG157592	Pan trogl
C 112	267.4	5.4	3287	4	CR858848	Homo sapi
C 113	267.4	5.4	5404	4	HSM808938	
C 114	267	5.3	858	5	BQ422295	AGENCOURT
C 115	266.8	5.3	722	9	AS93981	RPCI-11-4
C 116	266.8	5.3	766	3	BQ000089	UI-H-DP0-
C 117	266.8	5.3	2930	4	CR627462	Homo sapi
C 118	266.8	5.3	2930	4	AL390135	Homo sapi
C 119	266.6	5.3	6896	4	CR857559	Pongo pyg
C 120	266.2	5.3	802	8	CX786439	HESCA_60
C 121	266.2	5.3	988	3	BM905331	AGENCOURT
C 122	266	5.3	671	6	CD270132	1009099 H
C 123	266	5.3	877	6	CD515864	AGENCOURT
C 124	265.8	5.3	443	9	AQ164853	HS_2180_A
C 125	265.8	5.3	970	3	BM468547	AGENCOURT
C 126	265.8	5.3	1921	4	AF370377	Homo sapi
C 127	265.6	5.3	830	9	AQ897240	HS_3144_A
C 128	265.4	5.3	5157	4	CR857078	Pongo pyg
C 129	265.2	5.3	626	3	BM990577	UI-H-DP0-
C 130	265.2	5.3	820	6	CD653272	AGENCOURT
C 131	265	5.3	4087	4	BC024593	Homo sapi
C 132	265	5.3	4756	4	CR857077	Pongo pyg
C 133	264.8	5.3	622	5	BX505562	DKFZp688P
C 134	264.8	5.3	788	3	BM013486	603638941
C 135	264.8	5.3	835	5	BU933013	AGENCOURT
C 136	264.8	5.3	3804	4	HSM802182	
C 137	264.6	5.3	600	5	BX507478	DKFZp686A
C 138	264.6	5.3	680	9	AQ356404	CITBI-E1-
C 139	264.6	5.3	1345	1	AV762220	AV762220
C 140	264.6	5.3	3204	4	CR858951	Pongo pyg
C 141	264.6	5.3	4071	4	AL833113	Homo sapi
C 142	264.4	5.3	714	8	CR872940	HESCA_74
C 143	264.4	5.3	729	6	CF127074	UI-HF-ET0
C 144	264.4	5.3	778	1	AV764490	AV764490
C 145	264.2	5.3	872	9	BZ608878	WHABK92TR
C 146	264.2	5.3	910	5	BQ681678	AGENCOURT
C 147	264	5.3	1033	3	BM456793	Homo sapi
C 148	263.6	5.3	712	6	CF146965	UI-HF-C80
C 149	263.6	5.3	3466	4	AL832055	Homo sapi
C 150	263.4	5.3	857	9	AQ896568	HS_3134_A

ALIGNMENTS

RESULT 1	BU785306	599 bp	mRNA	linear	EST 11-OCT-2002
LOCUS	in43909.y1	HR85	islet	Homo sapiens	cdna clone IMAGE:6125008 5'
DEFINITION	similar to SW:PA21_HUMAN P04054 PHOSPHOLIPASE A2 PRECURSOR ; mRNA sequence.				
ACCESSION	BU785306				
VERSION	BU785306.1	GI:23831050			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				

REFERENCE	Hominidae: Homo.
AUTHORS	1 (bases 1 to 599) Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, L., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y., and Bowers, Y. Endocrine Pancreas Consortium Unpublished (2003) Other ESTs: in43909.x1 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138 Tel: 617-495-1812 Fax: 617-495-8557 Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu) Seq primer: -40RP from Gibco High quality sequence stop: 448. Location/Qualifiers 1..599 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6125008" /tissue_type="Purified pancreatic islet" /lab_host="DH10B" /clone_lib="HR85 islet" /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
FEATURES	source
Query Match	10.4%; Score 520.2; DB 5; Length 599;
Best Local Similarity	98.7%; Pred. No. 3.7e-34;
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QY	1821 AAAATGATCAAGTGGTGGTATCCCGGGAGTACCCCTTTTGGAAATACAAACATACGCG 1880
Db	70 AAAATGATCAAGTGGTGGTATCCCGGGAGTACCCCTTTTGGAAATACAAACATACGCG 129
QY	1881 TGCTACTGTGGTGGCGGCTCAGGCACCCCGCTGGATGAACCTGGAAGTAACTGATC 1940
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Db	250 ACGAGGCATACAAAGGGGACTTGCATATCTGCTAAGGATAACATATTTTCACTCTTGTC 309
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 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.
 REFERENCE 1 (bases 1 to 507)
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kastner,K.,
 Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,
 Williams,T., Jackson,Y. and Bowers,Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Dr. Hiroshi Inoue
 (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 443.

FEATURES
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 /clone_lib="HR85 islet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site 1:
 NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
 Size selected on agarose gel. Average insert size ~1kb. 5'
 XhoI site was destroyed after directional cloning.
 Amplified once. Contact information: Hiroshi Inoue, MD,
 Metabolism Div. (Alan Permutt Lab), Washington University
 School of Medicine, Box 8127, 660 South Euclid Ave., St.
 Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
 314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 10.1%; Score 505.4; DB 5; Length 507;
 Best Local Similarity 99.8%; Pred. No. 6.7e-33;
 Matches 506; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 QY 4066 TAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCGCAGAGAAATACAC 4125
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 genomic survey sequence.

ACCESSION AQ017732
 VERSION AQ017732.1 GI:3196468
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homnidae; Homo.

REFERENCE 1 (bases 1 to 349)
 AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
 Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
 Simon,M. and Venter,J.C.
 TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
 Building (1998)

JOURNAL Unpublished (1998)
 COMMENT Other GSSs: CIT-HSP-2308L15.TF
 Contact: Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: mdamas@tigr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page:
 http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.
 Location/Qualifiers
 1..349
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FEATURES
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ACCESSION  AL713681
VERSION    AL713681.1 GI:19584382
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1 (bases 1 to 3990)
            Ansoorge,W., Krieger,S., Regiert,T., Rittmueller,C., Schwager,B.,
            Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
            Wiemann,S.
            The German cDNA Consortium
            Direct Submission
            Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
            Neuherberg, GERMANY
            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by EMBL (European Molecular Biology Laboratories,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp76100217) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp76100217
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
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RESULT 7
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ACCESSION AL708471
VERSION AL708471.1 GI:19691826
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 347)
AUTHORS Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
TITLE EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp686J1752) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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/db_xref="taxon:9606"
/clone="DKFZp686J1752"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686" (synonym: hlcc3)"
/note="Vector: pTriplex2; Site_1: SfIA; Site_2: SfIIB;
cDNA-collection"
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Query Match 6.7%; Score 334; DB 1; Length 347;
Best Local Similarity 99.1%; Pred. No. 1e-18;

COMMENT	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd., Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp469P012) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering: http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp469P012 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/. Location/Qualifiers 1. .3095 /organism="Pongo pygmaeus" /mol_type="mRNA" /db_xref="taxon:9600" /clone="DKFZp469P012" /tissue_type="kidney" /clone_lib="469 (synonym: pkidl). Vector pSport1_Sfi; host DH10B; sites SfilA + SfilB" /dev_stage="adult" /note="hypothetical protein (Homo sapiens)" 1. .3095 /gene="DKFZp469P012" 120. .533 /gene="DKFZp469P012" /codon_start=1 /product="hypothetical protein" /protein_id="CAH90562.1" /db_xref="GI:55727614" translation="MLSGRLVPLVSMAGRVLCQGSAGSAGVPEVAIRTKLEQAL SEVLELNESGGHVPVPSGTHFRVAVSSRFGLSPLOHRHLIHAALABELAGPVH ALAIQARTPAQWGENSOLDTSPPLGGNKTLTGP"					Db	2047	GAGTTTTCCTCTGTTGCCAGACTGGAGTGCATGGCCCCAATCTCAGCTCACTCAACACC	2106
FEATURES	source	Qy	3544	TCTGCCTCCCGGTTCAAGYGATTCTCTCCCTAAGCCTCCTGAGTAGCTGGAAATTACAA	3603				
		Db	2107	TCCGCTCCAGGTTCAAGCAATTTCTCTGCTCAGCCTCCGAGTAGCTGGGATTACAG	2166				
		Qy	3604	CGGTGCACCACTGCTTGGCTAAATTTTTTGTATTTTGTAGCAGAGATGGGTTTTACCAT	3663				
		Db	2167	GCTCCTGCGACCATGCGCTGGCTAA-TTTTGTGTATTTTGTAGTGAGACAAGGTTTCATCAT	2225				
		Qy	3664	GTTGCCCGAGGTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAA	3723				
		Db	2226	ATTGGTCAGGTGGTCTCAAACTCCTGACCTCAAGCATCGGCTCGGCTCAACCTTCCAA	2285				
		Qy	3724	AGTGTCTGGAATATATAGGCGTGAGTCACTGTGCTCGCTGGCC-GATTACTGTCTATTTTCTTTA	3782				
		Db	2286	GTTGCTGGGATTACATGCGTGAGCCACACACCCGCGCTGCTTTAAACATATATCTTGACCA	2345				
		Qy	3783	TTGCTATATCCCCAGATCTAGACAGTGTCTGTACATATAGTAGGTGCTCAATAAATAATT	3842				
		Db	2346	TTTCTAGCTGAAGAATTTAAGGTGCTATGGTTGGCGAGTAGGGAGTCAATTGACAAATTTT	2405				
ORIGIN	gene	Qy	3843	GATGAATGCACAGCCTAGATATAAATCTTCTTTTCTTTTAAAAACAATCTTGACAAC	3902				
	CDS	Db	2406	TGAGTACAGACATGCCAGAGAGCA-----TTTGGGGCGAGATGGATCTGGCAGT	2454				
		Qy	3903	TTTGCAGAAATAACAATCTTTCATTTCTGCTTTTTCACCTTATCACCTCTTTATGACTTTT	3962				
		Db	2455	GATGTGTGAGTGAATTGGCATGGGAGGTGGAGGACAGAGATCAATCCAGAGTGAAGGT	2514				
		Qy	3963	TTTCATATTTGCTCAAACTTTATTTGTTACTGTGTTTTTTCATTTGTTTACTATTTTATGCTG	4022				
		Db	2515	AGAAACCTTGACTTACAAAGTCATCTGTGGGAATGGAAGAAGAGGTTTATTTTGAGAGCTA	2574				
		Qy	4023	AATAATATGGCTTAATTTGGCTTATACATCTCTCTGCTCCACTTTTAGAAGGCCAAATTTAC	4082				
		Db	2575	CCATAAGTTCAGAAATATGGTTTGTATGGAAACAGAAATGGACTAGAGGGGAGTCAATGG	2634				
		Qy	4083	AAATCTGATGAAAGCTATGAACCTCTCTCCCAGAGAAATACACACACACACACTCA	4142				
		Db	2635	TA-----ACCCC	2641				
		Qy	4143	CACACAGTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTTG	4202				
		Db	2642	AAGGCAGTGGTTTTTCAGATTTTCTCAGGTAAAGAGCTCCCATAGAGATTG-----	2691				
		Qy	4203	TTCATATTAATTAATAATACTCAGTTGGGCAACAGTCACTCAAGCCTGTAAACACACAGTAC	4262				
		Db	2692	-----TTTAAATAATGAAGCTTCTGGCTGGGTGTGGTGGCTCACACCTGTAAATCCCAGCAG	2745				
		Qy	4263	TTTGGAGTCCCAAGGTGGGTGGATCACTTCAGGTGGAAGTTCGAGACCAAGCCTGGTCAA	4322				
		Db	2746	TTTGGAGGCCATGGCAGGCGGATTTGGTGAAGTTCAGAGTTTCAGACCAAGCTTTGGGCAG	2805				
		Qy	4323	TATGGTGAACCTTATCTCTACTAAAAATAACAAAAATTTAGCTGGGTGTAGTGTATGATGC	4382				
		Db	2806	CATGGTGAACCGGTATCTC-ACTAAAAATAACAAAAATTTAGTTGGGTGTGGTGGCAGCCAC	2864				
		Qy	4383	CTGTAGTCCCAGCTACTCGGGAGGCTGAGGACAGAGAAATTTGCTTGAACCTGGGAGGCAGA	4442				
		Db	2865	CTGTAATCCCAGCCTCTTTAGGCAGCTGAGGCAGAGAAATCACTTTGAACCTGGGAGGCAGA	2924				
		Qy	4443	GTTTCAGTGTAGCCAGATCCACCACTGCACCTCCAGCCTGGCGCACACAGCCAGACTCT	4502				
		Db	2925	GTTTCAGTGTAGCCAAAGATCAGCCACTGCACTCCAGCCTGGGCAACAAAGTGAACCTCT	2984				
		Qy	4503	ATCTCAAAAAATAATAATAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTC	4562				
		Db	2985	GTCTCAAAAAAATAATAATAATAAAGGATCGGAGAGAAACAAAACTAATAAGATTC	3044				
		Qy	4563	C 4563					
		Db	3045	C 3045					

[illegible]


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QY 3405 GCTACTTATTCTTTTACATTCATCTTCCAAATAGAATGTAAGATCCACAGACAGGAT 3464
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Db 4685 GCTTTTCTTTCTTTCTT-----TTTGAGATGGAGTGTCCTCTCT 4648

QY 3465 TACTGCTCATTTCTTCTCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTC 3524
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4647 CACCCAGGCTGGAGTCAGTGGTGCTAT----- 4620

QY 3525 CGTTAGCTCACTGCAACCTCTCCCTCCGGGTTCAAGYGAATTCCTCTCGCTAAGCCTCC 3584
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4619 --CTCAGCACACTGAAACCTCCACCTCCAGGTTCAAGGCAATTCCTCGCTCGGCTTCC 4562

QY 3585 TGAGTAGCTGGAATACAGCGTCGACCACTGCTTGGCTAATTTTGTATTTTGTAGC 3644
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Db 4561 CGAGTAGCTAGGAATAC--GGGTGCACCACTGACCCAACTAATTTTGTGTGTTT----- 4508

QY 3645 AGAGATGGGGTTTTTACCATGTTGCCAGGCTGCTCTCAAACCTCCTGACCTCAAGTGATCT 3704
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4507 -AGTAGAGAGTTTACAAATGTTGGTCAGGCTGGTCTTGAACCTCTGACCTCA--TGATCT 4451

QY 3705 GCCTGCTCAGTCTCCCAAGTCTCGAATATAGCGGTGAGTCACTGTGCGCTGGCCGAT 3764
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4450 GCCCGAGCTCACCTACCAAGTCTCGGATTTACAGGCATGAGCCACTGGGTCCAGCCCA- 4392

QY 3765 TACTGTCTATTCTTTTATTGCTATATCCCAGATCTAGAGCAGTGTCTGACATATAGTA 3824
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4391 -----TATCTATTATTTCTGTAATAATTTTATTATGACATATAAAATCACCTGTA 4337

QY 3825 GGTGCTCAATAAATAATGATGAATGCAGCCTAGATATAAACTTTCTTTTCTTTT 3884
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Db 4336 GTCAATTACAAATTAATTGGACATTTAAAG--TAACATAAGTGATAAATTACACTGTT 4279

QY 3885 TAAAACAATCTGCACAACTTTGCAGAAATAATACAACTCTGCAATTCGTCTTTTCACTTA 3944
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Db 4278 TGGAATAGAAAGATAAATGCTAGAGGTGATAGATACCTTATTATCCCTAAATGTAATTAC 4219

QY 3945 TCACCTTGTGTATGACATTTTTCATATTG-----CCTCAAACCTTTATGTTACTGTTTTT 3999
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Db 4218 TACATATTGATGCGCTGAATCAAAATATTCTCTATAAGACATATATACACTACTATATA 4159

QY 4000 CATTTGTACTATTATTAGTCACCTGAATAATATGSCCTT---AATTGGTTTATACATCTCTCT 4056
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4158 CTCACAAATAGTAATAATAAATTAAGAAAAAGATTAAAAAATTAACATAACGGGAACAAT 4099

QY 4057 GCTCCACTTTAGAGGCCAAATTTACAATCTGATCAAAAGCTATGAACCTCTCCCCACA 4116
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4098 ATTCTTCAATTGCGATTTTCTGCAAAAGTGATTACTAGTGATGACATTCCACTACATACC 4039

QY 4117 GAAATACACACACACACACTCACACAGTTTTTTTTTTTAATG----- 4162
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4038 AATAGTATACTTCTTCCATCTTTTGGTTACACCAATTTGATGAAGCCGGATAGGTTAA 3979

QY 4163 -----TTTGCAACTAAGACAAGAAACCTGCAATTAGAGGATGTTGTTTCATATTAAATTA 4216
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3978 GTTAGTGGCGCTAATAATGCTTCAATTAATGCACAATAGTTTTAAGATGCAAAAAATAAA 3919

QY 4217 AATAACTCAGTTGGCGCAGTCACTCAAGCCTGTAACACAGTACTTTTGGAGTCCAG 4276
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3918 ATAAAAATTAGCTGGACATATTGGCTCACACCTTATAATCCCAACTTTTGGAGAGCCCGAG 3859

QY 4277 GTGGGTGGATCACTTGAGGTGAGAAAGTTCGAGACCAAGCCTGGTCAATATGGTGAAACCTT 4336
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Db 3858 GTGGGTGGATCGTTGAGCTCAGAGTTTGGAGACTAGCCTGACCAATATAGGGGAACCC 3799

QY 4337 ATCTCTATAAAAAATACAAAAATTAGCTGGGTGATGATGATGCTGTAGTCCAGCT 4396
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Db 3798 ATGTCTATAAAAAATATAAAAAATAGCCAGGCGTGGTGTCAAGCACTGTAGTCCCACT 3739

QY 4397 ACTCGGGAGCTGAGCGCAGAGAAATGCTTGACCTGGGAGCGAGGTTGGAG-----TG 4452
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3738 ACTCGGAGGCTGAGGAGAGAAATTTCTTGAACCTTGGGAGGTGGAGTTGCAGTCAATTG 3679

QY 4453 AGCCGAGATCCCACCTGCACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAA 4512
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Db 3678 TGCTGAGACTGCAGCTGCTGCCCTCAGCCTGGGTGACAGCAAGACTCCATCCCAAAG 3619
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4513 AATAAATAAATAAATAAAGGATCGGAGAGAAACAAAACATAAAGATTCTCGAAGGTAA 4572
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3618 AAAAGTTAAGTAAATAAATAAATAAGTTAAGTTTCAACATAAATCTAAACAATTTTAAATAT 3559
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4573 GCAGAGATACGTAATTTATATGTAATAAGTTTAAATGCAATTTAACTGTAATCTTATTG 4632
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3558 ATTGCATTTTATTACGTAAACAGTAAAAATAGTAAAAAATAATTGATATACTTTAATTTATAA 3499
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4633 TTTATTTTGGTTATAAAAAGTAAACAA 4658
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3498 TTTCTTTCTCTCAGTATATGTAGAA 3473
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
CR591254 1654 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DF001YF08 of Fetal brain of Homo sapiens
DEFINITION (human).
ACCESSION CR591254
VERSION CR591254.1 GI:50472061
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1654)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope 2 (bases 1 to 1654)
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source 1..1654
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF001YF08"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"
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ORIGIN

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Query Match 6.1%; Score 307; DB 4; Length 1654;
Best Local Similarity 72.0%; Pred. No. 6.3e-17;
Matches 450; Conservative 0; Mismatches 155; Indels 20; Gaps 3;

QY 477 ATTTTACTTTTATTTTATTTTGGAGCGGGCTCACTCTGTGCGCCAGGCTGGAGTGGCT 536
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 394 ACTTTTATTTTATTTTATTTTGGAGCGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGT 453
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 537 GCGGTGATCTCAGATCACTACAACCTCCATCTCTCGGGTTCAAAATAATTTCTTCCCTCA 596
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 454 GCGCGATCTCGGCTCACTGCAAGCTCGCCTCTCGGGTTCAAGCAATTTCTCTGCCTCA 513
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 597 GCCTCTCAAGTAGTGGGACTTTAGCTCTCAAGTAGTGGCACACACACCATGCCAG 656
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 514 GCCTCCCAAGTAGTTCGGACT-----ACAGGCGTCTCCACCATGCCTGG 558
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Db 1542 TGTAAGTGGTCAATCTCAGCTCACTGCAACATCCATCTCCGGATTCCACTTTATCTCTC 1483
Qy 3218 ACCTAGCCTCCCAAGTAGCTGGACTAGAGCGTGCACACGCGCTGGCTAATAA 3277
Db 1482 GCTCAGCCTCTCAGTAGCTGGATATAGGGTGCCTGCATAATAGCCCACTCAATTTT 1423
Qy 3278 AAAATTTTTTTGAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAAACTCCTGG 3337
Db 1422 GTA--CTTTTAGTAGACGGGTTTCCACCATGTTGGCCAGGCTGTCTCAAACTCCTGG 1365
Qy 3338 CTTCAAGCAATCCTCTACTCTGGCATCCAAAGTCTGGATATCAGGGGTGAGCCACC 3397
Db 1364 CTTCAAGTATCCACCTGCTTGGCTCCCAAGTCTGGATATCAGGTGTGACCACTG 1305
Qy 3398 ATGTGGGGTACTATTCTTTACATTCATCTTCCATAGATGTAAGATCCACAGAA 3457
Db 1304 CACCTGGCTGAATTTCTCATTTCTCCCA-----CACACCGCTCAGGTTCTCTTCC 1250
Qy 3458 CAGGGAATTAATCTTCTTCTTCTTTTGGAGACAGAGTCTCACTTCATCACT 3517
Db 1249 TGATCATTCAGCGTTTCTTTTCTTTTGGAGACAGCATCTCACTGTCTCACCC 1190
Qy 3518 CAACCTCCGTTCA-----GCTACTGCAACCTCTGCTCCCGGGTTCAGAGY 3563
Db 1189 AGACTGGAGTGCAGTAGTGAATCTTTGGCTCACTGAAACCTCTTCTCCAGCCTCAAGC 1130
Qy 3564 GATTCTCCTGCTTAAGCCTCCTGAGTAGCTGGAATTTACAGCGTGCACACCATGCTGG 3623
Db 1129 GATTCTCCTGCTCAGCCTCCGAGTAGCTGGATTTACATGTGTGCACCATTAACACCCA 1070
Qy 3624 CTAATTTTTTGTATTTTGGAGAGATGGGGTTTTTACCATTGTGGCCAGGCTGGTCTCAA 3683
Db 1069 GATAATTTTGTACTTTTAGTAGAGATGGGTTTGACCATATTGGCCAGACTGGTCTTGA 1010
Qy 3684 ACTCTGACTCAAGTAGTCTGCTGCTCAGTCTCCCAAGTGTGGAATTTATAGGGT 3743
Db 1009 ATTCTGACTCAGGTGATCCGCCACCTCAGCCTCCCAAGTGTGGGGTTATAGGGCT 950
Qy 3744 GAGTCACTGTGCTGCGCGATTACTGTCTATTCTTTAT 3783
Db 949 GAGCCACTGCACCGCGCCCTTCTTCACTTAGTCAAT 910

RESULT 20
CR599842
LOCUS
DEFINITION
CR599842 1863 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DA002Y006 of Neuroblastoma of Homo
sapiens (human).
ACCESSION
CR599842
VERSION
CR599842.1 GI:50480649
KEYWORDS
HTC; CNSLT cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1863)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
JOURNAL
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE
2 (bases 1 to 1863)
Genoscope.
Direct Submission
AUTHORS
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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division of Invitrogen.
FEATURES
source
1. 1863
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA002Y006"
/tissue_type="Neuroblastoma"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 6.0%; Score 301.2; DB 4; Length 1863;
Best Local Similarity 56.9%; Pred. NO.1.7e-16;
Matches 811; Conservative 1; Mismatches 509; Indels 105; Gaps 10;
Qy 3124 GAGCAGGGTCTTGCTGTCTCAGCCAGGATGAGCAGAGTGGTGCACCATAGGTCACTG 3183
Db 496 GGGTCAGAGTCTCACTCTGTTTCCAGGCTGGAGTTCTGTGGCACCGTGTGGTCACTG 555
Qy 3184 CAGCCTCAACCTCTCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGAG 3243
Db 556 CAACCTCGCTCTCTGGGTTCAAGCAATCTCTTGGCTCAGCCTCCAGAGTAGTGGAT 615
Qy 3244 TACGAGCGTGCACCAACCAAGCTGCTTAATAAATTTTGTAGAGACTGGGTCT 3303
Db 616 TACAGGTGCCACCAACCAACCGGCTAAATTTTATATTTTAGTAGACACGGGTTT 675
Qy 3304 TACTAGCTTGGCCAGGCTTGTCTTAACTCTGCTTCAAGCAATCTCTTCACTTGGCA 3363
Db 676 CACCATGTTGGCCAGGCGGCTTTGAATCTGTGAGTGTGACGTCAGGTGACCCGCTTGGCC 735
Qy 3364 TCCAAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTTATTTTACAT 3423
Db 736 TCCAAAGTGTGGGATTACAGGTCCAGATTTTGAACAAATCTCGCTAGAGATTGAACAG 795
Qy 3424 TCCATCTTTTCCAATAGAAATTAAGATCCAGAGACAGGGATTTACTGCCTATTTTCTCT 3483
Db 796 AGCTGCGCTGGATCCCGCCACAGTGAGGAGACCTGAAAGACAGAGAAACACAGCAAC 855
Qy 3484 TTCCTTTTGGAGACAGATCTCACTTCACTCACTCACTCGGTTCAGTCACTGCAAC-C 3542
Db 856 GGAGTCTTGTCTGTGTTCAGGCTGGAGTGTAGTGGCGATCTCGGCTCCCTCAAGA 915
Qy 3543 CTCTGCTCCCGGGTTCAAGYATTTCTCTGCCTAAGCCTCTCGTAGTGTGGAATTACA 3602
Db 916 ATCTGCTCCAGATTCAGGCCATTTCCACACTCAGCCCTGGAGTAGTGGAGTAGACA 975
Qy 3603 AGCGTGACCAACCATGCTTGGCTAAT----TTTTGTATTTTGTAGCAGAGATGGGGTTT 3658
Db 976 GGCTCCCGCCACCAACCGCTGCTAATTTTGTATTTTGTATTTTGTAGTAGAGACGGGTTTC 1035
Qy 3659 ACCATGTTGCCAGGCTGCTCAAACTCTGACCTCAAGTGTGCTGCTGCTGCTGCTGCT 3718
Db 1036 ACTGTTTGTAGTAGAGTGTCTCGATCTCTGACCTCA--TGATCCATCCGCTTGGGCT 1093
Qy 3719 CCCAAAGTGTGGAATTATAGCGTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3778
Db 1094 CTCAAAGTGTGGGATTACAGGCATGAGCCACCGCACCTGGCTG-----TTTT 1141
Qy 3779 TTTATTGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGTGTGCTCAATAAT 3838
Db 1142 TTCATTTCTATATGATTTTCTGTGGAATGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1201
Qy 3839 AATTGATGAATGCACAGCTAGATATAAACTTTCTTTTCTTTTAAAAAACAATCTTGA 3898
Db 1202 TTTATAAAGCTGAATAGTGTCTGTATGTGACGACCCCTAGTGTGAGTGTGAGTGTGAGT 1261
Qy 3899 CAACCTTTCAGAAATAAATAAATACTTGTGATTTTGTGCTTTTTCACCTTATCACCTTGTATGA 3958
Db 1262 CTCCTGTGTGATAGATGGGGGCTGTCCACACCCCAATCTCTGGGTTCCCGCTGCC 1321
Qy 3959 CTTTTCATATTTGGCTCAAACTTTATTTGTACTGTTTTTTCATTTTGTACTTATTTTATGTC 4018
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Db 1322 GCACCTGAAGGTACCCACAGAGTGTCTGTCTCACTGCCCTCCATCCACCTTTCTTGTGTGT 1381
QY 4019 ACTGAATAATATGGCTTAATTTGCTTATATACATCTCTCTGCTCACTTTTGAAGGCCAAAT 4078
Db 1382 TCTCATGTTTCTGCTCTC-----CCTAGAGACCAATTTCTCTCTACAGCAGTAG----- 1428
QY 4079 TTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAAATATACACACACACACACA 4138
Db 1429 -----TTTCCATAGAAATATACATCCAGACACAT 1459
QY 4139 CTCACACACAGTTTTTTTTTAATGTTTGAACCTAAGACAAGAACCTGCATTAGAGGATG 4198
Db 1460 C-----GTCAATTTAGATTTCTAGTAGTCACTTTTAGAAAAGCTGAAAAGAGGCCA 1510
QY 4199 TTTGTTTCATATTAATTAATAATACTAGTTGGGCACAGTCAAGCTGAACCTGAACCCACA 4258
Db 1511 GCTG-----CACTGGCTCACACCTGTAATCCCA 1538
QY 4259 GTACTTTGGAAGTCCAAGTGGGTGGTCACTTTGAGGTGAGAAAGTTTCGAGACACAGCCTGG 4318
Db 1539 GCATTTTGGNAGGCTGAGTGGGTGGATCAC--GAGGTGAGNGATCGAGACCATCTCTGG 1596
QY 4319 TCAATATGTTGAACCTATCTCTACTATAAAATAC--AAAAATTTAGCTGGGTGTAGTATG 4377
Db 1597 CCAACATGTTGAACCTCTCTCTACTAAAAATACAAAAATTTAGCTGGGTGGTGGCA 1656
QY 4378 CATGCTCTAGTCCAGCTACTCTGGGAGCTGAGGCAAGAGAAATGCTTGAACCTGGGAG 4437
Db 1657 GCGCCTGTAGTCCAGCTACTCTGAGAGGCTGAGGAGGAGAAATGCGCTGAACCTGGGTAG 1716
QY 4438 GCAGAGTTTGCAGTGAGCGGAGATCCACCACTGCACCTCAGCCTGGGCGACACAGCGAG 4497
Db 1717 GCAGAGCTTGCAGTGAGCGGAGATGCGGCACCTGCACTCAGCCTGGGCGACAGAGGAG 1776
QY 4498 ACTCTATCTCAAAAAATAAATAAATAAATAAAGGATCGGAGAGA 4543
Db 1777 ACTCCATCTCAAAAAATAAATAAATAAAGGTTACAAAGAAACAGGTGAAA 1822

RESULT 21

BQ958903
LOCUS BQ958903 946 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_10035485 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6483214
5', mRNA sequence.

ACCESSION BQ958903

VERSION BQ958903.1 GI:22374381

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

1 (bases 1 to 946)

NIH-MGC <http://mgi.nhl.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabbs@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2667 row: 9 column: 23

High quality sequence stop: 534.

Location/Qualifiers

1..946

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6483214"

FEATURES

source

/tissue type="carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"

/note="Organ: prostate; Vector: pOTB7; Site: 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match	Score	300.6;	DB 5;	Length	946;	
Best Local Similarity	69.1%;	Pred. No. 3e-16;	Indels	11;	Gaps	4;
Matches	468;	Conservative	1;	Mismatches	197;	
QY	3096	AGTTTGGGTTTTTTTTTGTGTTTGTAGACAGAGGTCCTGTGTGTCACCCAGGCATG	3155			
Db	24	AGNTTTTTTTTTTTTTTTTTTTTTTTTGACACAGAGTCCTGTGTGTCACCCAGGCTGG	83			
QY	3156	AGCAGAGTGTGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGC	3215			
Db	84	AGTGCAGTGGTG---CGATCGCTCACTGCAACCTCAGCCTCTGGATTAAAGTGATCTC	140			
QY	3216	TGACCTCAGCCTCCCAAGTAGCTGGGACTAGAGCGTGACACACACCCCTGGCTAAATTA	3275			
Db	141	CTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGTGTGCACACCATGCCCCGGCTAATTT	200			
QY	3276	AAAAAATTTTTTTGTAGAGACTGGGTCTTACTAGTTGGCAGGCTGTCTTAAACTCCT	3335			
Db	201	TTTTGTATTTTGTAGTGAGACAGAGGTTTTCACCATGTTGCCAGGCTGTCTCGAACTCCT	260			
QY	3336	GGCTTCAAGCAATCTCTCTACTTTGGCATCCCAAGTCTCTGGATTACAGGCGTGAGCCA	3395			
Db	261	GACCTC--GTATCGGCTGCTCAGCCTCCCAAGTCTGGGATTACAGGTTGAGCCA	318			
QY	3396	CCATGTGGGCTACTTATTTCTTTACATTTCCATCTTTCCAATAGAATGTAAGATCCACAG	3455			
Db	319	CCACGCTGGGCCCCAGTCCAAAATATTTAAAGATTGTTTCTCTAGTGTCTTGAAGTTTG	378			
QY	3456	AACAGGGATTACTGCCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACTTCAATCAC	3515			
Db	379	CACA-----AAATCTTTTTTGTAGATGGAGTCTCACTGTCAACCCAGGCTGGAGTGC	433			
QY	3516	CTCAACCTCCGTTCACTCACTGCAACCTCTGCTCCCGGTTCAAGYATTCTCCTGCC	3575			
Db	434	AGTGGCGTGTCTTTGGCTCACTGCAACCTCTGCTCTGGGTTCAAGCAATTTCTCCACC	493			
QY	3576	TAAGCTCTCTGAGTAGCTGGAATTAACAAGCGTGACACCATGCTTGGCTAATTTTTTGT	3635			
Db	494	TCAGCTCCCAAGTAGCTGGGATTACAGACGTGTGCCACCATACCTGGGTAATTTTTTGC	552			
QY	3636	ATTTTGTAGACAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTGACCTC	3695			
Db	553	ATTTTGTAGGAGAGGAGTTTCAACCATGTTGGCAGGCTGCTTGAACCTCTGACCTC	612			
QY	3696	AAGTATCTGCTGCTCAGTCTCCCAAGTCTGGAATTAAGCGTGAGTCACTGTC	3755			
Db	613	AGGTGATCTCTGCTGCTGCTCCCAAGTCTGGAATTAAGCGTGAGTCACTGTC	672			
QY	3756	CTGGCCGATTAATCTGTCT 3772				
Db	673	TCAGCCGCANAAATTCCT 689				

RESULT 22

BUS68843/c
LOCUS BUS68843 820 bp mRNA linear EST 16-SEP-2002
DEFINITION AGENCOURT_10400218 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6616116
5', mRNA sequence.
ACCESSION BUS68843
VERSION BUS68843.1 GI:22919143

Db	2922	CTCAGGCTCCGAGTAGCTGGGACACAGTGCCTCCGACACCGCCGCTAATTTTTT	2863
Qy	977	GTATTTTAAAGACGGGGTTTCATCGTGTAGCCAGGATGGTCTCGATCTCATGACC	1036
Db	2862	GTATTTTGTAGAGACGGGGTTTACCGGTGTAGCCAGGATGGTCTCGATCTCTGACC	2803
Qy	1037	TTGTGATCCGCTCGCTCCGCTCCCAAGTGTCTGGGATACAGGATGAGCACCCTGC	1096
Db	2802	TCATGATCCGCTCGCTCCGCTCCCAAGTGTCTGGGATACAGGATGAGCACCATGC	2743
Qy	1097	CGGGCTTATACATTTATTTATTTATTTATTTCTCCCACTAGTGTCTAAGCTCCATG	1156
Db	2742	CGGGCCACATCTGCTGTGTTCACATCATTTAACTAGGATTAAGATGTTGGCCAGC	2683
Qy	1157	AGGTTAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	1216
Db	2682	ACGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGCAGGTGGACCTGA	2623
Qy	1217	GTTCACTGCTGTATCTCTAGCTCTAGGACAGAGCCCTGGACATAGTAGTGTCTA-ATA	1275
Db	2622	GGTCAAGAGTTCAAGACCCAGCTGACTAATCATGGTGAACCCCATCTCTATTAATAATACA	2563
Qy	1276	AATATTCACTGGATAAACAGTCAGATAGTTTAAACTATCTGACCTAGGAGGCTGAGG	1335
Db	2562	NAGACATTAGCCAGGTGTAGTGGCGCATGCTGTATCCAGCTACTTGGGAGGCTGAGG	2503
Qy	1336	CAGGAGAAATGGGTGAACCCGGGAAGCAGAGTTTGCAAGTGAAGTGTCTCACTGC	1395
Db	2502	CAGGAGAAATGGTTGAGCCCGGAGGTGGAGTTGCAGTGAACCAAGATTGGCCACTGC	2443
Qy	1396	ACTCCAACTGGGCAAC-AGAGCAAGCTCCATCTCAAAAAAAAAAAAAAAAAAAAA	1446
Db	2442	ACTCCAGCTGGGCAACAAGAGCAAACTCTGTCTCAAAAAAAAAAAAAAAAAAAAA	2391
RESULT 30			
CX780936			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			

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/mol_type="mRNA"			
/db_xref="taxon:9606"			
/clone="IMAGE:30928759"			
/sex="male"			
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/cell_type="human embryonic stem cells"			
/cell_line="BG01"			
/lab_host="DH10B-T1 phage-resistant E. coli"			
/clone_lib="NIH_MGC_260"			
/note="Vector: pExpress-1; Site 1: NotI; Site 2: EcoRV; RNA obtained from human embryonic stem cells isolated from the inner cell mass of blastocyst stage embryos. Cell line id and NIH Registry designation is BG01. Positive for SSEA3, SSEA4, Tra 1-60, Tra 1-81, CD9, Alk Phos, Oct4 and Nanog expression; negative for SSEA1 expression. Passage number 21. cDNA primed using oligo-dT primer: 5'-pGATGATGTTAGATCGGAGCGGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. This primary library is non-normalized (normalized primary library is NIH_MGC_261). It was constructed by Express Genomics (Frederick, MD). Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Note: this is a Mammalian Gene Collection library."			
ORIGIN			
Query Match 5.9%; Score 293.6; DB 8; Length 736;			
Best Local Similarity 66.9%; Pred. No. 1.3e-15;			
Matches 464; Conservative 1; Mismatches 220; Indels 9; Gaps 3;			
Qy	3099	TTGGGTTTTTTTCTGTTGTAGAGACAGGGTCTGTCTGTCAACCCAGGCATGAGC	3158
Db	1	TTTTTTTTTTTTTTTTTTTGTAGATGAGTCTCCTCTGTGCCGCGCTGAAGT	60
Qy	3159	ACAGTGGTGAACCATAGTCACTGCAGCCCTCAACCTCCTGAGCTCAAGGGATCTGTGA	3218
Db	61	GCAGTGGCGGATCTCGGCTCACTGCAACCTCTGCTCTCTGGGTTCAAGCACTTCTTCTG	120
Qy	3219	CCTAGGCTCCCAAGTAGCTGGGACTACAGCGTGCACCACCGCTGGCTTAATAAAA	3278
Db	121	CTTCAGCCCCCTGAGTAGCTGGGATTACAGGCACCCACCCAGCCCTGGATACCTT--TT	178
Qy	3279	AAATTTTTTTGTAGAGACTGGGTCTTACTAGCTTGGCCAGGCTTGTCTTAAACTCCTGCG	3338
Db	179	TGTATTTTTTGTAGTAAATAGGGTTTGTCTATATTGGCCAGGCTGTCTCAAACTCCTGAC	238
Qy	3339	TTCAAGCAATCCTCTACTCTTGGCATCCCAAGTCTGGGATTACAGGGGTGAGCCACCA	3398
Db	239	CTCAGGTGATCCACCTGCCTAAGCCTGCAAGTCTGGGATTACAGGCATGAACCACCA	298
Qy	3399	TGTGGGCTACTTATTTCTTTACATTCCTCTTTTCCATAGATCTTTTCCATAGATCCAGAAC	3458
Db	299	TGCCAGGCTCTTATTTCTTTTAAATATATACAAAGTTATTTATTTATTTATTTATTTA	358
Qy	3459	AGGGATTACTGCCTATTTTCTTCTTTTGTGAGACAGAGTCTCACTTTCATCACCTC	3518
Db	359	TTTATTTATTTTGTAGATGGAGTTTGGCCCTTGTGGCCAGCTGGAGTCAATGGCAC	418
Qy	3519	AACCTCCGTTGAGTCACTGCAACCTCTGCTCCCGGTTCAAGYATTTCTCTCTGCTTAA	3578
Db	419	GATC-----TCAGTCACTCAACCTCCACCTCCCGGGTTCAAGTGATTTCTCTGCTCA	473
Qy	3579	GCCTCTGAGTAGCTGGGAATTACAGCGTGACCACTGCTTGGCTAATTTTGTATT	3638
Db	474	GCCTCTGAGTAGCTGGGATTACAGGCACATGCCATCATGCTCTGGCTAA--TTTGTCAIT	531
Qy	3639	TTTAGCAGAGATGGGGTTTTTACCATGTTGCCAGGCTGTCTCTCAAACTCCTGACCTCAAG	3698
Db	532	TTTAGTAGAGACAGAGTTTCTCCATGTTGGTCAGGCTGTCTTGAACCTCTGACCTCAGG	591
Qy	3699	TGATCTGCTGCTCAGTCTCCCAAGTCTGGGAATATAGCGGTGAGTCACTGTGCTGTG	3758
Db	592	TGATCTGCTGCTCAGTCTCCCAAGTCTGGGATTATAGGCATGAGCCACCGTCCCA	651

/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_181"
/note="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(destroyed); Library is oligo-dr primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 5.7%; Score 287; DB 6; Length 688;
Best Local Similarity 68.3%; Pred. No. 4.9e-15;
Matches 428; Conservative 0; Mismatches 195; Indels 4; Gaps 2;
QY 480 TTACTTTATTTATTTTGGAGAGCGGGCTCACTCTGTGCGCCAGGCTGGAGTGC-GGTGG 538
DB 682 TTTTATTTTATTTTTCAGATAGAGTCTTGTCTTGTGCGCCAGGCTGGAGTGCATATGG 623
QY 539 CTGTATCTCAGATCACTACAACTCATCTCTGGGTTCAAATAATTCCTTGGCTCAGC 598
DB 622 AGCAATCTTGGCTCAATGCAACTCTGCTTCCCTAGTTCAGCGATTCCTTGGCTCAGC 563
QY 599 CTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGCACACACCACCTGCCAGCT 558
DB 562 CTCTGAGTAGCTGGGATTACAGGCAAGCACCACGC---CTGGCTCATTTTGTATTTC 506
QY 659 AATTTTTCGTGTGTTTTTTTGGTAGACAGAGTGTTCACCATGTTGGCCAGGCTGGGTG 718
DB 505 AGTAGAGTGTTCATCATTTTGGCCAGGCTGTCTCGAACTCTCGACCTCAGATGATCCG 446
QY 719 ACTCCCTTTTATGATTCCTCATCTGCTCTATTCTTCCCTTTCTAATGAGATCA 778
DB 445 CCGGCTCAGCTGCCAAAGGGCTGGGATTACAGGCATGAGCCACCGTGCCCGGCTACT 386
QY 779 GTTTCCTTACTTATCATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 838
DB 385 TTTTCTTTTTCGTGTTTTTCTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 326
QY 839 GTCCGCAAGCTGGAGTACAGTGGTGGCATCTCGGCTCACTCGCAAGCTCCACTGCTGG 898
DB 325 GTTGGCCAGCTGGAGTGAGTGAGTGTGATCTTGGCTCACTCGCAAGCTCCGCTCCGG 266
QY 899 TTACGCCATTTCCGGCTCAGCTCCAGCTCCAGTAGCTGGGATTAAGGGCGCTGCCACA 958
DB 265 TTACACACATTTCTCTGCTCAGCTCCGAGTAGCTGGCACTACAGGGCGCGGCCACCA 206
QY 959 CCGCCGCTAAATTTTGTATTTTATTAAGACGGGTTTCATCGTTAGCCAGGAT 1018
DB 205 CGCCTGGCTAAATTTTGTATTTTATTAAGACGGGTTTTCATCGTTAGCCAGGAT 146
QY 1019 GGTCTCGATCTCATGACCTTGTGATCCGCTGCTCGGCTCCCAAGTGGCTGGGATTAC 1078
DB 145 GGTCTCAATCTCTGACCTGGTGTATCCGCTACCTCGGCTCCCAAGTGGCTGGGATTAC 86
QY 1079 AGGCATGAGCCACCGTGCCCGGCTTA 1105
DB 85 AGGTGTGAGCCACCGTGCCCGGCTTA 59

RESULT 40

HSM808459/c 4088 bp mRNA linear HTC 22-SEP-2004
LOCUS
DEFINITION Homo sapiens mRNA; cDNA DKFZp686I19131 (from clone DKFZp686I19131).
ACCESSION BX648311
VERSION BX648311.1 GI:34367470
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 4088)
REFERENCE
Bloecher, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B., Amid, C.,
Osanger, A., Fobo, G., Han, M. and Wiemann, S.

CONSRMT
TITLE

The German cDNA Consortium
Direct Submission
Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
Sponsored by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
This clone (DKFZp686I19131) is available at the RZPD Deutsches
Resourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp686I19131
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES

source

1..4088
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="RZPD:DKFZp686I19131Q"
/db_xref="taxon:9606"
/clone="DKFZp686I19131"
/tissue_type="uterus"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfiII + SfiIB"
/dev_stage="adult"
/note="unspliced mRNA, 5' and 3' truncated"

ORIGIN

Query Match 5.7%; Score 285.2; DB 4; Length 4088;
Best Local Similarity 56.9%; Pred. No. 2.2e-15;
Matches 619; Conservative 1; Mismatches 459; Indels 9; Gaps 5;
QY 3452 ACAGACAGGAGTACTGCCTATTCTCTCTCTTTTGGAGACAGAGTCTCACTCA 3511
DB 1504 AAAAAAAGCTGGTTTCAGGAATATTGATTTGTTGTTTGGAGATGGAGTCTCCCTTG 1445
QY 3512 TCACCTCAACCTCCGT----TCAGCTCACTCAACCTCTGCCTCCCGGTTCAAGYGATT 3567
DB 1444 TCGAGTGCAGTGGTGTGATCTCGCTCACTCGACCTCCGCTCCAGGCTCAAGCGATT 1385
QY 3568 CTCCTGCTTAAGCTCTCTGAGTAGCTGGAATATACAGCGTGACACCATGCTTGCTTAA 3627
DB 1384 CTCGCGCTCAGCCGCCGCGGCGGATCACAGGTGTGGCCACACACCCAGCTAA 1325
QY 3628 TTTTGTGATTTTGTAGCAGAGATGGGTTTACCATGTTGCCAGGCTGCTCAAACTC 3687
DB 1324 -CCTCTGATTTCTTAGTAGACAGGCTTCACCATGTTGGCCAGGCTGCTTGAACATC 1266
QY 3688 CTGACCTCAAGTGATCTCCCTGCCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGAGT 3747
DB 1265 CCGACCTCATATGATCCGCGGACCCAGCTCCCAAGCGTTGGGATTACAGCGCTGAGC 1206
QY 3748 CACTGTGCTGGCGGATTAATGCTATTTCTTTATTGCTATATCCCCAGAGTCTAGAGCA 3807
DB 1205 CACCACACTGGGCCCCAAGGCATTTATGTTTAATGTTCAATTTCCCTGGACATCCACATTC 1146
QY 3808 GTGTGTGACATATAGTAGGTCTCAATAAATAATTTGATGAATGCACAGCTAGATATAA 3867
DB 1145 ATGTTCTCTTTCGAGAAATGCTAAGAAATTTCTAAAAAGAAAGGAATGATT--ATGTAAA 1088
QY 3868 CTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTGACAGATAAATAACAATCTTGCA 3927
DB 1087 CATACCTAACTATGTCTAGTTAACTTAGGCAACAACACTAGTGCACCCAGTCAAAACAGAC 1028
QY 3928 TTCTGCTTTTTCATTAATCACTTGTGTTAAGACTTTTTCATATTTGCTCAAACTTTATG 3987
DB 1027 ATCAATAATCCATGGAGTAAAAATTCCTATACCTTTAGTAGAGGCTGCTGTTTACTC 968
QY 3988 TTACT-GTTTTTTCATTTGTTACTATTTTAGTCACTGATATATATGGCTTAATTTGCTTAT 4046
DB 967 CTCTAGCAGTTATAAATTTAATAAATCTAGTCTTCTACTTTCTAGTCTATATTAAATTA 908

This clone (DKFzp459D2020) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFzp459D2020>
Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

FEATURES
source

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1. .2128
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/mol_type="mRNA"
/db_xref="taxon:9600"
/clone="DKFzp459D2020"
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/clone_lib="459 (synonym: pcorl). Vector pSport1_sfi; host DH10B; sites SfiIa + SfiIb"
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/note="hypothetical protein (Homo sapiens)"
1. .2128
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20. .364
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ORIGIN

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Best Local Similarity 71.0%; Pred. No. 5e-15;
Matches 455; Conservative 0; Mismatches 160; Indels 26; Gaps 5;

Qy 478 TTTTACTTTATTTATTTTGTAGACAGGGGCTACTCTGTGCGCCAGGCTGGAGTGGGGTG 537
Db 2125 TTTTATTTTATTTTCTGTAGACAGAGTCTCACTCTGTGCGCCAGGCTGAAGTGCAGTG 2066

Qy 538 GGGTATCTCAGATCACTACACCTCCATCTCTCTGGTTCAATAATTTCTTGGCTCAG 597
Db 2065 GCATATTTTGGCTCTACTGCAACCTCCACTCCGGATTCAGTGATTTCTGCTCTAG 2006

Qy 598 CTCTCAAGTAGCTGGAGCTTGTAGCTCTCAAGTAGCTGGCCACACACACACATGCCACG 657
Db 2005 GCCCCCAAGTAGCTGGAGCT-----ATAGGCATGCACCATCACACCCAGC 1961

Qy 658 TAATTTTGTGTGTTTTTTTGTGTAGACAGAGTTTTCACCATGTGTCAGGCTGGGT 717
Db 1960 TAATTTTT-----GTATTTTGTAGTAGACAGGGTTTCATCATGTGTCAGGCTGGTC 1907

Qy 718 GACCTCCCTTTTAGATTTCTCTCATCTCTCTATTCTTCTCCCTTTCTAATGCAGTATCC 777
Db 1906 TGAATCTCTGACTTCAAGTAGATCTGCCACCTCCAGCTCCCAAGTAGTCTGGATTCAG 1847

Qy 778 AGTTTCTTTACTTATCACAATTTATTATTATT--CTTATTATTATTGAGACAGAGTCTTGC 835
Db 1846 GAGTAGAGCGCTGGCGGGATATTCTTATTATTATTATTATTATTGAGATGAGTCTGCG 1787

Qy 836 TTGTGCGCAAGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGCTCAACTGCT 895
Db 1786 TCTGTGCGCCAGGCTGGAGTGCAGTGGCGACGATGTTGGCTCACTGCAACTCTGCTGCC 1727

Qy 896 GGTTTCACGCCATTCTCCGCGCTCAGCCTCCCGAGTAGCTGGAGCTAAAGCGCGCTGCCA 955
Db 1726 GGGTTCAGCGGATTTCTCTGCGCTCAGTCTCCGAGTAGTGGAGCTACAGGACCGGCCA 1667

Qy 956 CCACGCGCCGCTAAATTTTGTGATTTTAAAGACGGGGTTTCATCGTGTAGCCAG 1015
Db 1666 CCACGCGCCAGCTAA--TTTTTGTATTTTGTAGTGCAGGAGTTTCACCATGTGGCCAG 1609

Qy 1016 GATGCTCTGATCTCATGACCTTGTGATCGGCTGCGCTCGGCTCCCAAGTGTGGGAT 1075
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Qy 1076 TACAGGCATGAGCCACCGTGCCTGCGCCCTTATCACATTATT 1116
Db 1549 TACAGGTGTAGCCACACCGCTGCCCCAGGATATTCTTT 1509
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RESULT 43
CR859576

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LOCUS          CR859576          3165 bp      mRNA      linear      HTC 12-NOV-2004
DEFINITION     Pongo pygmaeus mRNA; cDNA DKFZp468A085 (from clone DKFZp468A085).
ACCESSION     CR859576
VERSION       CR859576.1  GI:55730029
KEYWORDS       HTC.
SOURCE         Pongo pygmaeus (orangutan)
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ORGANISM

Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Pongo.

REFERENCE

1 (bases 1 to 3165)

AUTHORS

Ansorge, M., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
Wiemann, S.

CONSRMT

The German cDNA Consortium

TITLE

Direct Submission

JOURNAL

Submitted (12-NOV-2004)

MIPS, Ingolstaedter Landstr.1, D-85764

Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.

This clone (DKFZp468A085) is available at the RZPD Deutsches

Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.

Please contact RZPD for ordering:

<http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp468A085>

Further information about the clone and the sequencing project is

available at <http://mips.gsf.de/projects/cdna/>.

Location/Qualifiers

1. 3165

/organism="Pongo pygmaeus"

/mol_type="mRNA"

/db_xref="taxon:9600"

/clone="DKFZp468A085"

/tissue_type="heart"

/clone_lib="468 (synonym: phrt1). Vector pSport1_sfi; host

DH10B; sites SfiIa + SfiIb"

/dev_stage="adult"

/note="hypothetical protein (Homo sapiens), differentially

spliced"

1. 3165

/gene="DKFZp468A085"

34. .687

/gene="DKFZp468A085"

/codon_start=1

/product="hypothetical protein"

/protein_id="CAH91740.1"

/db_xref="GI:55730030"

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SKKSPADPTNYKFKGEAGTWTLSQFTLHEKDQETASRLGLNETELLHKSHV

SGEKTKLRATPEAIQNRQDIEBRIERQIRICLPORFAKSKQLTRKMEIEKSLFQ

GADRHSFLKALYYQYHKKTSADKYMTSMRKIKLGTKALLVCSQTAMKKYRLDNF"

Query Match 5.7%; Score 283; DB 4; Length 3165;

Best Local Similarity 67.9%; Pred. No. 3.9e-15;

Matches 515; Conservative 1; Mismatches 176; Indels 67; Gaps 6;

Qy 3106 TTTTTCCTTCTGTTTGTAGACAGAGGCTCTTCTCTGTCAACCCAGGATGAGCAGTGG 3165

Db 2300 TTTTATTATTATTTTGTAGACAGAGGCTCTTCTGTGTAATCCAGGCTGGATGAGTGA 2359

Qy 3166 TGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGTCACCTCAGC 3225


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ACCESSION CR860168
VERSION 1
KEYWORDS GI:557311191
SOURCE HTC
ORGANISM Pongo pygmaeus (orangutan)

REFERENCE
AUTHORS Pouska A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M. and
Wiemann S.
CONSRMTM 1 (bases 1 to 3259)
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKFZp459B2023) is available at
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in
Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp459B2023
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.

FEATURES
Location/Qualifiers
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/db_xref="taxon:9600"
/clone="DKFZp459B2023"
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/clone_lib="459 (synonym: pcor1). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
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/note="calcium-binding protein p22 (Homo sapiens)"
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125..712
/gene="DKFZp459B2023"
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ORIGIN
Query Match 5.6%; Score 281.4; DB 4; Length 3259;
Best Local Similarity 69.5%; Pred.No.5.1e-15;
Matches 455; Conservative 1; Mismatches 187; Indels 12; Gaps 5;

QY 3107 TTTTGTGTTGTTTGTAGACAGAGGTCTGTCTGTCTACCCAGGCGATGACACAGTGGT 3166
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Db 1828 TTTTGTGTTTGTGAGACAGAGTCTGTCTGTCTACCCAGGCGTGGTGCAGTGGT 1887
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QY 3167 GCAACCATAGTCACTGCAGCCTCAACCTCTGAGTCAAGGATCTGCTGACCTCAGCC 3226
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Db 1888 G---CGATCGCTCACTGCAACCTCAGCCTCTCTGGGTTTAAGTGATTCTCTCGCTCAGCC 1944
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QY 3227 TCCCAAGTACGTGGGACTAGCGCTGACACACCGCTGCTTAATAAAAAATTTT 3286
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Db 1945 TCCCAAGTACGTGGGATTAACAGTGTFACACACCACTGATGCGCGGCTAATTTTGTGTA 2003
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QY 3287 TTGTAGAGACTGGGTCTTACTAGTTGGCGCAGGCTGTCTTAACTCTCTGGCTTCAAGCA 3346
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Db 2004 TAGTGAGACAGGTTTTCACCATGTTGGCCAGGCTGTCTCGACTCTCTGACTTC--GTG 2061
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QY 3347 ATCCTCTTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGC 3406
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QY	863	TGCGATCTCGGCTCACTGCAAGCTCCACCTGCTGGGTTTCAAGCAATTCCTCCGCTCAGC	922
Db	2936	TGCAACTTCAGCTCAATGCAACTCTACCTCCGGGTTCAAGCAATTCCTCGCTCGC	2877
QY	923	CTCCCAAGTAGCTGGGACTAAAGCGCGCTGCGCACACCGCCGCTAAATTTTGTATTT	982
Db	2876	CTCCCAAGTAGCTGGGACTATAGGCGCTGCCACACCGCCGCTAAATTTGTCT-TTT	2818
QY	983	TTAATAAAGACGGGTTTCATCTGTAGCCAGGATGCTCGATCATGACCTTGCGA	1042
Db	2817	TTAGTAGAGTTGGGGTTTCATCATGTGTGGTCAGGATGGTCTCAATCTCTGACCTCGTA	2758
QY	1043	TCGCGCTCGCTCGGCTCCCAAGTGTCTGGGATTTACAGGCATGAGCCACCGTCCCGGCC	1102
Db	2757	TCGCGCGCTCGGCTCCCGATATGCTGGGATTTACAGGTGAGAGCCACACACCGCC	2698
RESULT 48			
CA431692			
LOCUS			
DEFINITION	CA431692	672 bp mRNA linear EST 07-NOV-2002	
ACCESSION	UI-H-DF0-bet-b-22-0-UI.s1	NCI CGAP DF0 Homo sapiens cDNA clone	
VERSION	UI-H-DF0-bet-b-22-0-UI.3	mRNA sequence.	
KEYWORDS	CA431692.1	GI:24794418	
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1	(bases 1 to 672)	
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
JOURNAL	Tumor Gene Index		
COMMENT	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs.r@mail.nih.gov		
	Tissue Procurement: Dr. Jose Mercuende		
	CDNA Library preparation: Dr. M. Bento Soares, University of Iowa		
	CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa		
	DNA Sequencing by: Dr. M. Bento Soares, University of Iowa		
	Clone Distribution: Clone distribution information can be obtained		
	from Dr. M. Bento Soares, bentso-soares@uiowa.edu		
	The following repetitive elements were found in this cDNA		
	sequence: 11-299, >ALU (matched complement) 378-667, >ALU (matched		
	complement)		
	Seq primer: M13 FORWARD		
	POLYA=Yes.		
FEATURES			
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	Location/Qualifiers		
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	/dev_stage="Adult"		
	/lab_host="DH10B (Life Technologies)"		
	/clone_lib="NCI_CGAP_DF0"		
	/note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a		
	modified polylinker; Site 1: EcoR I; Site 2: Not I;		
	NCI CGAP DF0 is a cDNA library containing the following		
	tissue(s): Subchondral Bone. The library was constructed		
	according to Bonaldo, Lennon and Soares, Genome Research,		
	6:791-806, 1996. First strand cDNA synthesis was primed		
	with an oligo-dT primer containing a Not I site. Double		
	stranded cDNA was ligated to an EcoR I adaptor, digested		
	with Not I, and cloned directionally into pT7T3-Pac		
	vector. The oligonucleotide used to prime the synthesis of		
	first-strand cDNA contains a library tag sequence that is		
	located between the Not I site and the (drl)18 tail. The		
	sequence tag for this library is GTTAAAGCGTC.		
	TAG_TISSUE=subchondral bone		
ORIGIN			
	Query Match		
	Best Local Similarity	5.6%; Score 280.4; DB 6; Length 672;	
	Matches 457; Conservative	1; Mismatches 198; Indels 19; Gaps 4;	
QY	3106	TTTTTTTGTGTTTGTAGACACGGTCTTGCTGTCACCCAGGCATGACAGTCGG	3165
Db	1	TTTTTTTTTTTTTTTTTGTAGATGGAGTCTCGCTCTGTGGCCAGGTGGAGTGG	60
QY	3166	TGCAACCATAGATGCTACTGCGCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGC	3225
Db	61	CAGGATCTCGGCTCACTGCAAGCTCTGCTCCGGGTTTCAAGCCATTTCTCTGCTCAGC	120
QY	3226	CTCCCAAGTAGCTGGGACTGAGGCGTGACACACCGCTGGCTAAATTTAAAAAATTTT	3285
Db	121	CTCTGAGTAGCTGGAACCTACAGGCGCGCCGACACCGCCGACTAAATTTTGTGA-TTT	179
QY	3286	TTTGTAGAGACTGGGCTTACTTACGTTGGCCAGGCTTGTCTTTAAACTCTCTGCTTCAAGC	3345
Db	180	TTAGTAGAGACGGGTTTCACTGTGTACAGGATGGTCGGGATCTCTGACCTCATG-	238
QY	3346	AATCTCTCTACCTTGGCATCCCAAGTGTCTGGGATTACAGGGGTGAGCCACCATGTGGG	3405
Db	239	-ATCCGCGCGCTCGGCTCCCAAGTGTGGGATTACAGGCGTGAGCCACCATCTTG	297
QY	3406	CTACTTATTTCTTTACATTCATCTTTTCCAATAGAAATGTAAGATCCACAGACAGGATT	3465
Db	298	CCATAATATGTCTTTTAAAAATTACAATTAATCTTACTTGTATTTAATTTGATGCCAA	357
QY	3466	ACTGCTTATTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCACTCACTCAACCTCC	3525
Db	358	GTTTTGTGTTTATTTGTGTTTTTTTGGAGACAGGCTCTCACTATGTACCCAGGATGA	417
QY	3526	GTTC-----GCTCACTGCAACCTCTGCTCTCCCGGTTTCAAGYGATTCTC	3570
Db	418	GTGCAGTGGCCATGATCTTGGCTCACTGGAACCTCTGCTCCAGTGTTCAGTGATCTT	477
QY	3571	CTGCTTAAGCTTCTCTGAGTAGCTGGAATTAAGGCTGACACCATCTTGGCTTAATTT	3630
Db	478	ATGCTCTAGTCACTCTGAGTAGCTGGGATTACAGGCGTGTACCACTATGCCAGCTAA-TT	536
QY	3631	TTTGTATTTTGTAGCAGAGATGGGGTTTACCATGTTGCCAGGCTGTCTCAAACTCTCG	3690
Db	537	TTTGTATTTTCACTAGTACACAGGCGTTCGCCATGTTGGCCAGGCTGGTCTCGAATCTCTC	596
QY	3691	ACCTCAAGTGTCTGCTGCTCACTCTCCAAAGTGTGGAATTTATAGGCGTGAAGTAC	3750
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QY	3751	TGTGCTGCGCGATT 3765	
Db	657	CAAGCTCAGCCTAAT 671	
RESULT 49			
HS0800886			
LOCUS			
DEFINITION	HS0800886	3474 bp mRNA linear HTC 22-SEP-2004	
ACCESSION	Homo sapiens mRNA; cDNA DKFP434N174 (from clone DKFP434N174).		
VERSION	AL110229		
KEYWORDS	AL110229.1	GI:5817168	
SOURCE	HTC.		
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1	(bases 1 to 3474)	
AUTHORS	Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,		
	Fobo,G., Han,M. and Wiemann,S.		
CONSRMT	The German cDNA Consortium		

TITLE Direct Submission
JOURNAL Submitted (22-SEP-2004) MIPS, Ingolstaedter Landstr.1, D-85764
Neuerberg, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Agowa (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKF2p434N174) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKF2p434N174
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
FEATURES
Location/Qualifiers
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DH10B; sites NotI + SalI"
/dev stage="adult"
/note="hypothetical protein, N-terminus truncated, not
fully spliced"
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Query Match 5.6%; Score 280; DB 4; Length 3474;
Best Local Similarity 67.5%; Pred. No. 6.4e-15;
Matches 483; Conservative 1; Mismatches 221; Indels 11; Gaps 6;
QY 3103 GTTTTGTGTTGTTGTAGAGACAGGGTCTGTCTGTACCAGGCATGAGCAG 3162
DB 2101 GTTTTGTGTTTTCCTTTTGTAGATGGGCTTTTGCTCTTACCAGGC-TGAGTGCAG 2159
QY 3163 TGGTGAACCATAGGTCACTGACGCTCAACCTCTGAGCTCAAGGGATCTGTGACCTC 3222
DB 2160 TGGCAGATCATAGCTCAGTGCAGCTCAAACTCTGGGCTCAAGCCATCTTCCACGTC 2219
QY 3223 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACCAACCGCTGGCTAATTAATAAAT 3282
DB 2220 AGCCTCCAGGTAGCTGGGACTACAGGCACACACCAACACCTGGCTAATTTTAAAT- 2278
QY 3283 TTTTGTAGAGACTGGGCTTACTAGCTGGCAGGCTTGCTTAACTCTGGCTTCA 3342
DB 2279 TTTTGTAGAGATGAGGTCTACTGTGTGCCCGGGTATCTGAACTCCTAGCCTCA 2338
QY 3343 AGCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCATGTG 3402
DB 2339 AGCGATCCTCTGCTTCGGTCTCCCAAGTGTGGGATTACAGGCATGAGCCACCATCTC 2398
QY 3403 CGGCTACTATTCTTTTACATTCCTTTTCCAATA---GAATGTGAAGATCCACAGAA 3459
DB 2399 TGCCAGGAGTTTATATGATATCTGTGGATCTAGATCTCATGTGATTGCAAAAACCT 2458
QY 3460 GGGATTACTGCCTATTTCTCTCTTCTTTTGTGACAGAGCTCACTTCATCACTCA 3519
DB 2459 TATTTATTTATTTATTTTGAATGGAATCTTGTCTGTGCGCCAGGCTGGAGTGCA 2518
QY 3520 A---CCTCGGCTCAGCTCACTGCAACCTCTGCCCTCCGGGTTCAAGYGATTTCTCGCTC 3576
DB 2519 ATGGCGTGATCTGGGCTCACTGCAACTACCACTCTCGGTTCAAGGATTCGGCTGCT 2578
QY 3577 AAGCTCTCGAGTAGCTGGAATTTAAGCGGTGACCAACCATGCTTGGCTTAATTTTGTGA 3636
DB 2579 CAGCGTCTGAGTAGCTGGGACTTACAGGGCGGCACCAACCGCCAGCTAA-TTTTGTGA 2637
QY 3637 TTTTGTAGCAGAGTGGGTTTACCATTGTGCCAGGCTGGTCTCAAACTCTGACCTCA 3696
DB 2638 TTTTGTAGAGACGGGATTTCACTATGTGTGGTGGGATGGTCTTGATCTCTTGACCTC- 2696
QY 3697 AGTGATCTGCCTGCCTCAGTCTCCCAAGTGTCTGGAAATTATAGGCGTGAGTCACTGTGCC 3756

Db 2697 -GTGATCCACCACCTCGGCTCCCATAGTGCTGGATTACAGGTGTGAGCCACCGCACT 2755
QY 3757 TGGCGGATACTGCTTATTTTCTTTTATGCTATATCCCGAGATCTAGAGCAGTGTC 3812
Db 2756 CAGCTGATTTCAGAAAACCTTCTTCCATACTGTTGTTTCACTTCTCGGATAGTGC 2811
RESULT 50
CN359768/c 718 bp mRNA linear EST 16-MAY-2004
LOCUS 17000418008134 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
DEFINITION CN359768
ACCESSION CN359768
VERSION CN359768.1 GI:47359702
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 718)
AUTHORS Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
PUBMED 15146197
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 718 Std Error: 0.00.
FEATURES
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H9"
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and H9 (p26) maintained in feeder-free conditions"
ORIGIN
Query Match 5.6%; Score 279.2; DB 7; Length 718;
Best Local Similarity 68.1%; Pred. No. 2.1e-14;
Matches 403; Conservative 0; Mismatches 188; Indels 1; Gaps 1;
QY 514 TGTGCGCCAGGCTGGAGTGGGTGGCGTGATCTCAGATCACTACAACTCCATCTCCTGG 573
DB 690 TGTGCGCCAGGCTGGAGTGGCAATGGCGGATCTCAGCTCATCAACACTCCGCTCCTGG 631
QY 574 GTTCAATTAATCTCTTGCCCTCAGCCTCTCAAGTAGCTGGGACTTGTAGCTCTCAAGTAG 633
DB 630 GTTCAAGTGATTTCTGCTGCCTCAGCTTCTCCTGAGTAGTGGGACTACAGGCATGTGCCACC 571
QY 634 CTGGCAGACACACCATGCCAGCTAAATTTTGTGTGTTTGTGTGGTAGAGACAGGTT 693
DB 570 ATGCTGCTAATTTTGTATTCTGTAGAGATGGGGTTTCTCCATGTGTGTCAGGCTGGTCT 511
QY 694 TTCAACATGTTGGCAGGCTGGGTGACCTCCCTTTTAGATTCTCCTCAATCCTGCTCTATT 753
DB 510 TGAATCCCGACCTCAGTTGATCTGCCCGCTCAGCCCTCTCAAAGTGTGAGATTACAGG 451
QY 754 CTTCCCTTTCTAATGAGATATCCA-GTTTCTTACTTATCACATTTATTATTATTCTTA 812
DB 450 CATGAGCCATCATGCCCGCCCAATACTACTTCTTTTCTTTTCTTTTCTTTTCTTTT 391

Qy	766	AATGCAGTATCCAGTTTCCTTACTTATTCACATTTATTATTATTCTTATTATTATTTGAGAC	825
Db	548	TTATAGGGGTGAGCCACTGTGCTCAGCCTGAACATTTTATTCTATTATTATTTTTTGAGAC	489
Qy	826	AGAGTCTTGTTTGTTCGCAAGGCTGAGATACAGTGGTGGGATCTCGGCTCATCTGCAAGC	885
Db	488	GGAGTCTCGCTCTTTTCGCCAGGCTGAGTGCAGTGGGGTGATCGCTGCTCACTGCAAGC	429
Qy	886	TCCACCTGCTGGGTTTCACGCCATTCTCCCGCTCAGCCTCCCACTAGCTGGGACTAAAG	945
Db	428	TCCGCCCTCCAGGTTTCACGCTATTCTTCTGCCTCAGCCTCCGAGTACGTGGGACTACAG	369
Qy	946	CGCGCTGCCACACCGCCCGCTAAATTTTTTTGTATTTTTTAATAAGACGGGTTTTCATCG	1005
Db	368	CGCGCCGCCACCAACCTGGCGTAATTTTTTTTTTATTATTTAGTAGACACGGGTTTTCACCA	309
Qy	1006	TGTTAGCCAGGATGGTCTCGATCTCATGACCTGTGTATCGCCCTGCCTCGGCCCTCCCAA	1065
Db	308	TGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCTGCCTGCCTCAGCCTCCCAA	249
Qy	1066	GTGCTGGGATTTACAGGATGAGCCCGTGC CGCGCCTTATCATCATTTATTATTATTGT	1125
Db	248	GTGCTGGGATTTACAGGTGTGAGCCACCGCGCCCTGC AACATTTTATTTTTTAAAAAATTA	189
Qy	1126	TTTTTCTCTCCCACTAGTGTGT	1146
Db	188	AAATTTAATAACTCATTTGTAGT	168

RESULT 57	BX644719/c	BX644719	782 bp	mRNA	linear	EST 04-SEP-2003
LOCUS		DKFZp781N1434_r1	781	(synonym: hicc4)	Homo sapiens	cdna clone
DEFINITION		DKFZp781N1434_5'		mRNA sequence.		

accession	BX644719.1	GI:34479052
version	EST.	
keywords	Homo sapiens (human)	
source	Homo sapiens	
organism	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
reference	1 (bases 1 to 782)	
authors	Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.	
title	EST (lauber,J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)	
journal	Unpublished (2003)	
comment	Contact: MIPS	

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Db	745	TTTTATTTTGGAGCAGAGTCTCGCTCTGTTGCAGGCTGGAGTGGCGTGGCAATCTC	686	
QY	548	AGATCACTCAACCCCTCATCTCTGGGTTCAAAATAATTTCTTTGGCTCAGCCCTCTCAAGT	607	
Db	685	GGCTCACTCAACCCCTCGCTCCGGGTTCAAGTGATTTCTCTGCTCAGCCTCCTCGT	626	
QY	608	AGCTGGAGCTTGAGCTCTCAAGTAGCTGGCAGACACACCATGCCAGCTAATTTTTTG	667	
Db	625	AGCTGGGACT-----ACAAGCGCCGCCACACGCGCCAGCTAATTTTTTTG	581	
QY	668	TGTTGTTTTTTTTGGTAGAGACAGGTTTTTACCATTGTTGGCCAGGCTGGGTGACCTCCCTT	727	
Db	580	-----CATTTTTTAGTAGACAGGTTTTTACCATTGTTGGCCAGGATGGTCTCGATCTC--	528	
QY	728	TTAGATTCTCTCATCTCGTCTATTCTTCTCCCTTTCTAAATGCAGTATCCAGTTTCTCTTA	787	
Db	527	-----TTGACCTCGTGATCCACCTGCTCGGCTCCCAAAGTCTGGAATATAGGCGTG	473	
QY	788	CTTAATCAATTTATTTATTTCTTTATTTATTTATTTAGACAGAGTCTTGCTTTGCGCCAAG	847	
Db	472	AGTCACCGTGGCGGCTTTTTTTTTTTTTTTTTTTTTTTGGAGATGGAGTCTGCTGTGCGCCAG	413	
QY	848	GCTGGAGTACAGTGGTGGATCTCGGCTCACTGCMAGCTCCACTGCTGGTTCAGGCCA	907	
Db	412	GCTGGAGTGGAGTGGCATGATCTCAGCTCACTGCACTCTGCTCCCGGTTCAAGTGA	353	
QY	908	TTCTCCCGCTCAGCCCTCCCGTAGTCTGGGACTAAAGGGCGCTGCCACACGCCCGCT	967	
Db	352	TTCTCTGCTCAGCTCTCTGAGTAGTGGGATTAAGGTTGCCGCTACACGCCCTGGCT	293	
QY	968	AATTTTTTTGTAATTTTAAAGACGGGGTTTCATCGTGTAGCCAGGATGTTCTCGAT	1027	
Db	292	AATTTTTTTGTAATTTTATAGAGACGGGGTTTACACCATGTGCGCAGGCTGCTCAA	233	
QY	1028	CTCATGACCT--TGATGATCGCTGCTCGGCTCCCAAGTCTGGGATACAGGCATG	1085	
Db	232	CTCTGACCTCAGGTGATTCATCGGCTCAACTCTCTAAAGTCTGGGATACAGGCCTG	173	
QY	1086	AGCCACCGTGGCGGCTTATCATTTATTTATTTA	1121	
Db	172	AGCCACTGCTGGCCCAAGCAGGATTTCTTTA	137	
RESULT 58				
AQ743787/c				
LOCUS	AQ743787	942 bp	DNA	linear
DEFINITION	HS_5501_Al_E07_T7A RPOC-11 Human Male BAC Library Homo sapiens genomic clone Plate=1077 Col=13 Row=1, genomic survey sequence.			
ACCESSION	AQ743787			
VERSION	AQ743787.1	GI:5521309		
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.			
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)			
PUBMED	1049764			
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington			

401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieterdejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1077 row: I column: 13
Seq primer: T7
Clase: BAC ends
High quality sequence stop: 942.

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/notes="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 5.5%; Score 277.2; DB 9; Length 942;
Best Local Similarity 70.4%; Pred. No. 2.6e-14;
Matches 452; Conservative 0; Mismatches 163; Indels 27; Gaps 5;
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824 TTTTATTTTGTGAGACGGGGCTCACTGTCTGCCAGGCTGGAGTGGCGTGGATGC 765
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546 TCAGATCACTACAACTCCATCTCCGGTTCAAATAATCTTCTGCCCTCACTCAA 605
|||||
764 TCGGCTCACTGCAACTCTGTCTCCGGGTTCAGGTATCTCTCCCTCGGCTCCCGA 705
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606 GTAGCTGGGACTTGTAGCTCTCAAGTAGCTGGGCACACACCATGCCAGCTAATTTT 665
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704 GTAGCTGGGA-----TTACCCGATGTGTATCACGCTGGTTAATCTT- 661
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666 TGTGTGTTTTTTGTGAGACAGGTTTACCATGTTGGCAGGCTGGGTGACCTCCC 725
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660 -----ATATTTTATTAGACAGAGGGTTTCTCCATGTTGGTCAGGCTGGTCTGAAC 607
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726 TTTTAGATTCTCTCATCTGCTCTATTCTTCCCTTTCTAATGCAGTATCAGTTTCT 785
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846 AGGCTGGAGTACAGTGGTGGATCTCGGCTCACTGCAAGTCCACCTGTGGGTTCAAGC 905
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906 CATTCTCCGCTCAGCTCCAGTAGCTGGGACTAAAGGGCTCCGCCACCAAGCCGCG 965
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369 CTAA- TTTTGTATTTTAGTAGAGATGGGGTTTCACTGTGTAGCCAGGATGGATTG 311
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1026 ATCTATGACCTTGTGATCGGCTGCTCGGCTCCCAAAGTGTGGGATTTACAGGCATG 1085
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LOCUS Homo sapiens, Similar to hypothetical protein PRO1722, clone
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ACCESSION BC009270
VERSION BC009270.1 GI:14627272
KEYWORDS HTC
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1875)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-3590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susantha Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Nataesja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IMAGE Plate: 22 Row: J Column: 8
This clone has the following problem: retained intron.
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Matches 460; Conservative 1; Mismatches 189; Indels 30; Gaps 4;
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|||||
QY 3235 AGCTGGGACTACGAGCGTGCACCACTCCAGCTGGCTAAATTAATAAATTTTTTTGTAGAG 3294
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Db 966 AGCTGGGATTACAGGCACGCTCCACACACCCGGCTAAATTTTTTGTATTTTAGTAGAG 1025

QY 3295 ACTGGGCTTACTACGCTGGCAGGCTGTCTTAAACTCCTGGCTTCAAGCAATCTCTCT 3354

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QY 3475 TTTCTTCTCTCTTTTTTGGAGACAGAGTCTCACTTCATCACTCAACCTCC----- 3525

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Db 1249 ATCTCAACTCACTGCAACCTCCACCCGCGGGTCCCTGTGATTTTCCCACTCAGCCTCC 1308

QY 3585 TGAGTAGCTGGAATTAACAAGCTGCAACACCATGTCTGGCTAATTTTTTGTATTTTAGC 3644

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Db 1368 AGAGACGGGGTTTACCAATGCTCAGGCTGTCTGAAACTCTGGCTGAAAGTGATCC 1427

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RESULT 60

BI868328

LOCUS 603392289F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5402038 5', mRNA linear EST 11-OCT-2001

DEFINITION mRNA sequence.

ACCESSION BI868328

VERSION BI868328.1 GI:16042001

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 744)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: ARCC
cDNA library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLAM12025 row: b column: 23
High quality sequence stop: 741.
Location/Qualifiers
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FEATURES

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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 5.5%; Score 276.8; DB 3; Length 744;
Best Local Similarity 71.5%; Pred. No. 3.2e-14;
Matches 455; Conservative 0; Mismatches 157; Indels 24; Gaps 6;

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QY 537 GGCGTGATCTCAGATCACTACAACCTCCATCTCTGGGTTCAAAATAATTTCTTTGCCTCA 596

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QY 597 GCCTCTCAAGTAGCTGGGACTTTAGCTCTCAAGTAGCTGGCACACACCATGCCAG 656

Db 202 GCCTCCCAAGTAGCTCGGACT-----ACAGGCGTCTCTCCACATGCCTGG 246

QY 657 CTAATTTTTTGTGCTGTTTTTTTGGTAGACAGAGTTTTTCAACATGTTGGCCAGGCTGG 716

Db 247 CTAATATTT---GGTATTTTTTAGTAGACGGGGTTTTACCGTGTAGCCAGGAT--GG 301

QY 717 TGACCTCCCTTTTATAGATTCTCTCATCTGCTCTATTCTTCCCTTTCTTAATGCAGTATC 776

Db 302 TCTCGATCTCTAACTCGTGATCGCCCGCTCGGCTCCCAAAGTATGGGATTAACC 361

QY 777 CAGTTTCTTACTATACATTTATTTATTTATTTATTTATTTAT--TGAGACAGATCTTGC 835

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QY 836 TTTGTGCGCAAGGCTGGAGTACAGTGGCGGATCTCGGCTCACTCAAGCTCCACTGCT 895

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QY 1074 ATTACAGGCATGAGCCACCGTGGCCGCGCTTATCAC 1109

Db 661 ATTACAGCGGTGAGCCACCGCGCGCGCGGCGGCGAAACAC 696

Search completed: May 12, 2006, 15:20:22
Job time : 12171 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 12, 2006, 12:01:43 ; Search time 577 Seconds
(without alignments)
15406.561 Million cell updates/sec

Title: SEQ1-4500-9500-7328G

Perfect score: 4997.8

Sequence: 1 cttgcatcatcgattctttt.....tttgaccacgctggacaa 5001

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 150 summaries

Database :

Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 9	420.4	8.4	32068	3	US-09-949-016-12973
C 10	420.4	8.4	32068	3	US-09-949-016-12974
C 11	420.4	8.4	32068	3	US-09-949-016-12975
C 12	420.4	8.4	32068	3	US-09-949-016-14436
C 13	420.4	8.4	32068	3	US-09-949-016-14437
C 14	420.4	8.4	32068	3	US-09-949-016-14438
C 15	420.4	8.4	32068	3	US-09-949-016-14439
C 16	420.4	8.4	32068	3	US-09-949-016-14440
C 17	420.4	8.4	32068	3	US-09-949-016-14441
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Sequence 16790, A
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Sequence 719, App
Sequence 14577, A
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c 136	356.2	7.1	140844	3	US-09-949-016-14399	Sequence 14399, A
c 137	356	7.1	33908	3	US-09-949-016-15104	Sequence 15104, A
c 138	356	7.1	106199	3	US-09-949-016-12393	Sequence 12393, A
c 139	356	7.1	107980	3	US-09-949-016-14370	Sequence 14370, A
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c 141	355.4	7.1	45842	3	US-09-949-016-12550	Sequence 12550, A
c 142	355.4	7.1	45842	3	US-09-949-016-17327	Sequence 17327, A
c 143	354.8	7.1	64137	3	US-09-949-016-14831	Sequence 14831, A
c 144	354.8	7.1	64171	3	US-09-949-016-12502	Sequence 12502, A
c 145	354.6	7.1	24645	3	US-09-949-016-14062	Sequence 14062, A
c 146	354.6	7.1	127280	3	US-09-949-016-14857	Sequence 14857, A
c 147	354.6	7.1	132266	3	US-09-949-016-14860	Sequence 14860, A
c 148	354.6	7.1	150833	3	US-09-949-016-14859	Sequence 14859, A
c 149	354.6	7.1	159963	3	US-09-949-016-14858	Sequence 14858, A
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ALIGNMENTS

RESULT 1
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; Sequence 11957, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

;	PRIOR APPLICATION NUMBER: 60/231,498	
;	PRIOR FILING DATE: 2000-09-08	
;	NUMBER OF SEQ ID NOS: 207012	
;	SOFTWARE: FASTSEQ for Windows Version 4.0	
;	SEQ ID NO 11957	
;	LENGTH: 64813	
;	TYPE: DNA	
;	ORGANISM: Human	
;	US-09-949-016-11957	
	Query Match	8.9%; Score 444.4; DB 3; Length 64813;
	Best Local Similarity	54.1%; Pred. No. 3e-91;
	Matches 1225; Conservative	3; Mismatches 987; Indels 51; Gaps 14;
QY	2291	AGCCAGGCGCGTCTGCTGTAATCCAGCACTTTGGGAGCGCGGCGG 2350
DB	7028	AGCCAGGCGGTATGGCTCATGCTGTATCCAGCACTTTGGGAGCGCGG 7087
QY	2351	ATCAGCTTGAGGTTCAGAGTTCGAGACCAGCCTGGCCAAACATGGTGA 2410
DB	7088	ATCAGCTGAGGTTCAGAGTTCGAGAACAGCCTGGCCAAACATGATGAA 7147
QY	2411	TAAAAAATACAAAAATAGCCGACATGGTGGAGCGCC-----TGTA 2465
DB	7148	T-AAAAATACAAAAATTAGTGGCGTGTGGCAGACACCTATAGTCTAG 7206
QY	2466	TTGGAGAGTAGTTGGAGGTTTCAAGTGGCCAAAGTGTGCTGCTGCTCC 2525
DB	7207	TTGGAGGCTGAGGCGGGAATCGTTTGAACCCGGAGGTAGAGGCTGA 7266
QY	2526	GTAACAGAGCACTCTGTCTAAA---AAAAAAATATGCTTTCAATAA 2581
DB	7267	ATCACACCACTGCATCCAGCCTAGGTGACAGCAAGGCCTCATCTCAA 7326
QY	2582	AAGGACTTATATTTTTCAGCCATAGGATCATTTCTCTGAAGCATCTT 2641
DB	7327	GTGGCCAGGACGGTGGCTACGTCAGTAATCCAGCACATTTGGAGGCC 7386
QY	2642	TCCCACCTGTTCTTGAGAGTGGGAGGTGAGGCTGACCTATTGCTGCA 2701
DB	7387	AGATCATGAGGTTCAGAGATCAAGACCATCTCTGGGTAAACCGGTGA 7446
QY	2702	TATCTCAGTGTCTCCACCTTTCCAGTGTGTCAGACACATGACAACCT 2761
DB	7447	TAAAAATACAAAAATTAGCCGGCATCGTGTGGCGCCTGTAATCCAGC 7506
QY	2762	AGGCCAAGAAGCTGGACAGCTGTAAATTTCTGTGCGACAMMCCGTGAC 2821
DB	7507	AGGCTGAGCGGGAATGGCGTGAACCCGGAGCGGAGCTTGCAGGAGCG 7566
QY	2822	CATCTCTGCTCTGGCTGGCAATCAGCTGTAGCAGTAGGTTTATCCCTT 2881
DB	7567	CATCTCTGGCTCCATTCAGCCTGGGAGACAGAGTGAGACTCCATCTCA 7626
QY	2882	ATGAATTCAGTTGGTTCTCAGTAGCGCGGGGAAATAATAGTAAC----- 2933
DB	7627	AAACAAAACAAAAGTGGTGGGCGATGCTCTTAATCCTAGCTACTTGG 7686
QY	2934	CCATGATTTAGTGTAAATTTTCTTGGTTCTGGGAGTGTCTCCTTTAAT 2993
DB	7687	GCAGGAGAATCGTTGAACCCCGGAAGCAGAGGCTGCAGTGAGCAAGAT 7746
QY	2994	CAGTATGGATAGGT-ACAAATTATCCTCACTTAACAGATAAGAAAACTG 3052
DB	7747	TACTCCAGCCTGGGTGACAGAACGAGACTCTCCATAAGTTCACATGAAA 7806
QY	3053	GCTGAGCTATTTCGCCCAAGATCACACAGCTTCTAAGTGGTGACAGTTT 3112
DB	7807	TCTAATCCGACACCCAGAGATTTACTCTAGCCTTCAACCATGTCCATCT 7866
QY	3113	GTGTGTTTATAGACAGAGGTTTCTCTGTGACCCAGGCATGACACAGTGG 3172
DB	7867	TCTCTAATGCTGAGATGGAGTCTCACTCTGTCAACCCAGGCTGAGTGAG 7926

3173 ATAGGTCACTGACGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAGCTCCCAA 3232
Db |||||-----CCTCCACCTCCAGGTTCAGCGATCTCTCGCTCAGCTCC-TG 7974
3233 GTAGCTGGACATACGAGCTGACACACCGCTGGCTAATTAATAAATATTTTGTAG 3292
Db GTAGCTGGGAATACAGCGCTGCACCACTATGCGCGCTAATTTTATA--TTTTCAGTAG 8032
3293 AGACTGGGTCTTACTAGTTGGCCAGGCTTGCTTAACTCTCGGCTTCAAGCAATCTC 3352
Db |||||-----CCTCCACCTCCAGGTTCAGCGATCTCTCGCTCAGCTCCCAA 8092
3353 CTACCTTGGCATCCCAAGTGTGGGATACAGGGGTGAGCCACCATGTCGGCTACTTA 3412
Db CCGCCGACGCTCCCAACGCTGTGGGATTAAGGGGTGAGCCACTGCACCTGGCTTCT 8152
3413 TTTCTTTATCATTCATCTTTTCCAAATGAGATGTAAGATCCACAGACAGGGATTA 3472
Db GTACTCTTTATCTATTCTCACTGCTCTTTTCTTTTGGTTTCAGTATCATAGTACTTTG 8212
3473 ATTTCTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCTCGGTCAGC 3532
Db TTTCTGTAGCTTAAATAT--ATATATTTTAAGACTGGAATGAGTGGCATGATCTCAGC 8270
3533 TCACTGCAACCTCTGCTCCCGGTTCAAGYGATCTCTGCTTAAGCTCTCTGAGTAGC 3592
Db TCACTGCAACCTCCACTCCAGGCTCAATATTTCTGTGACTAGCTCTGAGTAGC 8330
3593 TGAATTAACAGGTCACACCATGCTTGGCTAATTTTGTATTTTGTAGCAGATGG 3652
Db TGGGATTAACAGGTCACACCATGCTTGGCTAATTTTGTATTTTGTAGCAGATGG 8389
3653 GGTTTTACATGTTGGCCAGGCTGCTCAAACTCTGACCTCAAGTATCTGCTGCT 3712
Db AGTTTACCATGTTTCTAGGCTGATCTTAACTCTGACCTCGAGTATCGCCGCGT 8449
3713 CAGTCTCCAAAGTGTGGAATTAAGGCGTGAGTCACTGTGCTGGCGGATTAAGTCT 3772
Db CAGCTCCCAAGTGTGGGATAACAGGATTAAGCTGCTGCTGAGCTCTTCTGTATTC 8509
3773 ATTTCTTTATGCTATATCCCAAGTCTAGACAGTGTCTGACATATAGTAGGTCTCA 3832
Db TTTATTTCTGTTTCATTGATCTGTTCTTTTGGTTTCAGTATCATATACTATTTTGT 8569
3833 ATAAATAATGATGATGACACGCTTAGATATAAACTTTCTTTTCTTTTAAACAA 3892
Db TTTCTATAGCTTAAATAATATGTTT---TTTGTAGATAGGCTCTCACTGTCTACCC 8626
3893 TCTTGACAACTTTGCAGAAATAAATACTTGTGATCTGCTTTTTCATCTATCACTTG 3952
Db GCTGGAGTGTACTGGTGTGATCATGCTCACTGCTCACTCAACCTCTATCTCA-ATTG 8685
3953 TTAAGTATTTTTCATATGCTCAAACTTTATTTGTTACTGTTTTCATTTGTTACTAT 4012
Db ATCTTCCCACTCAGCTCCCAAGTGTGACCACTGTTTGGCTAATTTTAAATTT 8745
4013 TTAGTCACTGAATAATATGCTTAATTTGTTTATATATCTCTGCTGCACCTTTAGAAG 4072
Db TTTGTAGAACACAGAGCTTGGCATGTCACCCAGGCTGGTCTTGAACCTCTGGGCTGA 8804
4073 CCAAAATTTTACAACTCTGATGAAAGCTATGAACCTCTCCCAAGAGAAATACACACA 4132
Db --AGATCCGCTGACCTCATCTCCCAAGTGTGGAATTAAGGTTGACCACTTGGC 8862
4133 CACACTCACACAGTGTTTTAAATGTTTGTGCAACTAAGACAAGAA-----ACC 4184
Db CAGCCAAAATAATGTTTGGCAGATCACTGAGTGGGAGTTCAAGACCAGCTTGGC 8922
4185 TGCAATTAGAGGATGTTTGTTCATATTAATTAATAAATCACTAGTTGGGACAGTCA 4244
Db AACATGGCAAAACCTTGTCTCTACTAAAGAAATACAAAATATTTCTGGGCGCAGCTCA 8982

4245 AGCCTGTAAACACAGTACTTTTGGAGTCCAAAGTGGTGGATCACTTGGAGTGAGAGTT 4304
Db TGTCTGTAATCCAGTACTCTGGAAGGCCAAGGAGGTGGATCACCTCAGGTGAGAGTT 9042
4305 CGAGCAGCCTGTGTAATATGTTGAAACCTTATCTTACTTAAATAATCAAAAAATAGCT 4364
Db TAAGACCAAGCTGGCCAACTGGTGAACCTCTCTACTTAAATAATCAAAAAATAGCT 9102
4365 GGGTGTAGTGTGATGCTGCTGTAGTCCAGTCTCTCGGAGGCTGAGGCAAGAGAAATTGC 4424
Db GGGCGTGTGACCGGTGCTGTATCCAGTCTCTCAGAGGCTGAGGAGAGAGTACAC 9162
4425 TTGAACCTGGAGGAGAGGTTGCAAGTGGAGGAGATCCCACTGCACTCCAGCTGG 4484
Db TTGAACCTGGAGGTTAGAGGTTGCAAGTGGAGGAGATCATGCCATTGCACTCTAGCTGG 9222
4485 GGCACACAGCAGAGTCTTATCTCAAAAAAATAAATAAATAAATAA 4530
Db GTGACAGAGCGAGATTCTGTCTCAAAAAAAGAAAAAAGAAAAA 9268

RESULT 2
US-09-949-016-16064
; Sequence 16064, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16064
; LENGTH: 70131
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16064

Query Match 8.9%; Score 444.4; DB 3; Length 70131;
Best Local Similarity 54.1%; Pred. No. 3.1e-91;
Matches 1225; Conservative 3; Mismatches 987; Indels 51; Gaps 14;

4245 AGCCTGTAAACACAGTACTTTTGGAGTCCAAAGTGGTGGATCACTTGGAGTGAGAGTT 4304
Db TGTCTGTAATCCAGTACTCTGGAAGGCCAAGGAGGTGGATCACCTCAGGTGAGAGTT 9042
4305 CGAGCAGCCTGTGTAATATGTTGAAACCTTATCTTACTTAAATAATCAAAAAATAGCT 4364
Db TAAGACCAAGCTGGCCAACTGGTGAACCTCTCTACTTAAATAATCAAAAAATAGCT 9102
4365 GGGTGTAGTGTGATGCTGCTGTAGTCCAGTCTCTCGGAGGCTGAGGCAAGAGAAATTGC 4424
Db GGGCGTGTGACCGGTGCTGTATCCAGTCTCTCAGAGGCTGAGGAGAGAGTACAC 9162
4425 TTGAACCTGGAGGAGAGGTTGCAAGTGGAGGAGATCCCACTGCACTCCAGCTGG 4484
Db TTGAACCTGGAGGTTAGAGGTTGCAAGTGGAGGAGATCATGCCATTGCACTCTAGCTGG 9222
4485 GGCACACAGCAGAGTCTTATCTCAAAAAAATAAATAAATAAATAA 4530
Db GTGACAGAGCGAGATTCTGTCTCAAAAAAAGAAAAAAGAAAAA 9268

Qy	2642	TCCCACTGTTTCTGAGATGGCGAGGTGAAGGGCTGACCTATTGCTTGCACTTACTTC	2701
Db	13041	AGATCATGAGGTGAGGAGATCAAGACCATCCTGGCTAAACACGGTGAACCCCGCTCTCTAC	13100
Qy	2702	TATCTCAGCTGTCCTCCCATCTTCCAGGTGCTGCAGACACATGACAACCTGCTAYGACC	2761
Db	13101	TAAAAATACAAAATAATAGCCGGCATCGTGTGGCGCCTGTAACTCCAGCTACTTGGG	13160
Qy	2762	AGGCCAAGAAGCTGGACAGCTGTAAATTTTCTGTGGACAMMCCGTACACCCACACCTATT	2821
Db	13161	AGGCTGAGCGCGAGAAATGCGCTGAACCCGGGAGCGGAGCTTTCAGGGAGGGAGATCG	13220
Qy	2822	CATACTGTGCTCTGCTCGGCAATCACCTGTAGCAGTAGGTTTTATCCCTTCCTTTGACCT	2881
Db	13221	CACTGCTGCGCTCCAATTCAGCCCTGGGAGACAGATGAGACTCCATCTCAAAACAAAACA	13280
Qy	2882	ATGAATCTAGTTGGTTCTCAGTAGGCGGGGGGAAATAATAGTAAC-----AACAG	2933
Db	13281	AACAAACAAAACAAGATGGTGGGCGATCGCTTAATCCTAGCTACTTTGGAAGGCTGAG	13340
Qy	2934	CCATGATTAGTGTAAATTTTCTTGGTTCTGGGCACTGTCCTCTTAATCTCTCAGAACAA	2993
Db	13341	GCAGGAAATCGCTTGAAACCCCGAAGCAGAGGCTGCAGTGAGCCAGNACACCACTG	13400
Qy	2994	CACATGCGGATAGGT-ACAAATTATCCTACTTAACAGATAAGAAACCTGAGGCTCAGAAG	3052
Db	13401	TACTCCAGCCTGGGTGACAGAACGAGACTCTCCATAAGTTTCATATGAAAAATACCACCAAT	13460
Qy	3053	GCTGAGCTATTTGCCCAAGATCACACAGCTTGTAGTGGTGACAGTTGGGTTTTTTTTT	3112
Db	13461	TCTAATCCGACCGCAAGATTTACTCTAGCTTCAACATGTCCATATCTTTAACTCCTT	13520
Qy	3113	GTTGTGTTTAGAGACAGGGTCTTGCTCTGTCAACAGGATGAGCAGAGTGGTGCAACC	3172
Db	13521	TCCTAATGCTGAGATGGAGTCTCACTGTCAACCGAGCTGGAGTGCAGTGGTGTGATC	13580
Qy	3173	ATAGGTCACCTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCOA	3232
Db	13581	TCA-----CCTCCACCTCCAGGTTCAAGCGATTCTCTCGCTCAGCCTCC-TG	13628
Qy	3233	GTAGCTGGGACTAGGAGCTGCACCAACCGCTGGCTAAATTAATAAATTTTTTTGTAG	3292
Db	13629	GTAGCTGGGAATACAGCGGTGCACACCATATGCCGGCTAAATTTTATA--TTTTCAGTAG	13686
Qy	3293	AGACTGGGTCTTACTACGTGGCCAGGCTGTCTTAACTCCTGGCTTCAAGCAATCTCTC	3352
Db	13687	AGTCGAGTTTACCATGTTTCCAGGCTGGTCTCAAACTCTGACCTCAAGTGATCCAC	13746
Qy	3353	CTACCTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGCGGCTACTTA	3412
Db	13747	CCGCGCAGCCTCCCAACGTCGTGGGATATAGGGGTGAGCCACTGCACTTGGCCTTTCT	13806
Qy	3413	TTTCTTTACATTCATCTTTTCCAAATAGAATGTAAGATCCACAGAACAGGGATTACTGCCT	3472
Db	13807	GTACTCTTTATTTCTATTTCACTGGTCTGTTTTCTTTGGTTTCAGTATCATAGTACTTTTG	13866
Qy	3473	ATTTTCTCTCTTTTTFITFAGACAGAGTCTCACTTCATCACTCAACCTCCCGTTCAGC	3532
Db	13867	TTTCTGTAGCTTAAAAATAT--ATATATTTTAAGACTTGGAAATGCAGTGGCATGATCTCAGC	13924
Qy	3533	TCACGTCAACCTCTGCTCCCGGTTTCAAGYANTTCTCTGTGCTTAAGCCTCTGATGAGC	3592
Db	13925	TCACGTCAACCTCCACTCCAGGCTCAAATATTCTTGTACTCAGCCTCTCTGATGAGC	13984
Qy	3593	TGGAATTTACAAGCGTGCACCAACATGCTTGGGTAAATTTTTTGTATTTTTTAGCAGAGATGG	3652
Db	13985	TGGGATTTACAGGAGGACCAACATGCCCACTAA--TTTTTGTATTTTCAGTAGAGTGA	14043
Qy	3653	GGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTGACCTCAAGTGATCTGCCTGCCT	3712
Db	14044	AGTTTTACCAATGTTTCTAGGCTGTACTTTAAATCTCTGACCTCGAGTGATCCGCCGGT	14103

RESULT 3

US-09-949-016-15371

US-09-949-016-15371 : Sequence 15371. Application US/09949016

Sequence 13371, April 1997
Patent No. 6812339

; Patent No. 6812339
: GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE METHODS OF DETECTION AND USES THEREOF

: TITLE OF INVENTION: WITH HUMAN DISEASE METHODS OF DETECTION AND USES THEREOF

; TITLE OF INVENTION: WIT
 : FILE REFERENCE: CI.001307

FILE REFERENCE: CL001307
CURRENT ADDICTION NUMBER: IIS/08/848 016

; CURRENT APPLICATION NUMBER: US/0

; CURRENT FILING DATE: 2000-04-14
 ; PRIORITY APPLICATION NUMBER: 60/341 755

; PRIOR APPLICATION NUMBER: 60/300,100

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/3

; PRIOR FILING DATE: 2000-10-03

Db 258572 TTGAGACACAGTCTTCTGCTGTTGGCCCAAGCTGGAGTACCGTGGCCACAAATCTTGGCTCAC 258631
Qy 3537 TGCACACTCTGCTCCCGGGTTCAGYGATTCCTCGCTTAAGCTTCCCTGAGTAGTGGA 3596
Db 258632 TGAACCTTCCACCTCTCGGTTCAAGCGATTCCTCCATCTCAGCCCTTCGAGTAGCTGG 258691
Qy 3597 ATTACAAGCGTGCACACCATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTT 3656
Db 258692 ACTACAGATGCACACGATGCCAGCTAA- TTTTATATTTTGTAGTAGACGGGTT 258750
Qy 3657 TTACCAATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTCCCTGCCTCAGT 3716
Db 258751 TCACCATGTTGGCAGGCTGGTCTGAACTCCTGGCATCAAGCAATCTCCCTGCTTCAGC 258810
Qy 3717 CTCCCAAGTGTGGAATATATAGGCTGAGTCACTGTGCTGCTGCCGATTAATCTGTCTATT 3776
Db 258811 CTCCCAAAATGCTGGGATTTACAGGCATGAGACATGCTGCTAGCCTTAAAAAATATTTTG 258870
Qy 3777 TCTTTATTGCTATATCCCCAGAT- ---CTAGACAGTGTCTGACATATAGTAGTGCTCA 3832
Db 258871 ATAGCTATTTTATACAAAGGTAACTTGCAGCCCTTCTATTTTGTATGCAITTTACA 258930
Qy 3833 ATAAATAATTTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAA 3892
Db 258931 AGCCTTTATGCATAAAATAAAATAGCCAGCACTATTCTCACATGGCCAAAGTTTCATGCA 258990
Qy 3893 TCTTGACAACTTTGCAGATAAATAACAATCTTGCATCTGCTTTTTCATCTATCACCTT- 3951
Db 258991 CACACAAAGATATAGTTGGCTGAGTGGCTGCACACCTGTAAATCCCAACACTTTG 259050
Qy 3952 -----GTTATGACTTTTTCATATTTGCTCAAACTTTATTTGTTACTGTTTT 3997
Db 259051 GGAGACAGAGTGGTGGATCATGAGTCAAGAGATCCAGACACACCTTGGCCAAATGTT 259110
Qy 3998 TTCAITGTTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATPACATCTCTCG 4057
Db 259111 GAAACCCCATCTCTACTAAAAAGTACAAAAATTAGCTGGTGTGGCGCATGCTGTA 259170
Qy 4058 CT-----CACTTTAGAAGCCNAATTTACAATCTGATGAAGCTATGAACCTCTCCC 4112
Db 259171 GTCTCAGTACTCGGAGGCTGAGGAGGAGATCAATTTGAACGTGGGAGGCGAGTTG 259230
Qy 4113 CAGAGAAATACACACACACACACTCACACACAGATTTTTTTTAAATGTTTGCAACTA 4172
Db 259231 CAGTGAGCGAGATCTTGCACCTGCACTCCAGCTGGTGACAGAGTGAGACTCCATCTC 259290
Qy 4173 AGACAAGAA--ACCTGCATTAGAGGATGTTTGTTCATATTAATTTAAAAATAACTCAGTTG 4230
Db 259291 AATAAATAAATAAATTAATAATTAATAATTAATAATTTATTTTAAAAAATTTGGGGCTG 259350
Qy 4231 GGACAGTGAAGTCAAGCCTGTACACAGTACTTTTGGAGTCAAGGTGGTGGATCCT 4290
Db 259351 AGTGTATGGCTCACACCTGTAAATCCCGCAGTTTGGGAGCTTTGAGGAGGCGAGATCCCT 259410
Qy 4291 TGAGGTGAGAAGTTTCAGACAGCCTGTTCAATATGTTGAACCCCTATCTCTACTAAAAA 4350
Db 259411 TGAGGTGAGAGTTCAAGACCGCTTGGACAACATGTTGAACCCCGTCTCTACTAAAAA 259470
Qy 4351 TACAAAAATTTAGTGGGTGTAGTATGATGCTGATGCTTGTAGTCCCAAGTACTCGGAGGCTGA 4410
Db 259471 TACAAAAATTTAGCCAGGATGTTGGCTGTGCTGTAATCCCAAGTACTCGTGAAGCTGA 259530
Qy 4411 GGCAAGAGAAATTCCTTGAACCTGGGAGGAGGAGGTTGCAAGTGGCCAGATCCCACT 4470
Db 259531 GGCCCAAGCATCTCTTTGAACCTGTGAGCGGAGGTTGCAAGTGGCCAGATGCAACAGT 259590
Qy 4471 GCACTCAGGCTGGGACACACGAGACTCTATCTCAAAAAATAATAATAATAA 4526
Db 259591 GCACTCAGGCTGGGTGACAGAGTGAGACTTTGTTCTCAAAAAATAATAATAATAA 259646

US-09-949-016-15786
; Sequence 15786, Application US/09949016
; Patent No. 6812319
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15786
; LENGTH: 35629
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(35629)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15786

Query Match 8.5%; Score 424.6; DB 3; Length 35629;
Best Local Similarity 54.1%; Pred. No. 7.9e-87;
Matches 1272; Conservative 3; Mismatches 922; Indels 156; Gaps 14;
Qy 2283 TCGCTTTTCAGGCGAGCGGTGCTCATGCTGTAATCCAGACACTTTTGGGAGGCGGAG 2342
Db 26911 TCTACTTTTGGTGGTGGCTCAGCTGTAATCCAGACACTTTTGGGAGGCTGAG 26970
Qy 2343 GCGGCGGATCACTTTGAGTTCAGAGCTTCGAGACAGCCTGCGCAACATGTTGAAACCT 2402
Db 26971 GCAGTGGATCAC--AAGTCAAGAGATCGAGACCATCTCGCTAACAGGGTGAACCT 27028
Qy 2403 GTCTCTACTAAAAATACAAAAATTTAGCGGACATGTTGGCGAGCGCTGTAAACCCAGC 2462
Db 27029 GTCTCTACTAAAAATACAAAAATTTAGCGGCGGTGGTGGCACAGAGCTGTATTCACG 27088
Qy 2463 TACTTGGGAGACT-----GAGTTGGAGTTTTCAGTGAGC 2496
Db 27089 TACTAGGAGGCTGAGGAGAGAAATCGTTGAACCTGGGAGGCTGAGGTTGAGTGAGC 27148
Qy 2497 CAAGTCTGTGTCACTGTCTCCAGCTTGGGTAACAGAGC--AACTCTGTCTCAAAAAA 2554
Db 27149 CGAGATCGCAGCTGCACTCCAGCTTGGGACAGAGAGAGCTCCGTTTCAGAAAAA 27208
Qy 2555 AAAATGCTTTCATATAATATATGATAAAAGGACTTATATTTTTCAGCCATAGATCAT 2614
Db 27209 AAAAAAATAATACCTTACTTTAGCTAAACAAACCCCTTTTACCTCTTTCAGACAC 27268
Qy 2615 TTCTCTCCTGAGCATCTTGGCGAAGTCATCCCAAC-----TGTTCT 2656
Db 27269 TAACTCTGAGCATTTTGGAGATTTTAAATGTAATTTGTTTCTGGATTTCTCAA 27328
Qy 2657 GAGAGTGGCGAGTGGGCTGACCTATTTGCTCTGCACCTTACTCTATCTCAGCTGTCCC 2716
Db 27329 TATAGTTTAGGATTTGGCTTTCTCCAGTCCACTACACTAACCGTACTCTTCCATGCT 27388
Qy 2717 TCCCACTTTCAG-----GTGCTGCCAGACACATGACAACTGCT 2755
Db 27389 TTCTAACTTGCAGAAATTAATTAATAATTTTGTGAGACGGTTTTCGCTCTG 27448
Qy 2756 AYGCACAGGCCAAGAGCTGGACAGCTGTAAATTTTCTGCTGGACAMMCGTACACCCACA 2815
Db 27449 TCGCCAGGCTGGAGTGAGTGCGCAACTCTCGGCTCACTGCAACCTCCACCTCTGGGT 27508
Qy 2816 CCTATTCACTCTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCT 2875

Db 27509 TCATGCCATTCTCTGCTCAGCTCCCGAGTAGCTGGGACTACAGGTGCCCCCAACAT 27568
QY 2876 TGACCTATGAATTTCTAGTGGTTCTCAGTAGGCGGGGGAATAATAGTAACAACAGCC 2935
Db 27569 GCCCAGCTAATTTTTGTAATTTTTCAGTAGATACGGGTTTCACTGTGTTAGCCAGGATGG 27628
QY 2936 ATGATTTAGTGTAAATTTTCTGGTCTGGGAGTGTCTCTTAAATCTCTCAGAACACA 2995
Db 27629 TCTCAATTCCTGACCTCGATGCTGCTTGCCTTCCCAAGTGTGGGATACAG 27688
QY 2996 CTATGGGATAGGTACAATATCTCACTTAACAGATAAGAAAACTCAGGCTCAGAAGGCT 3055
Db 27689 GCCTGAGCACCGGCTGCACTAATCTGCAAAATTAATTTTAA----- 27735
QY 3056 GAGCTATTTGCCAAGATCACAGCTGTGAAGTGTGAGAGTTTGGGTTTTTTTTTGT 3115
Db 27736 -----ATCTTCTCTGATGCTCCCTTCTTTAGAGTCTTGGGTGGGTTGTTGTGTC 27790
QY 3116 GTTGTTTAGAGACAGGCTCTGCTCTGTACCCAGGATGAGCACAGTGTGCAACCAT 3175
Db 27791 ATTGTTTTTGAGACAGTCTTGTCTGTGACCCAGGCTGGAGTGCAGCAGCAATCTTG 27850
QY 3176 GGTCACTGACGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAGCTCCCAAGTA 3235
Db 27851 GCTCACTGCAACCTCCGCTCCAGGTTCAAGCAATCTCTGCTCAGCTCCTGAGTA 27910
QY 3236 GCTGGGACTACGAGCGTGCACACACGCTGCTGCTAAATAA--AAAAATTTTTTTGTAGA 3293
Db 27911 GCTGGGACTACAGCGACGACCCGCCACCATGCCAGCTAAATTTTGTATTTTAGTAGA 27970
QY 3294 GACTGGGTCTTACTAGTGTGGCAGGCTGTCTTAACCTCCTGGCTCAAGCAATCCTCC 3353
Db 27971 GCGGAGTTTTTACATGTTGTCAGGCTGTCTTGAACCTCCTGACCTCAAGTGTATCGCC 28030
QY 3354 TACTTGGCATCCCAAGTCTGGGATTAACAGGGTGAGCCACCATGTGCGCTACTTAT 3413
Db 28031 TGCTTGGCTCCCAAGTTAAGGATTACAGGTGTGAGCCACTGCACCTGGCCAGAGTT 28090
QY 3414 TTCTTTACATTCATCTTTTCCAATAGAAATGAAGATCCACAGAACAGGGAATTAAGTCCCTA 3473
Db 28091 TTGGTGTTTTGTGTTTTTTTTTTTGTAGAGGGA----- 28125
QY 3474 TTTTCTCTCTTTCTTTTGTAGACAGTCTCACTTCATCACCTCAACCTCGCTCAGCT 3533
Db 28126 --GTCTCACTCTGTGCGCCAGGCTGGAGTGCATGGCAGCATC-----TCAGCT 28172
QY 3534 CACTGCAACCTCTGCTCCCGGTTTCAAGYATTCTCCTGCCCTAAGCCTCCTGAGTAGCT 3593
Db 28173 CACTGCAACCTCTGCTCGTGGGTTCAAGCAATTTCTCTGCCCTCAGTCTCCTGAGTAGCA 28232
QY 3594 GGAATTACAAGGTGCACACCATGCTGTGGCTAAATTTTTTGTATTTTGTAGCAGATGGG 3653
Db 28233 GG-ACTACAGGATGTGCCACCGCCAGCTAAATTTTGTATTTTGTAGTAGAGACGG 28291
QY 3654 GTTTTACCATGTTGCCAGGCTGTCTCAACTCTGACCTCAAGTATCTGCTCCCTC 3713
Db 28292 GTTTCACCATGTAGCCAGATGCTCTATCTCTGACCTC--GTGATCTGCTGCTGC 28349
QY 3714 AGTCTCCAAAGTCTGGAAATTATAGCGGTGAGTCACTGTGCTGGCCGATTAAGTCTCTA 3773
Db 28350 AGCTCTTAAGTCTGGGATTACAGGCTGAGCCAGCCGCGCCCGCCAGCCGGTTT 28409
QY 3774 TTTTCTTTA-----TTGCTATATCCCCAGATCTAGAGCAGTGTCT 3813
Db 28410 TTTTAAACAAGATTCAAGACATCCAAATTTGGATGCTGCTTCTCTCAAAATCTCTTGCC 28469
QY 3814 GACATAGTAGTGTCTCAATAAATAATTCATGAATGCACAGCTAGATATAAATTTCT 3873
Db 28470 CATAGTTTCAAGCCCTCTCTATTTCTTTACATATGACGAGCGAATCTGTTTATATTC 28529
QY 3874 TTTTCTTTTTTAAACAATCTTTGACAATTTT-----GCAGATAAATAACAATCTTCATTT 3929

Db 28530 TATATCTATAGTTATGATACCTGAAGTCTTTAGGGTCTGATTTCTGATAACCACTTGA 28589
QY 3930 CTGCTTTTTCTATACCTTGTATGACTTTTTTCATATTCCTCAACCTTTTATTGTT 3989
Db 28590 CTGCTGGTTCCCATCATATGTGGCTTGTCTTATTTTTTGTCTTGAATTTTATT 28649
QY 3990 ACTGTTTTTTCATGTTACTATTATTAGTCACTGAATAATATGG--CTTAATTTGCTTATA 4047
Db 28650 TATTTTACTATATGATGAATTCAGCATGCTCCTTTATTTGAGAGTTAATTTGGGCGCTG 28709
QY 4048 CATCTCTCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCT 4107
Db 28710 GGTGAAGTTGAATTCATTTAGAAATTTGTTTTTTTTTTTTTTTTTTTCTCTAGGG 28769
QY 4108 CTCCTCAGAGAATACACACACACACATCTCACACAGTTTTTTTTTAATGTTTGC 4167
Db 28770 CACTACCACTGTTTACCATTTTTTAAATAAATAATCTCCACTTGAGAAATTTGTAGGAAATAC 28829
QY 4168 AACTAAGACAAGAAACCTGTCATTAGAGGATTTTGTTCATATTAATTAATAAATAACTCAG 4227
Db 28830 AACATAAATTTGGGCTCCAAATCCAAAGCAGGCTTATGGTTGTAATAACTCGAGTGT 28889
QY 4228 TTGGCACAAGTCAAGCCTGTAAACCACAGTACTTTTGGAAAGTCCAAAGTGGGTGGATC 4287
Db 28890 CTGGGTAGGTGGCTCATGCTTATTAATCCAGCACTTTGGGAGGCCAAGGTGAGAGGATC 28949
QY 4288 ACTTGAAGTGAAGATTTGAGACAGCCTGTGTCATATATGTTGAAACCTATCTCTACTAA 4347
Db 28950 ACTTGAGCCCAAGGATTTGAGACAGCCTGGGCAACATATTAATAACCCCGTCTCTACAA 29009
QY 4348 AATAACAAAAATTAGCTGGGTGTAGTGTGATGCTGTAGTCCAGCTACTCTCGGAGGC 4407
Db 29010 AATTTAAATAATAGCCCAATGCGATGCGTGTAGTCCAGCTACTTTGGGAGC 29069
QY 4408 TGAGCAAGAGAAATTTGTAACCTGGAGGAGAGGTTGCAAGTGGAGAGATCCAC 4467
Db 29070 TGAGGTGGAGGATTTGTTAGCCGAGGAGGTGGAGGCTGCAGTGAATCATGCTGC 29129
QY 4468 ACTGCACTCCAGCTGGGAGCAGCAGGCTCTATCTCAAAAAATAAATAAATAA 4527
Db 29130 ACTGCACTCCAGCTGGGTGAGCAAGAACCCCTCTCTCAAAAAAACAACAA 29189
QY 4528 TAAAGGATCGGAG 4540
Db 29190 AGTCGCTGGGCG 29202

RESULT 6

US-09-949-016-12970/c
; Sequence 12970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12970
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12970

Query Match 8.4%; Score 420.4; DB 3; Length 32068;

Best Local Similarity 60.7%; Pred. No. 6.9e-86; Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;									
QY	3104	TTTTTTTTTGTGTTGTTTGTAGACAGGGCTTGCTC-TGTCA	CCCGCATGAGCAGACAG 3162						
Db	27493	TTTTTCTTCTTTTTTTTGAGCGGAGTTGCTCTTTGTTGCC	CAGGCTGGAGTGCAA 27434						
QY	3163	TGGTGCAACATAGGTCACTGACGCTCAACCTCTCTGAGCT	CAAGGGATCTGCTGACCTC 3222						
Db	27433	TGGTGCAATCTTGGCTCACCGCACTTCGCTTCTCGGTT	CNAGCAATTCCTCGCTC 27374						
QY	3223	AGCTCCCAAGTAGCTGGGACTACGAGCGTGACACCA	CGCTGGCTTAATTAATAAAAT 3282						
Db	27373	AGCTCCCAAGTAGCTGGGATTACAGCATGCGCCACCA	CTGCGGCTAGTTTGTGA--- 27317						
QY	3283	TTTTTTGTAGAGACTGGTCTTACTAGCTTGGCAGGCT	TGCTTAACTCCTGGGTTCA 3342						
Db	27316	TTTTTTGTAGAGACAGGGTTTCTCATGTTGGTCAGGCT	GTATCGGAATCCCGACTTCA 27257						
QY	3343	AGCAATCCTCTACCTTGGCATCCCAAGTGTCTGGGATT	TACAGGGGTGAGCCACATGTG 3402						
Db	27256	GGTGATTCGGCTGCTTGGCTCCCAAGTGTGGGATTAC	CGGCTGAGCCACTCGCGCC 27197						
QY	3403	CGGCTACTTATTTTATCATTCATCTTTTCCAATAGA	ATGTAAAGATCCACAGAACAGGG 3462						
Db	27196	CAG---CTGATTTTCTCTTTCAGTATGTCCAATGAT	GTCTCTGAGCCGCTTATACCT 27140						
QY	3463	ATTACTGCCTATTTTCTCTTCTTTTGTAGACAGAGT	CTCATTCTATCACTCAACC 3522						
Db	27139	TATTTTTTTTTTTTGAGATGGAGTTTGTCTTGTG	CCCCAGGCTGGAGTGCAATGAGG 27080						
QY	3523	TCGGTTTCAGCTCACTGCAACCTCTGCTCCCGGTT	CAAGYGATTTCTCTGCTAAGCCT 3582						
Db	27079	TGATCTCGGCTACCGCAACCTCCACTCCAGGTTCA	GCAATTTCTCTGCTCAGCCT 27020						
QY	3583	CTTGAGTAGCTGGAATTACAAGCGTGCACCACTGCT	TTGGCTAAATTTT-TTGATTTTT 3641						
Db	27019	CCTGAGTAGCTGGGATTACAGGCATGCACCACCA	CGCCGCTAAATTTTGTATTTTTT 26960						
QY	3642	AGCAGAGATGGGGTTTACCATGTTGCCAGGCTGT	CTCAAACTCCTGACCTCAAGTGA 3701						
Db	26959	AGTAGAGACGGGGTTTCTCATGTTG---AGGCTAG	CTCTAACTCCCGACCTCAGGTGA 26903						
QY	3702	CTGCTGCTGCTAGTCTCCCAAGTGTCTGGAATTA	TATAGGCGTGAGTCACTGTGCGCC 3761						
Db	26902	TCGCTGCTGCTCGGCTCCCAAGTGTGGGATTAC	AGGTGTGAGCCACGTCGCGGCC 26843						
QY	3762	GATTACTGTCTATTTTCTTTATTTGCTATATCCC	CAGATCTAGACGAGTGTCTGACATATA 3821						
Db	26842	TATACCT---TATTTTCATCAATAAAATATATG	ACCTTTAACTACCTGTGTACTTTA 26786						
QY	3822	GTAGGTGCTCAATAAATAATTGATGATGCACAGC	CTAGATATAAATTTCTTTTCITT 3881						
Db	26785	TTAAAAATGAGACCATTTAAACACCAAGTATT	CACTTAAATAAAAAAAATTTAAAGTCAAAA 26726						
QY	3882	TTTTTA---AAACAACTTTGACAACTTTGCAGA	ATAATAATACATCTTGCTTTT 3937						
Db	26725	ATTAATCTAAACATTTGTTTCTTGTCAGATCT	TAGCCCAATGCTCTGTCTCTCT 26666						
QY	3938	TCACTTATCACCTTGTATGACTTTTTCATATTG	CCCTCAAACTTTATTTGTTACTGTTTT 3997						
Db	26665	TCGCGCTCAATGCTTCTATCTTCCCTACATGT	TACTAGCTTCGAGTGGCTTCCCA 26606						
QY	3998	TTCAATTTGTACTATTTTAGTCACTGA--ATA	TATATGGCTTAATTTGCTTATACATCTCC 4055						
Db	26605	TTCAITTAATAATACACCTTAACAGACCGTA	AGATGATTTGAAGATTTGTTACTAATGA 26546						
QY	4056	TGCTCCACTTTAGAAG-----GCAAAATTT	TACAAATCTGATGAAGC 4097						
Db	26545	GTATCAAGTTATTAACCTATTTTATGTTATTT	CAACAACTATTTCTTAGTCAATTTGCAAT 26486						
QY	4098	TATGAACCTCTCCCGAGAGAAATACACACACA	CACACACTTCACACACAGTTTTTTTTT 4157						

RESULT 7

US-09-949-016-12971/c
; Sequence 12971, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12971
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12971

Query Match 8.4%; Score 420.4; DB 3; Length 32068; Best Local Similarity 60.7%; Pred. No. 6.9e-86; Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;									
QY	3104	TTTTTTTTTGTGTTGTTTGTAGACAGGGCTTTGCTC-TGT	CACCCAGGCATGAGCAGACAG 3162						
Db	27493	TTTTTCTTCTTTTTTTTGAGCGGAGTTTCGCTCTTGT	TGCCCGCAGGAGTGCAA 27434						
QY	3163	TGGTGCAACCATAGGTCACTGACGCTCAACTCTCT	GAGCTCAAGGGATCTGCTGACCTC 3222						
Db	27433	TGGTCAATCTTGGCTCACCGCAACTCCGCTTCTCG	GTTCGAAATTTCTTCCCTGCTC 27374						
QY	3223	AGCTCCCAAGTAGCTGGGACTACGAGCGTGACCA	CCACCGCTCGGCTTAATTAATAAAAT 3282						
Db	27373	AGCTCCCAAGTAGCTGGGATTACAGGATGCGCCAC	CACTAGCCCGCTAGTTTTGTGA--- 27317						
QY	3283	TTTTTTGTAGAGACTGGGTCTTTACTACGTTG	SGCCAGGCTGTGCTTTAAACTCTCGGCTTCA 3342						

Db 26842 TATACCT---TATTTTCATCAATAAATAATATATGACCTTAACTACTGCTGCTACTTAA 26786
Qy 3822 GTAGTGTCTCAATAATAATTTGATGATGACAGCCCTAGATATAAATACTTTCTTTCTTT 3881
Db 26785 TTAATAATGAGACCATTAATAACACAGATTTTCTACTAATAAATAAATAAATAAATAA 26726
Qy 3882 TTTTA----AAACAATCTTGACAACTTTTGAGAAATAAATAAATAAATAAATAAATAA 3937
Db 26725 ATTAATACTAAACATTTGTTTCTTGTGACAGATCTAGGCCAAATGCTCTGTCTCTCT 26666
Qy 3938 TCACTTATCACTTGTGATGACCTTTTTCATATTTGCTCTCAAACTTTTATTTGTTACTGTTT 3997
Db 26665 TCTGGCTTCAATGCTTTCTATCTTTCCCTACATGATATAGCTTGCAGTGGCTTCCAC 26606
Qy 3998 TTCATTGTTTACTATTTTACTGCTGA--ATAATATGCTTAAATTTTGTCTTATACATCTCC 4055
Db 26605 TTCATTACTAATCTACACCTAAACAGCCGTAAGATGTTTGAAGATTTGTTACTAATGA 26546
Qy 4056 TGCTCCACTTTAGAG-----GCGAATTTTACAAATCTGATGAAGC 4097
Db 26545 GTATCAAAAGTTATAACCTATTTTATGTTATTTCAACAACATTAATCTTAGTCAATTTGCA 26486
Qy 4098 TATGAACCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTCTTTT 4157
Db 26485 TCTGCTTAGATTTCTAAGACAAAGATAGAGGTTAAAGCTAGACTCAGAGCTATCTC 26426
Qy 4158 TAAATGTTTGAACATAAGACAAAGAACTGCTATTTAGAGGATGTTTGTCTATATTAATAA 4217
Db 26425 AACACGTGCTTCAGTAGAACAAGGTTAAGAAATTTAGCTTAAAGGCAATGACGTATT 26366
Qy 4218 AATAACTCAGTTGGGA----CAGTGACTCAAGCTGTAAACACAGTACTTTGGAAGTCC 4273
Db 26365 AAAAAACATTAAGCCAGGTGCACTGCTCACGCTGTAAATCCAGCAGCTTTGGGAGGCC 26306
Qy 4274 AAGTGGGTGGATCAGCTTGAGGTGAGAAAGTTGAGACCCAGCTGCTCAATATGGTGAAC 4333
Db 26305 TAGCAGGAGATCAC--GAGGTGAGGATGAGACCATCTTGGCTTACACAGGTGAAC 26248
Qy 4334 CCTATCTTCTAAAAATAC-AAAAATTAGCTGGGTGATGATGATGCTGCTAGTCC 4392
Db 26247 CCTATCTTCTAAAAATACAAAAATTTAGCCGTGATGTCACACAGCTGTAGTCC 26188
Qy 4393 AGCTACTCGGAGGCTGAGCAAGAGATTTGCTTGAACCTGGGAGGAGGTTGCAAGT 4452
Db 26187 AGCTACTTGTGGGCTGAGCAGGAGAAATGGTGTGAACCCGGAGGAGGAGCTTGCAGTA 26128
Qy 4453 AGCCGAGATCCCACTCCAGCTCCAGCTGGGCGACACAGCGAGACTCTATCTCAAAA 4512
Db 26127 AGCCAGATATGCCACTGCACTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAA 26068
Qy 4513 AATAAATAAATAAATGAGATCGGAGAGAAACAAACCTAATAAGATTCTCTGAAGT 4570
Db 26067 AAAAAAACAACAAAAAACCACAAAAACCAAAAAACAAAAAAGAACACAAACGAATGT 26010

RESULT 10
US-09-949-016-12974/c
; Sequence 12974, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12974
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12974

Query Match 8.4%; Score 420.4; DB 3; Length 32068;
Best Local Similarity 60.7%; Pred. No. 6.9e-86;
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;

Qy 3104 TTTTCTTTTGTGTTTGTAGACAGAGGCTCTTGTC-TGTCAACCCAGGATGAGCACAG 3162
Db 27493 TTTTCTTTTGTGTTTGTAGACAGGATTTGCTCTTGTGTTCCAGGCTGAGTGCAA 27434
Qy 3163 TGGTCAACACATGAGTCTGAGGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTC 3222
Db 27433 TGGTCAACATCTTGGCTCACCGCAACCTCGCTTCTCGGTTCAAGCAATCTCTGCTC 27374
Qy 3223 AGCTCCCAAGTAGCTGGGACTACGAGCTGACACACAGGCTGGCTAATTTAAAAAAT 3282
Db 27373 AGCTCCCAAGTAGCTGGGATTTACAGGATGCGCCACCATGCGCGCTAGTTTGTGA--- 27317
Qy 3283 TTTTGTAGAGACTGGGCTTTACTAGTTGGCCAGGCTTGTCTTAAACTCTCGGCTTCA 3342
Db 27316 TTTTGTAGAGACAGGTTTCTCCATGTTGGTGAAGCTGATCTGGAACCTCCGACTTCA 27257
Qy 3343 AGCAATCTCTCACTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTG 3402
Db 27256 GGTGATTCGCTGCTTGGCTCCCAAGTGTGGATTTACCGGCTGAGCCACTGCGCC 27197
Qy 3403 CGGCTACTTATTTCTTACATTTCCATCTTCAATAGATGTAAGATCCACAGNACAGGG 3462
Db 27196 CAG---CTGATTTTCTTTTCTGATGATGTCCAATGATGTTCTGAGCCGCTTATACCT 27140
Qy 3463 ATTTACTGCTATTTTCTTCTTTTGTGAGACAGAGTCTCACTTCACTCACTCAACC 3522
Db 27139 TATTTTGTGAGATGGAGTTTGTCTTGTGGCCAGGCTGGAGTGCATGAGG 27080
Qy 3523 TCCGTTGAGTCACTGCAACCTCTGCTTCCCGGTTCAAGYGAATCTCTGCTCAAGCT 3582
Db 27079 TGATCTGCTCACCAGCAACCTCCACTCCAGGTTCAAGCAATTTCTCTGCTCAGCT 27020
Qy 3583 CTTGAGTCTGGAATTAACAGCTGCACCACTGCTTGGCTTAATTTT-TTGTATTTT 3641
Db 27019 CTTGAGTCTGGAATTAACAGCTGCACCACTGCTTGGCTTAATTTT-TTGTATTTT 26960
Qy 3642 AGCAGAGATGGGTTTACCATGTTGCCAGGCTGCTCTCAAACTCTGACCTCAAGTGA 3701
Db 26959 AGTAGAGCGGTTTCTCCATGTTG---AGCTAGTCTTAACCTCCGACCTCAGGTGA 26903
Qy 3702 TCTGCTGCTCAGTCTCCAAAGTGTGGAATTTAGCGGTGAGTCACTGCTGCTGGCC 3761
Db 26902 TCCGCTGCTCGGCTCCCAAGTGTGGAATTTACAGGTTGTCAGCCAGCTGCGCGGCC 26843
Qy 3762 GATTACTGCTATTTTCTTATTTGCTATATCCCAGATCTAGGCGAGTCTGACATATA 3821
Db 26842 TATACCT---TATTTTTCATCAATAAATAATATATGACCTTAAACTCTGTGCTACTTA 26786
Qy 3822 GTAGTGTCTCAATAAATAATGATGAATGCACAGGCTTAGATATAAACTTTCTTTCTTT 3881
Db 26785 TTAATAATGAGACCAATTAACACAGATTTTCACTAATAAATAAATAAATAAATAA 26726
Qy 3882 TTTTA----AAACAATCTTGACAACTTTGCGAATAAATAAATAAATAAATAAATAA 3937
Db 26725 ATTAATACTAAACATTTGTTTCTTGTGAGATCTAGCCCAAAATGCTCTGTCTCTCT 26666
Qy 3938 TCACTTATCACTTGTGATGACTTTTTCATATTTGCTTCAAGCTTATTTGTTACTGTTT 3997
Db 26665 TCTGGCTTCAATGCTTTCTTATCTTTCCCTTACATATAGCTTGCAGTGGCTTCCAC 26606
Qy 3998 TTTCAITGTTTACTATTTTAGTCACTGA--ATAATATGCTTAAATTTTGTCTTATACCTCC 4055

[illegible]

RESULT 12

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US-09-949-016-14436/C
; Sequence 14436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14436
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14436

```

Query Match	8.4%	Score 420.4;	DB 3;	Length 32068;
Best Local Similarity	60.7%;	Pred. No. 6.9e-86;		
Matches 910;	Conservative	1;	Mismatches 542;	Indels 45; Gaps 12;

Qy	3104	TTTTTTTTTCTGTTGTTATGAGACAGAGGTCCTTGTCTC-TGTGACCCAGGCGATGAGCACAG	3162
Db	27493	TTTTTCTCTCTTTTTTTTTTTGAGACGAGATTTTCGTCTTTGTCGCCAGGCTGGAGTGCAG	27434
Qy	3163	TGTTGCAACCATAGGTCACTGACGCTCAACCTCTGTAGCTCAAGGGATCTGCTGACCTC	3222
Db	27433	TGGTGCANATCTTGGCTCACCGCAACTTCGCGCTTCTCGGTTCAAGCAATTTCTCTGCGCTC	27374
Qy	3223	AGCTCTCCCAAGTAGCTGGGACTACGAGCGTGCACACACGCGCTGGCTAAATTAATAAAAT	3282
Db	27373	AGCTCTCCCAAGTAGCTGGGATTAACAGCGATGGCGCCACCATGCGCCGCTAGTTTGTGTA---	27317
Qy	3283	TTTTTTTGTAGAGACTCGGTTCTACTAGTTTGGCCAGGCTTGCTAAACTCTCGCTTCA	3342
Db	27316	TTTTTTAGTAGACAGGTTTTCTTCATGTTGTTGTCAGGCTGATCTGGAACTCCGACCTTCA	27257
Qy	3343	AGCAATCTCTCTACCTTGGCATCCCAAGTAGCTGGGATTTACAGGGGTGAGCCACCATGTG	3402
Db	27256	GGTGATTCGCTCGCTTGGCTCCCAAGATGTTGGGATTAACGGGTGAGCACTGCGCC	27197

Db 26127 AGCCAGATCATGCCACTGCACTCCAGCTTAGGAGACAGAGCAAGACTGTCTCAAAAAACA 26068
Qy 4513 AATAAATAAATAAATAAAGGATCGAGAGAAACAAACAACTAATAAGATTCTTGAAGGT 4570
Db 26067 AAAACAAAACAAAAAACCACAAAAACCAAAAAACAAAAAACAAGAAACAAACGAATGT 26010

RESULT 13

US-09-949-016-14437/c
; Sequence 14437, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14437
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14437

Query Match 8.4%; Score 420.4; DB 3; Length 32068;

Best Local Similarity 60.7%; Pred. No. 6.9e-86; Indels 45; Gaps 12;
Matches 910; Conservative 1; Mismatches 542;

Qy 3104 TTTTCTTTTGTGTTGTTGTTAGACAGAGGTCTTGCTC-TGTCAACCAGGCGATGACACAG 3162
Db 27493 TTTTCTTTCTTTTGTGAGACAGAGTTTTCGCTCTTGTGCCCAGGCTGGAGTGCAA 27434
Qy 3163 TGGTGCAACATAGGTCACTGAGCGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTC 3222
Db 27433 TGGTGCAATCTTGGCTCAGCGAACCTCGCGCTTCTCGGTTCAAGCAATCTCTGCTC 27374
Qy 3223 AGCTCCCAAGTAGCTGGGACTACGAGCTGACACACAGCGCTGGCTAATTAATAAAT 3282
Db 27373 AGCTCCCAAGTAGCTGGGATTAACAGGCATGGCCACCATGGCCGCTAGTTTGTGA--- 27317
Qy 3283 TTTTGTAGAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAAACTCTCGGCTTCA 3342
Db 27316 TTTTGTAGAGACAGGTTTCTCCATGTTGGTCAGGCTGATCTGGAATCCCGACTTCA 27257
Qy 3343 AGCAATCTCTACTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCAATGTG 3402
Db 27256 GGTGATTGCGCTGCTTGGCTCCCAAGTGTGGGATTACCGGCTGAGCCACTCGGCC 27197
Qy 3403 CGGCTACTTATTTCTTACATTCATCTTCCATAGATGTAAGATCCACAGAACAGGG 3462
Db 27196 CAG---CTGATTTTCTTTTCAGTATGTCCAATGATGTTCTGAGCCCGCTTATACCT 27140
Qy 3463 ATTACTGCGCTATTTCTCTCTTTTGTGAGACAGAGTCTCACATTCACTCACTCAACC 3522
Db 27139 TATTTTGTGAGATGGAGTTTGTCTTGTGTCAGGCTGGAGTGAATGAGG 27080
Qy 3523 TCCGTTCACTCACTCAACCTCTGCTCCCGGTTCAAGYATTTCTCTGCTCAAGCTT 3582
Db 27079 TGATCTCGGCTACCCGCAACCTCCACTCCAGGTTCAAGCAATTTCTCTGCTCAGCCT 27020
Qy 3583 CTTGAGTGTGAATTAACAGCGTGCACCACTGCTGGCTAATTTT-TGTATTTTTT 3641
Db 27019 CTTGAGTGTGGGATTACAGGATGACCAACCGCCGCTAATTTTGTATTTTTTTT 26960

RESULT 14

US-09-949-016-14438/c
; Sequence 14438, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Qy 3642 AGCAGAGATGGGGTTTTTACCATTGTTGCCAGAGCTGGTCTCAAACTCTCGACCTCAAGTGA 3701
Db 26959 AGTAGAGAGCGGGTTTCTCCATGTTG---AGGCTAGTCTCTAACTCCGACCTCAGGTGA 26903
Qy 3702 TCTGCTCGCTCAGTCTCCCAAGTGTGGAAATATATAGGCGTGAGTCACTGTGCGCTGGCC 3761
Db 26902 TCCGCTCGCTCGGCTCCCAAGTGTGGGATTAACAGGTGTGAGCCACCGTGGCCGGCC 26843
Qy 3762 GATTACTGTCTATTTTCTTTTATGCTATATCCCCAGATCTAGAGCAGTGTCTGACATATA 3821
Db 26842 TATACCT---TATTTTTCATCAATAAATAATATATAGCTTAACTACCTGTGTCACTATA 26786
Qy 3822 GTAGGTGCTCAATAAATAAATGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTT 3881
Db 26785 TTAATAATGAGACCAATTAACACCCAGTATTCATAAATAAAAAAATTTAAAGTCAAAA 26726
Qy 3882 TTTTAA---AAACATCTTGACAACTTTTGCAGATAAATAAATCTTGCATTTCTGCTTTT 3937
Db 26725 ATTAATACTAAACAATTTGTTTCTTGTGAGATCTAGCCCAATGTCTCTGTCTCTCT 26666
Qy 3938 TCACATTATCACCTTGTATGACTTTTTCATATTTGCTCAAACTTTTATTTGTTACTGTTTT 3997
Db 26665 TCTGCTTCAATGCTTTCTATCTTTCCCTACATGATGATAGCTTGCAGTGGCTTCCAC 26606
Qy 3998 TTCATTGTTACTATTTTAGTCACTGA--ATAATATGGCTTAAATTTGCTTTATACATCTCC 4055
Db 26605 TTCATTACTAATCTACACCTAACACAGCGTAAGATGTATGAAAGATTTGTTACTAATA 26546
Qy 4056 TGCTCACCTTTAGAAG-----GCTTATGTTTATTTTCAACAACATTTTCTTAGTCAAT 26486
Db 26545 GTATCAAAAGTTATAACCTTATTTTATGTTTATTTTCAACAACATTTTCTTAGTCAAT 26486
Qy 4098 TATGAACCTCTCTCCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTT 4157
Db 26485 TCTGCTTAGATTTCTAAGACAAAAGATAGAGTTAAAGCTAGACTCAGACCTATCTC 26426
Qy 4158 TAATGTTTGCACCTAAGACAAAGAACCTGCATTTAGAGGATGTTGTTCTATATAATAA 4217
Db 26425 AACCACTGTTGCTTCAAGTAAACAAAGTTTAAAGATTTGTTAGCTTAAAGCAATGACGTAT 26366
Qy 4218 ATAACTCAGTTGGGCA---CAGTGACTCAAGCTGTAAACCACAGTACTTTTGGAGTCC 4273
Db 26365 AAAAAACATTAAGGCGAGGTGCGAGTGGCTCAGCTGTAAATCCAGCACTTTTGGGAGGCC 26306
Qy 4274 AAGTGGGTGGTCACTTGGGTGAGAAATTCGAGACAGCGCTGTCTAATATGGTGAAC 4333
Db 26305 TAGGACGAGCATCAC--GAGTCAAGAGATCGAACCATCTCTGGCTAACCGTGAAC 26248
Qy 4334 CCTATCTCTCTAATAAAATAC-AAAAATAGCTGGGTAGTGTGATGATGCTGTAGTCC 4392
Db 26247 CCTATCTCTCTAATAAAATACAAAAATTTAGCGTGCATGGTGGCACACGCTGTAGTCC 26188
Qy 4393 AGCTACTCGGAGGCTGAGGCAAGAAATTTGTTGAACCTGGGAGGAGAGTTGCAAGT 4452
Db 26187 AGCTACTTGTGCGGCTGAGGCAAGAAATGTTGTTGAACCCCGGAGGAGCTTGCAAT 26128
Qy 4453 AGCCAGATCCCACTGCACTCCAGCTGGCGGCACAGCGAGACTCTATCTCAAAAA 4512
Db 26127 AGCCAGATCATGCGCACTGCACTCCAGCTTAGAGACAGAGCAAGTGTCTCAAAAA 26068
Qy 4513 AATAAATAAATAAAGGATCGAGAGAAACAAAACTAATAAGATTTCTTGAAGGT 4570
Db 26067 AAAACAAAACAAAAAACCACAAAAACCAAAAAACAAAAAAGAACACAAACGAATGT 26010

FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14438
LENGTH: 32068
TYPE: DNA
ORGANISM: Human
US-09-949-016-14438

Query Match 8.4%; Score 420.4; DB 3; Length 32068;
Best Local Similarity 60.7%; Pred. No. 6.9e-86;
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;

3104 TTTTCTTTCTTTTGTGTTAGACAGGGTCTTGCTC-TGTCAACCAGGATGACAG 3162
3163 TGGTGAACCATAGGTCACCTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTC 3222
3223 AGCTTCCCAAGTAGCTGGGACTACGAGCGTGACACCAACCGCTGGCTAATTAATAAAT 3282
3283 TTTTGTAGAGACTGGTCTTACTAGCTGGGTCAGCTTGTCTTAACTCTGCTGGCTTCA 3342
3343 AGCAATCCTCTACCTTGGCATCCCAAGGCTGGGATACAGGGTGGAGCCACCATGTG 3402
3402 GGTGATTCGGCTCGCTTGGGCTCCCAAGGCTGGGATACCGGCTGAGCCACTCGGC 3462
3462 CGGCTACTTATTTCTTTACATTCCTATCTTCCCAATAGATGTAAAGATCCACAGAACGG 3462
3462 CAG--CTGATTTTCTTTCTTTAGTATGCTTCAATGATGTTCTGAGCCGCTTACCT 3462
3463 ATTACTGCTTATTTCTTTCTTTCTTTTGTGAGACAGTCTCCTTATCCTCAACC 3522
3522 TATTTTCTTTTGTGAGATGGAGTTTGTCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3582
3582 TCCGTTTCCAGCTCACTGCAACCTTGGCTCCCGGTTTCAAGYGATTTCTGCTTGAAGCTT 3582
3582 TGATCTGGCTTCCCGCAACCTTCACTTCCAGGTTCAAGCAATCTCTGCTGCTGAGCTT 3642
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3696 AGCAGAGATGGGTTTACATGTTTGGCCAGGCTGCTTCAAACTCTGCTGACCTCAAGTGA 3701
3701 AGTAGAGACGGGTTTCTCCATGTTG--AGGCTAGTCTTAACTCCCGACCTCAGGTGA 36903
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3761 TCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 36843
36843 GATTACTGCTGCTTATTTCTTTTATTTGCTATATATATATATATATATATATATATATAT 3821
3821 TATACCT--TATTTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 26786
3822 GTAGGTGCTCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 3881
26785 TTAATAATGAGACCATTAATAACACCATGATTCTCACTTAATAAATAAATAAATAAATAAATA 26726

3882 TTTTA---AAACAATCTTGACAACTTTGCGAGATAAATAACAATCTTGCAATCTTCTGTTTT 3937
3937 ATTAATACTAAACAACTTTTCTTCTGTCAGATGAGCCAAATGCTCTCTGCTCTCTCT 26666
3938 TCACCTTATCACCTGTTATGACTTTTTCATATGCTGCTCAAACTTATTTGTTACTGTTTT 3997
26665 TCTGGCTTCAATGCTTCTTCTTCTTCCCTACATGATATAGTCTTGCAGTGGCTTCCAC 26606
3998 TTCATTTGTTACTTATTTTGTACTGCA--ATAATATGCTGCTTAAATTTGCTTATACATCTCC 4055
26605 TTCATTTGTTACTTATTTTGTACTGCA--ATAATATGCTGCTTAAATTTGTTTACTTAATGA 26546
4056 TGCTCCACTTTAGAAG-----GCCAAATTTTACAAATCTCTCATGAAGC 4097
26545 GTATCAAAAGTTATTAACCTTATTTTATTTTATTTTCAACAACATTTATTTAGTTCATTTGCAT 26486
4098 TATGAACCTCTTCCCAAGAGAAATACACACACACACACACACACACACACACACACACACAC 4157
26485 TCTGCTTAGATTTCTTAAGACAAAAAGATAGAGGTTTAAAGCTTAGACTCAGAGCCTATCTC 26426
4158 TATGTTTTCGAACCTAAGACAAAGAACTTGCATTAGAGGATGTTTCTTATTAATTAATAA 4217
26425 AACCACTGCTTCACTAGTAAACAAAGGTTAAGATTTGTTAGCTTAAAGCAATGACGTATT 26366
4218 AATAACTCAGTTGGCA---CAGTGACTCAAGCCTGTAACCAACACACACACACACACACAC 4273
26365 AAAAACTTAAAGCCAGGTCAGTGGCTCAGCCTGTAATCCAGACACCTTTGGGAGGCC 26306
4274 AAGTGGTGGATCACTTTGAGTGAGAGTTCGAGACACACACACACACACACACACACACAC 4333
26305 TAGGCAGGACGATCAC--GAGGTCAGGAGATCGAGACCATCTCTGGCTAACACGGTGAAC 26248
4334 CCTATCTCTTAAATAATAC--AAAAATTTAGTGGTGTAGTATGATCATGCTGCTGTTAGTCCC 4392
26247 CCCATCTCTTAAATAATACAAAAATTTAGCCGTCATGTTGGTGCACACGCTGTAGTCCC 26188
4393 AGCTACTCGGAGGCTGAGGCAAGAGATTTGCTTCAACTGGGAGGACAGAGTTGCAAGT 4452
26187 AGTACTTGTGGGCTGAGGAGGAGATGTTGTGAACCCGGGAGGACAGAGTTGCAAGT 26128
4453 AGCCGAGATCCACACCTGCTCAGCTCCAGCTGGGCAACACAGGACGACTCTATCTCAAAAA 4512
26127 AGCCAAAGATCATGCTCAGCTCCAGCTTCCAGCTTAGGACACAGACAGACTGTCTCAAAAA 26068
4513 AATAAATAAATAAATAAAGGATCGGAGAGAACAAAACTAATAGATTTCTTGAAGGT 4570
26067 AAAAAACAAAAAAACCCCAAAAAACCAAAAAACAAAAAGAAACAAAAACGAATGT 26010

RESULT 15
US-09-949-016-14439/C
Sequence 14439, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14439
LENGTH: 32068
TYPE: DNA
ORGANISM: Human
US-09-949-016-14439


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QY 3283 TTTTGTAGAGACTGGTCTTACTAGCTTGGCCAGGCTGTCTTAAACTCCTGGCTTCA 3342
Db 27316 TTTTGTAGAGACAGGGTTTCCATGTGTGGTCAGGCTGATCTGAACTCCCGACTTCA 27257
QY 3343 AGCAATCCTCCTACCTTGGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCATGTG 3402
Db 27256 GGTGATCGGCTGGCTTGGCTCCCAAGTGTGGGATTACCGGCTGAGCCACTCGGCC 27197
QY 3403 CGGCTACTTATTTCTTACATTCCTTTCCAAATAGAAATGTAAGATCCACAGAAACAGG 3462
Db 27196 CAG---CTGATTTTCTCTTCAGTATGTCCAATGATGTCTCGAGCCGCTTATACCT 27140
QY 3463 ATTACTGCCATTTTCTCTCTTTTGGACAGAGTCTCACITCATCACTCAACC 3522
Db 27139 TATTTTTTTTTTGGATGGAGTTTGTCTTTTGGCCAGGCTGGAGTGAATGAGG 27080
QY 3523 TCGGTTTCAGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTTCTCTGCCCTAAGCCT 3582
Db 27079 TGATCTGGGCTCACCGCAACCTCCACCTCCAGGTTCAAGCAATTTCTCTGCCCTCAGCCT 27020
QY 3583 CTTGAGTAGCTGAATTTACAAAGGTGCAACCACCATGCTTGGCTAAATTTT-TTGATTTTT 3641
Db 27019 CTTGAGTAGCTGGGATTACAGGATGCACCAACCGCCGCTAAATTTTGTATTTTTTT 26960
QY 3642 AGCAGATGGGTTTTACCATGTGCCAGGCTGCTCAAACTCTCAAACTCTGACCTCAAGTGA 3701
Db 26959 AGTAGAGCGGGTTTTCTCATGTG---AGGCTAGTCTCTAACTCCCGACCTCAGGTGA 26903
QY 3702 TCTGCTTCGCTCAGTCTCCCAAGTGTGGAATATATAGGCGTGAGTCACTGTGCTGGCC 3761
Db 26902 TCCGCTGCCTCGGCTCCCAAGTGTGGGATTACAGGTGTGAGCCACCGTCCCGGCC 26843
QY 3762 GATTACTGTCTATTTCTTTATTTGCTATATCCCCAGATCTAGAGCAGTGTGACATATA 3821
Db 26842 TATACCT---TATTTTCATCAATAAATAATATATGACCTTAAACTACCTGTGTATACTTA 26786
QY 3822 GTAGGTGCTCAATAAATAATTGATGATGCACAGCTTAGATATAAACTTTCTTTTCTTT 3881
Db 26785 TTAATAGAGACCATTAACACAGATATTCCTAAATAAATAAATAATTTAAAGTCAAA 26726
QY 3882 TTTTA----AAACAATCTTGACAACTTTGCAGAAATAATAACAATCTTGCAATCTGCTTTT 3937
Db 26725 ATTAATACTAAACATTTGTTTCTGTGTCAGATCTAGCCAAATGTCTCTCTCTCT 26666
QY 3938 TCATTATACCTTGTATGACCTTTTCATATTTGCCTCAAACTTTATTTGTTACTGTTT 3997
Db 26665 TCTGGCTTCAATGCTTTCTATCTTTCCCTACATGTATACTAGCTTGCAGTGGCTTCCAC 26606
QY 3998 TTCAATGTTACTATTTTGTACTGA--ATAATATGCTTAAATTTGCTTATACATCTCC 4055
Db 26605 TTCAATTAATCTACACCTTAACAGCCGTAGATGTTTGAAGATTTGTTACTAATGA 26546
QY 4056 TGCTCCACTTTAGAG-----GCCAAATTTACAAATCTGATGAAGC 4097
Db 26545 GTATCAAGTTATAACCTATTTTATGTTATTCAACAACATTTCTTAGTCAATTTGCA 26486
QY 4098 TATGAACCTCTCCCGAGAAATACACACACACACACACTCAACACACAGTTTTTTTT 4157
Db 26485 TCTGCTTAGATTTCTAAGACAAAGATAGAGTTAAAGCTAGACTCAGAGCCTATCTC 26426
QY 4158 TAATGTTTGAACATAACACAAGAAACCTGCAATTAGAGATGTTTGTTCATATTAATAA 4217
Db 26425 AACCACTGGCTTCAGTAGAACAAAGGTTAAGTAATTTAGCTTAAGGCAATGACGTATT 26366
QY 4218 AATAACTCAGTTGGCA----CAGTGACTCAAGCCTGTAAACCAACAGTACTTTGGAAGTCC 4273
Db 26365 AAAAAACATTTAAGCCAGGTGAGTGGCTCACGCTGTAATCCAGCACTTTGGGAGGCC 26306
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QY 4334 CCTATCTCTCTATAAAATAC-AAAAATTAGCTGGGTAGTGTGATGATGCCTGTAGTCCC 4392
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QY 4393 AGCTACTCGGAGGCTGAGGCAAGAAATTTGCTTGAACCTTGGGAGCAGAGTTTGCAGTG 4452
Db 26187 AGCTACTTGTGGGCTGAGGCAAGAAATGTTGTGAACCCGGGAGCAGAGCTTGCAGTA 26128
QY 4453 AGCCAGATCCACACCTGCACTCCAGCTGGGCGACACAGCAGACTCTATCTCAAAA 4512
Db 26127 AGCCAGATCATGCCACTGCCACTCCAGCTTAGGACACAGCAAGACTGTCTCAAAAACA 26068
QY 4513 AATAATAATAATAAAGGATCGAGAGAAACAAAACTAATAAGATTCTCTGAAGGT 4570
Db 26067 AAAACAAAACAAAAAACCCAAAAACCAAAAAACAAAAAGAACACAAACGAATGT 26010

RESULT 17
US-09-949-016-14441/c
; Sequence 14441, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14441
; LENGTH: 32068
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14441

Query Match      8.4%; Score 420.4; DB 3; Length 32068;
Best Local Similarity 60.7%; Pred. No. 6.9e-86;
Matches 910; Conservative 1; Mismatches 542; Indels 45; Gaps 12;
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QY 3104 TTTTTTTTGTGTTGTTTAGAGACAGGCTCTTGTC-TGTCACCCAGCATGAGCACAG 3162
Db 27493 TTTTTTCTCTTTTTTTTTTGAGACGGAGTTTCGCTCTTGTGCCCAGGCTGGAGTCAA 27434
QY 3163 TGGTCAACCATAGTCTACTGCAGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTC 3222
Db 27433 TGGTCAATCTTGGCTCACCGCACTTCGCTTCTCGGTTCAAGCAATTTCTTGCCTC 27374
QY 3223 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACCGCTGGCTAATTTAAAAAAT 3282
Db 27373 AGCCTCCCAAGTAGCTGGGATTACAGGCATCGCCACCATGCTCCGCTAGTTTGTGA--- 27317
QY 3283 TTTTTTGTAGACATGGGTCTTACTACGTGGGCGAGGCTTGTCTTAAACTCTGGCTTCA 3342
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QY 3463 ATTACTGCCATTTTCTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 3522
Db 27139 TATTTTTTTTTTTTGGATGGAGTTTGTCTCTTTGTCGCCAGGCTGGAGTGAATGAGG 27080
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Qy	3223	AGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACGCTTGGCTTAATTTAAAAAAT	3282
Db	38833	AGTCTCCCAAGTAGCTGGGACTATAGGAGCCTGCCACCAACGCTTGGCTTAATTTTGTGA	38774
Qy	3283	TTTTTTTGTAGAGACTGGGTCTTACTACGTTTGGCCAGGCTTGCTTAAACTCCTGGCTTCA	3342
Db	38773	ATTTTATAGTAGAGCGGGTTTACCATAATGGCCAGGCTGGTCTCGAACTCCTGAC--CT	38716
Qy	3343	AGCAATCTCTACTACCTTGGCATCCCAAAGTGTCTGGGAATTACAGGGGTGAGCCACCATGTG	3402
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Qy	3403	CGGCTACTTATTTCTTTTACATTCCTATTCCTATTTCCAAATAGAAATGTAAGATCCACAGAACAGGG	3462
Db	38655	TGCGCCAGTTAAATGTTTTTTTATAGATGTCTGCTGAAAGTTGTTTTTTC-----	38607
Qy	3463	ATTACTTGCCTATTTCTTCTCTCTTTTGTAGACAGAGTCTCACTTCATCACCTCAACC	3522
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Qy	3523	TCGGT-----TCAGCTCACTGCACCTCTGCTCTCCGGGTTCGAAGTGATC	3568
Db	38547	GGAGTGCAAATGGTGCATCTCGGCTCACTGCACAACTCCACCTCCAGGTTCAAGTGATTC	38488
Qy	3569	TCTTGCTTAAGCCTCTGAGTAGCTGGAATTACAGCGTGCACCACTGCTTCGGCTAA-	3627
Db	38487	TCTTGCTTCAGCCTCCCAAATAGCTGGGAATACAGCATGCACCACTATCCCGGTAAAT	38428
Qy	3628	---TTTTTTTGTATTTTTTAGCAGATGGGGTTTTACCATTGTGGCCAGGCTGGTCTCAAA	3684
Db	38427	CTTTTTTTTTGTATTTTTAGGAGACGGGTTTTTACCATTGTGGCCAGGCTGGTCTCGAA	38368
Qy	3685	CTCCTGACCTCAAGTAGATCTGCTGCTCAGTCTCCCAAAGTGTCTGGAATTTATAGGCGTG	3744
Db	38367	CCCTGACCTCAGGTGATCTGCCACCTCAGCTTCCCAAAGTGTCTGSAATTTATAGTGTG	38308
Qy	3745	AGTCACCTGTGCTTGGCGGATTACTGTCTATTTTCTTTATTGTCTATCCCCAGATCTAGA	3804
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Qy	3805	GCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACGCTAGATAT	3864
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Qy	4045	ATACATCTCCTCTCCACTTTAGAAGGCCAAATTTACAAATCTCATGAAAGCTATGAAC	4104
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Qy	4105	CCTCTCCCCAGAGAAATACACACACACACACTCAACAGATTTTTTTTTTAATGTT	4164
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Qy	4165	TGCAACTAAGACAAGAAACCTGCATTAGAGGATGTTGTTTCATATTAATTTAAATAACT	4224
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Qy	4225	CAGTTGGGCACGTACTCAAGCCTGTAAACCAAGTACTTTTGGAAAGTCCAAAGGTGGGTG	4284
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RESULT 21

RES001 ZI
US-09-949-016-13045/c

US-93-343-013-13043/C
: Sequence 13045, Application US/09949016

: Patent No. 6812339

FACEBOOK NO. 0812333
: GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENIER, J. CLAY ET AL.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

INVENTOR	ATTORNEY
<p> TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE METHODS OF DETECTION AND USES THEREOF </p>	<p> TITLE OF INVENTION: WITH HUMAN DISEASE METHODS OF DETECTION AND USES THEREOF </p>

; TITLE OF INVENTION: WIRE
; FILE REFERENCE: CI.001307; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: IIS/09/949 016

CURRENT APPLICATION NUMBER: US70
CIPBTT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14

30 PRIOR APPLICATION NUMBER: 607

; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 50/233775

;; PRIOR APPLICATION NUMBER: 607

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast:

; SEQ ID NO 13045

; LENGTH: 4

; TYPE: DNA

; ORGANISM

FEATURE:

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; NAME/KEY: misc_feature
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; LOCATION: (1) ... (45300)

OTHER INFORMATION:

Query Match 8.38: Score 415; DB 3: Length 45300;

Query Match	8.5%	Score 413, DB 3,
Best Local Similarity	60.7%	Pred. No. 1 4e-84:

Best Local Similarity 80.7%, Freq: NO, 1.4E-84,
Matches 877: Conservative 1: Mismatches 511: Indels 56: Gaps 10:

Ov 3104 TTTTCTTTCTGTTCTTTAGAGACACAGGGTCCTTGCTGTCACCACGCAT-GAGCACAG 3162

QY 3104 TTTTITGTTGTTTAGAGACAGGGCTTGCCTCIGTCACCCAGGCAT-GAGCACAG 3102

38953 TTTGGTATTGTTTCTCTGAGATGGAGTCTCACCTGTCCTTGGGGTGGAGGGCAG 38894

[illegible]

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

D5 38893 TGGCGCAATCTCAGCTCACTGCAACCTCTGCCCTCTGGGTCAAGCTATTCTCTCTGACTC 38834

Qy 3223 AGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACCAACGCTGGCTAATTAAAAAAAT 3282

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Qy 3283 TTTTGTAGACTGGGTCTTACTACGTGGCCAGGCTTGCTTAACCTCCTGGCTTCA 3342 Qy

Qy	2164	GGCA--GAATGTAGCAACAGTAAACATCACGAACTATCCACGTGTCAATTTCTAGCA	2220
Db	33460	GAATAACAAATGTCTACAAATGTGAGGGTTATTTCTGACTCTCACTTCTAATCAAATG	33401
Qy	2221	GTGGTGTCTCACTGCACCTCTCTGAATACAGAGTTTACTGTATCTTCTGCAACCATGTTAA	2280
Db	33400	GTCTATGTCTCTCTTGTGTCCAGTAAACAAATTTACTATTTGTCTTTATAGTAAGTTTAA	33341
Qy	2281	AATCGCTTTTCAGGCCAGCGCGGTGGCTCATGCTGTAAATCCAGCACCTTTGGGAGGCGG	2340
Db	33340	TTGAGAGTAAGCCAGGTACAGCTGCTCACACTGTATCTCAGCACCTTTGGGAGTCCA	33281
Qy	2341	AGCGGGCGGATCACCTTGAGGTTCAGAGTTCGAGACCGCTTGGCCAAACATGGTGAAC	2400
Db	33280	AGGAGACAGATGTTTCGAGCCGAGAAGCTCGAGACCGCTGGATAACTCGATGAAAC	33221
Qy	2401	CTGTCTCTACTAAAAATACAAAAATTTAGCCGACATGGTGGGAGCGCTGTAAACCCA	2460
Db	33220	CCATCTCTAC-AAAAAATACAAAAATTTAGCTGGACATGGTGTGCACGCTGTAGTCCCA	33162
Qy	2461	GCCTACTTGGGAG-----ACTGAGTTGGAGTTTCACTGAGC	2496
Db	33161	GCCTACTTGGAGGTGAGGTGAGGATCGTTAGCCAGGAGCGGAGAGCCAGTGAAC	33102
Qy	2497	CAAGGTCGTCTACTGTCTCCAGCCTGGGTAAACAG--AGCAACTCTGTCTCAAAAAAA	2554
Db	33101	TGAGATCATGCCACTGCACCTCCAGCCTGGGTGACTCGACGAGGCGCTGTCTCAAAAAAAT	33042
Qy	2555	AAAATGCTTCAATAAATATATGATAAAAGGACTTATATTTTTTCAGCCATAGGA----	2610
Db	33041	TAATAAAATAAAAATTGAGAAACATGAAGGCCAGCGCAGTGGCTCATGCTGTAAACCCA	32982
Qy	2611	----TCATTTCTCTCTGAAGCATCTCGCGAAGTCATCCCACTGTTCTCTGAGAGTGGGC	2666
Db	32981	GCATTTGTGAGGAGAGGTGGGTGGATCACTGAGGTGAGAGTTTGAGACCACCTGA	32922
Qy	2667	AGGTGAGGCGTACCTATTGCTCTGCACCTTACTCTCTATCTCAGCTGTCTCCCTCCCACTTTC	2726
Db	32921	CCAACTAGTGAAACCCCGSCTCTCTAAAAATPACAAAATTAGCTGGGTATGGTGTGCA	32862
Qy	2727	CAGGTGCTGCAGACATGACAACTCTTAYGACAGG-----CNAAGAGCTGACAGC	2781
Db	32861	TGCGTCAATCCCAAGTATTGTGGAGGCTAAAGCCGAGAAATCCCTTGAAACCCAGGAGGC	32802
Qy	2782	TGTAAATTTCTGCTGGACAMMCGTACACCCACACCTATTC-----ATACTCGTG	2831
Db	32801	AGAGGCTGCAGTGAGCTGAGATCGTGCCATTAACACTCCAGCCTGGCGACAAACAGTGAA	32742
Qy	2832	CTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTGACCTATGAATTTCTA	2891
Db	32741	CTCGTCTCAAAAAAANAANAAGAGAGAGGCTCAGGGTCTCTCAACTTGT	32682
Qy	2892	GTTGGTTCCTCAGTAGGCCGG-----GGGGAATAATAGTAACACAGCCATGATTTAG	2944
Db	32681	GTTTTTCAAGATTGTTTGGCTATTCCGGGTTCCTTCTATTCTTCTTCACTGTTTCTTA	32622
Qy	2945	TGTTAATTTTCTGGTCTCGGCAGTGTCTCCTTTAATCCTCAGAACACACTATGGGAT	3004
Db	32621	TCATGAAAAAGTGTCAAAATGTTTTTCTGTATTATCAAAAGGTGATCATGTGGTTCCTGT	32562
Qy	3005	AGGTACAATTTATCTCACTTAAACAGATAAGAAACCTGAGGCTCAGAGGCTCAGCTA---	3061
Db	32561	TGTTTAAATTTATTACCACAGTGTATTACATGATTAATGATCATATGTTGGAACCAACC	32502
Qy	3062	TTTGCCCAAGATCACACAGCTCTGTAAGTGGTGAAGTCTTTGGGTTTTTTTTTGTGTGTT	3121
Db	32501	TTCTCGGATAAATCCCACTTAGTCAATGATTATGATCTTTTTTGTGTTGTTGTTGTT	32442
Qy	3122	TAGAGACAGGGTCTTGCTGTGTACCAGGCATGACACAGTGGTGGCAACCATAGGTAC	3181
Db	32441	TTGAGACAGAGTCCCGCTGTGCACCTAGGCTGGAGTGGAGTGGCAAAATCTCGGCTCAC	32382

QY	3182	TGAGCCTCAACCTCTCTAGACTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGG	3241
DB	32381	CGCAATCTTCGCTCTCGGGTTTTAAGCAAAATCTCTGCTCAGCCTCTCGGTAGCTTGG	32322
QY	3242	ACTACGAGCGTGACACACACGCTCGCTAAATTTAAAAAAATTTTTTTGTAGAGACTGGGT	3301
DB	32321	ATTA--GTCAACCGCCACCAGCCGAGCTAAATTTTTTGTA--TTTTTGTGAGAGACGGGT	32266
QY	3302	CTTACTACGTTGGCCAGGCTTGCTTTAAACTCCTGGCTTCAAGCAATCTCTTACCTTGG	3361
DB	32265	TTCAACATGTTGCCAGGCTGGTCTCGAACTCTGACCTCATG--ATCCGCCACCTCAG	32208
QY	3362	CATCCCAAGTGTGGGATTAAGAGGGTGAGCCACCATGTGGGCTACTTATTTCTTTAC	3421
DB	32207	CCTCCCAAGTGTGGGATTTACAGGAGGAGCGAGCATGCCGGCTGATCTTTTTCATAT	32148
QY	3422	ATTCCATCTTTTCCAAATAGAATGAAGATCCACAGAACGGGATTACTGCTATTTTCTTC	3481
DB	32147	GTTACTGAATACAGTCATCTAGTATTTTGAAGACATGGCGGTACAAGCATACTTTTTTT	32088
QY	3482	CTTTCCTTTTTTGAGACAGAGTCTCACTTTCATCACCTCAACCTCCGT-----	3527
DB	32087	TTATTTTTTTGGATCAAGTCTCTCTCTCGTCCGCCAGGTGGAGTGCCATGGAGCAATC	32028
QY	3528	TCAGCTCACTGCAACCTCTGCTCCCTCC-----GGTTTCAAGYGATCTCTGCTTAAGCCTC	3583
DB	32027	TCAGCTCACTGCAACCTCTGCTCCCTCCCTGGGTTCAAGGCTATTTCTGTGCTCAGCCTC	31968
QY	3584	CTGAGTAGCTGGAAATTACAAGCGTGCAACCACTGCTTGCTTAAATTTTTTGTATTTTAG	3643
DB	31967	CCAAGTAGTCAGGATTACAGGCCACCAACCACTGTGCTCGCTGCTTAA--GTTTTGTATTTTAG	31909
QY	3644	CAGAGATGGGGTTTTTACCAATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATC	3703
DB	31908	CAGAGACGGGGTTTTTACCAATGTTGGCCAGCTAGTCTCAAACTCCTGATCTCA-----	31856
QY	3704	TGCTGCTCAGTCTCCCAAGTGCTGGAAATTATAGCGTGAGTCACTGTGCTGCGCCGA	3763
DB	31855	----CACCTTTGGCTCCCAAAGTGTGGGATTACAGGCATAAGTACTGTGCCAGGCCCA	31800
QY	3764	TTACTGCTATTT-----TTCTTTATTGCTATATATCCCCAGATCTAGAGCAGTCTGACAT	3818
DB	31799	TACTTGTGTTTTTAATCAGTAAAAAGTATCTCTAAATTTAAGACGAGGTAAATTTCCAAGTCC	31740
QY	3819	ATAGTAGTGCTCAATAATAATTTGATGAATGACAGCCTAGATATAAACTTTCTTTTTTC	3878
DB	31739	TGATCAATTAATCATACATCACTTCCTCTTTAAATTTCACTTCCCTAAAAAATGTCCC	31680
QY	3879	TTTTTTTTAAAAAATCTTGCAAACTTTGCAGAAATAATAACAATCTTGCAATCTGCTTTTT	3938
DB	31679	TAGAAATAAACTAGTAATGACCATGAGGACCTTTTCTTTGGACACAGATATGCTCTAAGT	31620
QY	3939	CACTTATCACCTTGTATGACT-----TTTTTCATATGCTCTCAAACTTTA	3984
DB	31619	CGTAGGTCTCCCTTTAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA	31560
QY	3985	TTGTTACTGTTTTTTCATTTGTTACTATTTTAGTCA-----CTGAATAATATGGCTTAAT	4039
DB	31559	CTAGGTGAACGTTCCCTCTAGTCTGCTGTTGGCTATATCTTGAATAATATGTCAGTAATG	31500
QY	4040	TGCTTATACATCTCTGCTCCACTTTTGAAGGCCAAATTTTACAATCTGTATGAAGCTA	4099
DB	31499	AATAAGTATTTTCTCCTATACCTATAGAAATGGCTGTAGTCAATTTTCCAAGTATAGCT	31440
QY	4100	TGAA-----CCCTCTCCCGAGAGAAATACACACA	4130
DB	31439	TTAAGAGGCCAAGTCCAGGCCACTAAGTAGTTCTCTACTTACTAGTATGAGAAAAATACTTT	31380
QY	4131	CACACACACTCACACACAGTTTTTTTTTAATGTTTGCACCTAAGACAGAACCTGCATT	4190
DB	31379	CAGAAAGGATAAGTGATCGCCTCAATAGCATCTCAACAAAGTAAGAGTAGAGCCCGGCT	31320
QY	4191	AGAGGATGTTGTTGTTATATTAATTAATAAAT--AACTCAGTTGGGCACAGTACTCAAGCC	4248


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Qy 4501 CTATCTCAAAAAATAAATAA 4522
Db 25514 CTGTCTCAAAAAATAAATAA 25493

RESULT 27
US-09-949-016-17289/c
; Sequence 17289, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17289
; LENGTH: 64518
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17289

Query Match 8.1%; Score 406.8; DB 3; Length 64518;
Best Local Similarity 59.8%; Pred. No. 1.2e-82;
Matches 874; Conservative 1; Mismatches 548; Indels 39; Gaps 10;

Qy 3081 CTTGTAAGTGGTGACAGTGTGGGTTTTTTTTTTTGTGTTTGTATAGACAGGGTCTTGCTC 3140
Db 26935 CCTAAAGGTACAAAACTTGCCTTTTTTTTTTTTTTTTTTTTTTTTGTGATGAAGTCTCACTC 26876

Qy 3141 -TGTCACCCAGGATGACAGTGTGGTGAACCATAGTGCACCTGCAGCCTCAACCTCCCTG 3199
Db 26875 TTGTTGCCAGGCTGCAAGTGGCAATCTGGCTCATTTGCAACCTCCACCTCCCG 26816

Qy 3200 AGCTCAAGGATCTGTGACTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCCACCAC 3259
Db 26815 GGTTCAGCGATTCTCTGCTCAGCTCCGAGTAGCTGGGTTACAGCGCGCTGCCAC 26756

Qy 3260 CACGCTCGGTAAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTAGTTGGCCAGG 3319
Db 26755 CACACCCAGCTAATTTTTTGTA--GTTTTAGTAGAGACAGGGTTTCACCATGTTGGCCAGG 26698

Qy 3320 CTTGTCTTAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTCTGGGA 3379
Db 26697 CTGGTCTCGAACTCTTGACCTCAGGCGATCTGCCACCTCAGCCTCCCAAGTGTGAGGA 26638

Qy 3380 TTACAGGGGTGAGCCACCATGTGCGGTACTTATTTCTTACATTTCCATCTTTTCCAATAG 3439
Db 26637 TTACAGCATGAGCCACCGTGGCCAGCAAACTTGCTGCTATTCTTTAGGCTT----- 26586

Qy 3440 AATGTAAGTCCACAGAACAGGGAATTACTGCCTATTTTCTTCTCTTTTGTGAGACAG 3499
Db 26585 ATTCTGGACTTACAAACAGACAAACCTGGCCTTTTGTGTTTTTTTGTGTTTTTGTGATGG 26526

Qy 3500 AGTCTCACTTCACTCACTCACTCCCTCGT-----TCAGCTCACTGCAACCTTGCCT 3550
Db 26525 AGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGATCTCGGCTCAGTGCACCTCCATCT 26466

Qy 3551 CCCGGGTTCAAGYATTTCTCTGCTAAGCTCCTGAGTAGCTGGGAATTAACAAGCGTGA 3610
Db 26465 TCCGGGTTCAAGCAATTTCTCTGCTCAGCTCCAAAGTAGCTGGGACTACAGCCACCAG 26406

Qy 3611 CCACCATGCTGGCTAATTTTTTGTATTTTGTAGACAGATGGGGTTTTTACCATGTTGCC 3670
Db 26405 CCACCATGCT-----AATTTTGTATTTTGTAGACAGGTTTTCACCTTATTGGTC 26351
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Qy 3671 AGGCTGGTCTCAAACTCCTGACCTCAAGTGATCTGCCTGCCTCAGTCTCCCAAAGTGTG 3730
Db 26350 AGGCTGCTCTCGAACTATTGACCTCAGGTGATCCACCACCTAGGCTCCCAAAGTGTG 26291

Qy 3731 GAAATTATAGGCGTGTGATCTGTGCTGCTGCCGCAATTAATGCTCTATTTTCTTTATGCTATA 3790
Db 26290 GGATTACAGGCGTGAGCCACCATGCGCGCC---AACCCCTAGCCTGTCTTTATCTCTATG 26234

Qy 3791 TCCCAGATCTAGACAGTGTCTGACATATAGTAGTGTCTCAATAAATTAATGATCAATG 3850
Db 26233 CAGATACCTTAAACACATCTACCAATTCAGAAAGTATTCAAAATCCAAACATGTAA 26174

Qy 3851 CACAGCTAGATATAAACTTTCTTTTCTTTTAAACAAATCTTTGACAACTTTGCACA 3910
Db 26173 CATCCAGTATTATTTGGGCCCATGTAATTCATTGTTTTCACCTTTATTCGTACAGTTAAAAA 26114

Qy 3911 ATAAATACAACTTTGCAATCTGCTTTTTCACCTTTTACCTGTTTATGACTTTTCAATTT 3970
Db 26113 AAAAAAATATCCGGGACATTTCTTCTGGAATTAATGCTATTTGGCATTAGAGGAGTTTC 26054

Qy 3971 GCCTCAAACTTTTATGTTTACTGTTTCTTTTCTATTGTTTCTATTGTTTCTGATTAAT 4030
Db 26053 GCGAACAGTCTACATCAAAACAGGGTGTCTGA--AGTCTCTGTGCTCTTCCCAAAGCACAG 25995

Qy 4031 GGCCTAATTTGCTTATACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4090
Db 25994 CCAGCCCTGGGGCACAGGAGGAGTCTCAAGTCCCAACCTGCCACAGAGCATAT 25935

Qy 4091 TGAAGAGTATGAACCTCTCTCCAGAGAAATACACACACACACACACTCACACA--CAG 4149
Db 25934 CAGTGTCTCACCATTGTTGTAAGAAACACAAAAAGGATAAAACCAAGAACTGATGTG 25875

Qy 4150 TTTTCTTTTAAATGTTTGCACCTTAAGACAGAAACCTGCACTTAGAGAT--GTTTGTTCATA 4208
Db 25874 ACTGTGATTTTGTCTCTTAGGACTACTGAAACACAGACCAACAACTAGGCGAGTTTCAA 25815

Qy 4209 TTAATTAATAATACTCAGTTGGGCACAGTCAAGCTCTGAAGCTCTTAACCAACAGTACTTGA 4268
Db 25814 AAGGTCCACAGTCTGAGCCAGGCACAACTCACACTGTAATCCAGCACCTTTGGG 25755

Qy 4269 AGTCCAAGTGGGTGGATCACTTGAAGTGAAGTTTCAGACAGCCTCGTCAATATGTT 4328
Db 25754 AGGCCAAGCAGGAGAAATCGCTTGAGCCAGGGTTTAAAGACAGCCTGGGCAAGAAGT 25695

Qy 4329 GAAACCTTATCTTACTATAAATAACAAAATTTAGCTGGGTGATGATGATGCTGCTAG 4388
Db 25694 GAGACTCCATCTCTGCAAAAAACACAAAAAATAGGCAAGTGTAGTGTGCTGCTAG 25635

Qy 4389 TCCCAGTACTCGGAGGCTGAGGCAAGAGAAATTTGCTTCAACCTGGGAGGCGAGAGTTGC 4448
Db 25634 TCCCAGTACTTGTGAGGCTGAGGTGGGAGATCACTTGAAGCCAGGATGTTGAGGCTGT 25575

Qy 4449 AGTGAGCCAGATCCCAACA-----CTGCACTCCAGCCTGGGCGACACAGCGAGACT 4500
Db 25574 AGTGAGCCAGATCACTACCTACCGCACTTCTGCACTTCAGGCTGGGTGAGACAGCGAGACT 25515

Qy 4501 CTATCTCAAAAAATAAATAA 4522
Db 25514 CTGTCTCAAAAAATAAATAA 25493
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RESULT 28

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US-09-949-002-843/c
; Sequence 843, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
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; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 843
; LENGTH: 64518
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-843

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Query Match 8.1%; Score 406.8; DB 3; Length 64518;
Best Local Similarity 59.8%; Pred. No. 1.2e-82;
Matches 874; Conservative 1; Mismatches 548; Indels 39; Gaps 10;

Qy	3081	CTTTGTAAGTGGTGACAGTTTGGGTTTTTTTTTTGTTGTTGTTTAGAGACAGGGTCTTGTC	3140
Db	26935	CCTAAAAGGTACAAAAAATTTGCCTTTTTTTTTTTTTTTTTTTGTAGATGAAGTCTCACT	26876
Qy	3141	-TGTCAACCCAGGCATGAGCACAGTGGTGCAACATAGGTCACTGACAGCCTCAACCTCGT	3199
Db	26875	TTGTGTGCCAGGCTGCAGTGCATATGTGCAATCTGGCTCATTTGCAACCTCCACCTCCCG	26816
Qy	3200	AGCTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAC	3259
Db	26815	GGTTCAAGCATTTCTCTCGCTCAGCTCCCGAGTAGCTGGGTTTACAGGCGCTGCCAC	26756
Qy	3260	CAGCCTGGCTAAATTAATAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTGTGCCAGG	3319
Db	26755	CACACCAGCTAATTTTGTGA--GTTTTGTAGACAGAGGTTTTCACCATGTTGGCCAGG	26698
Qy	3320	CTTGTCTTAAACTCTGGGTTCAAGCAATCTCTCACTTTGSCATCCCAAGTGTGGGA	3379
Db	26697	CTGGTCTCGNACTTTTGACCTCAGGCGATCTGCCACCTCAGCCTCCCAAGTGTCTAGA	26638
Qy	3380	TTACAGGGGTGAGCCACCACATGTGCGGCTACTTATTTCTTTTACATTTCCATCTTTTCCAATAG	3439
Db	26637	TTACAGGCATGAGCCACCGTGCCACGCCAAACTTGCCTATTCTTTAGGCTT-----	26586
Qy	3440	AATGTAAGATCCACAGAACAGGATTACTGGCTATTTTTCTTCCTTTCTTTTTTTAGACAG	3499
Db	26585	ATTCTCTGGACTTACAAACAGCACAAACCTGGGCTTTTGTTTTTTTTTTTTGTAGATGG	26526
Qy	3500	AGTCTCACTTCATCACTCAACTCAACTCGT-----TCAGTCTCACTGCAACTCTGCCT	3550
Db	26525	AGTCTGCTCTGTGCGCCAGGCTGGAGTGCATGATCTCGGCTCACTGCACTCCATCT	26466
Qy	3551	CCGGGTTCAAGYGATTCTCTGCTCAAGCCTCTGAGTAGTGGAATTTACAAGCGTGCA	3610
Db	26465	TCCGGGTTCAAGCGATTCTCTGTCTCAGCCTCCAAAGTAGCTGGGACTACAGGCACCAG	26406
Qy	3611	CCACCATGCTTGCTTAATTTTTTGTATTTTAGCAGAGATGGGTTTACCATGTTGCC	3670
Db	26405	CCACCATGCT-----AATTTTTGTATTTTGTAGAGACGAGGTTTCACTTATTTGTC	26351
Qy	3671	AGGCTGCTCAAACTCTGACCTCAAGTGATCTGCTGCCTCAGTCTCCCAAGTGCTG	3730
Db	26350	AGGCTGCTCTCGAATTAATTGACCTCAGTGATCCACCACTTAGGCTCCCAAGTGCTG	26291
Qy	3731	GAATTAATAGCGTGAGTCACTGTGCTGGCCGATTACTGCTATTATTTCTTTATTTGCTATA	3790
Db	26290	GGATTACAGCGTGAGCCACCATGCCCGCC---AACCCCTAGCCTGCTTTATCTCTATG	26234
Qy	3791	TCCCCAGATCTAGACAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGATGAATG	3850
Db	26233	CAGATACCTTAAAAACAATCTACCACAAATTCAGAAAGTATTCAAATTCCAAACCATGTAAA	26174
Qy	3851	CACAGCCTAGATATAAACTTTCTTTTTCTTTTTTAAAAACAATCTTGACAACTTTGCAGA	3910
Db	26173	CATCCAGTTAATTGGGCCCAATGTAATTGATGTTTCACTTAATTCGTACAGTTAAAAAAA	26114
Qy	3911	ATAAATACAATCTTGATCTGCTTTTTTCACTTATCACCTTGATGACTTTTTCATATT	3970

RESULT 29

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US-09-949-016-16766/c
; Sequence 16766, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 16766
; LENGTH: 32584
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16766

```

Query Match 8.1%; Score 404.4; DB 3; Length 32584;
Best Local Similarity 61.4%; Pred. No. 3.2e-82;
Matches 884; Conservative 1; Mismatches 512; Indels 43; Gaps 13;
Ov 3109 TTTTGTGTGTTTACAGACAGGGTCTTGTCTGTCTACCCAGGCATGAGCACACTGTGTC 3168

Db	11475	CTGGGATTACAGGCATAGACCACCGTGGCCAGCCT-----TTGTTTTTTTTTTTGAG	11424	Db	10425	CTCTACTAAAAATACAAAAATTAGCCAAAGCATGGTGGCAGGCACCTGTAATCCCGACTA	10366
Qy	824	ACAGAGCTTTGCTTTGTCGCCAAAGGCTGGAGTAGTACAGTGGTGGGATCTCGCTCACTGC	883	Qy	1896	GGGGCTCAGGCACCCCGTGGATGAACCTGGACAAGTAGTATCGGCTCGCAGGAAAT	1955
Db	11423	ACAGAGTTTCACTCTGTGCGCCACAGGCTGGAGTGCAGTGGCGGATCTTGGCTCACTGC	11364	Db	10365	TTCCGGAGGCTAAGGCAGGAGAAATCGTTGAACTCGCGGTGGAGATGCACTGAGCCAA	10306
Qy	884	GCTCCACCTGCTGGGTTCACGCCCATTTCTCCCGCTCAGCCTCCCAAGTAGCTGGGACTAA	943	Qy	1956	TGGAGTGTCTCGCGGGGCGGGTGGGCACACGCCAAAGGATCTCACGAGGCATACAAAG	2015
Db	11363	GCTCCGCTCCCGGGTTACGGGATTTCTCTGCTCAGCCTCCCAAGTAGCTGGGGCTAT	11304	Db	10305	GATTGCACATTTGCACTCCAGCCTGGGCAACAGATCAAACTCTGTCTCCCAAAAAA	10246
Qy	944	AGCGCTGTCACACACGCCCGCTAAATTTTTTTGTAATTTTAAATAAGACGGGTTTCAT	1003	Qy	2016	GGGACTTGCAATATCTGTCTAAGGATAACATATTTTTCACCTCTTTGTCAAAATAAATATG	2075
Db	11303	AGGCACTGCCACCATGCTCAGCTATATTTTTTTGTAATTTTAAATAAGACGGGTTTCAC	11244	Db	10245	AAAAAAGTTTTTTTAGAGATGCAGTCTCACTATGCTGCTAGGTGGTCTCAAACTCCT	10186
Qy	1004	CGTGTAGCCAGGATGGTCTCGATCTCATGACCTTGTGATCGCCCTGCTCGGCCCTCCCA	1063	Qy	2076	TTCCAAGAGGACCTGTAGCGNAACGACCCGTTAGAGATGGAACAATGACCGAGCTGC	2135
Db	11243	CGTGTAGCCAGGATGGTCTTGATCTCTGACCTCGCTGATCGGCCCATATCTCGGCCCTCC	11184	Db	10185	GGCCTCAAGTGTATCTCTGCTCTCTGATAGTAGTAGGATTACAGGCATAAGCCACAGCAC	10126
Qy	1064	AAGTGTGGGATTACAGGCATGAGCCACCGTGGCCCGCTTATCATCATTTATTTATTTAT	1123	Qy	2136	AAAAACAGTGGCGATGCTGCCCTCCAGTGGCAGAATGTAGCAACAGTAAACATCACAGCA	2195
Db	11183	ACGTGTGGGATCACAGGCATAAGCCACCGTGGCCCGGCCAAATTTTTTTTTTTGAGACG	11124	Db	10125	CHGGCAAAAAAATAATTTTAAATGTCACTTAATTCCTATTTCCCAAAAAATACTACC	10066
Qy	1124	GTTTTCTCTCCCACTAGGTGTGAAGCTCCATGAGGTTAGAGATTATTTATTTATTTAT	1183	Qy	2196	ACTATCCAGTGTCAATTTTCTAGCAGTGGTGTCTACTGCACCTTCTGAATAACAGGATTT	2255
Db	11123	GAGTCTTCTCGTGGCCAGACTGGAGTGAATGSCATGATCTCGCTCACTTCGCTC	11064	Db	10065	ATTAGCATTTGGTGAACATTTATTCAGACGCTCTCTCAATGCATTTTATAAAAAACACTGA	10006
Qy	1184	ATTATTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT	1243	Qy	2256	ACTGTATTTCTTGC-----AACCATGTTAAAAATCGTTTCAGGCCAGCGCGGTGCG	2307
Db	11063	CCGGTTCAAGCGATTTCTCTGCTCAGCCTCCCAAGTAGCTGGGATTATACGATGTAC	11004	Db	10005	GACATAGACTAACTTTAACTGCTTCCCTAAAAATAAAAAAGTATTTCAAGTCGGCGCAGTGGC	9946
Qy	1244	GACAGCCTGGCACATAGTAAAGTGTCTCAATAAATTTACTGGATAAAGAGTGCAGATA	1303	Qy	2308	TCATSCCTGTAAATCCAGCACCTTTGGGAGCGCGGCGGCGGATCACTTTGAGGTGAGCA	2367
Db	11003	CACCAAGCCTGGC-----TAAATTTTGTATTTTGTAGTAAATG	10965	Db	9945	TCACCCCTGTAGTCCAGCACCTTTGGAGGCTGAGCGCGATGATTTGCTGAGGTGAGCA	9886
Qy	1304	GTTTAAAACTATCTGACCTAGGAGGCTGAGGAGGAGATGCGTGAACCCGGGAAGCA	1363	Qy	2368	GTTCGAGACCAAGCTGGCCAAACATGCTGAAACCTGTCTCTACTAAAAATAACAAAAAT	2427
Db	10964	GGTTTTCACCTTGTGGTCAAGGCTGCTCGAACTCCTGACCTGATCTGCTGCTCCTC	10905	Db	9885	GTTCGAGACCAAGCTGGCCAAACATGAGAAAAACCTGTCTCTACT-AAAAATAACAAAACT	9827
Qy	1364	GAGTTGCAAGTGAATCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1423	Qy	2428	AGCCGCAATGCTGGGAGCGCTGTAAACCCAGCTACTTGGGAGACTGA-CTTGGAGGT	2486
Db	10904	AGCTCCCAAGTCTGGGATTACAGGAGTGAAGCACCACCCCGGATTTTCAGAAAAATA	10845	Db	9826	AGCCGGCATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	9767
Qy	1424	CCATCTCAAAAAAATAAAAAAATACTATCA-----GGCTAGCTGGTGGCACATGCTGTA	1479	Qy	2487	TTCACTGAGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2539
Db	10844	TTTATAGAAAAGTAGTACATGGTTTATTTTATCAGCTTTATTTTTCGTAATAAATTTA	10785	Db	9766	TTGCTTGAACCCAGGAGGAGGTTGCACTGAGTCACTTCCACCAAACTCAAGC	9707
Qy	1480	ATCTAGCTGAGCGGTAGGCTCCAGAGAAGAAGAAGAAGAAGAAGAAGAAGATATAT	1539	Qy	2540	CTGTCTCAAAAAAATAAATGCTTTCAATAATATATGATAAAGGACTTATTTTTTTC	2599
Db	10784	CATGCTCATTTAGAAAATGAAATTCATCAAAACAGTTTTATTTTATAGAGAGGCTTG	10725	Db	9706	CTGGGTGACAGAGCGAGACTCCATCTCAAAAAAGTAATAATAAAAAATAATAATAATAA	9647
Qy	1540	ATATATATACACACACAAGAATATAAATTTATATATATAAAGTTTTCATTTAAAAA	1599	Qy	2600	AAGCCATAGGATCATTTCTCTGGAAGCATCTTGGCGAAGTCAATCCCACTGTCTCTGAG	2659
Db	10724	CTCTGTATCCCGGCTGGAGTGCAGTGGTACAAATTTAATCACTACCACAGACTTGAATTC	10665	Db	9646	ATAAAAATAAAGTATCAATATAATTTTATTT- -TGAATTTACATATTATAGTTTCAGAA	9589
Qy	1600	AAAAAAACCTTACCCACT- -TTCACTTTACAGGTTCTGGTCCAGCGTCTTCAGA	1657	Qy	2660	AGTGGCAGGTGAGGCTGACCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2719
Db	10664	TGAGCGCAAGTGTATCTCTGCTTCACTTCCAGGTAGCCGGACTACAGGCATGACC	10605	Db	9588	AAAAACTCAATTTATTAGAACATGTTGAGTTTCACTACACATCTTCTTTTATGAAAA	9529
Qy	1658	GGAGGCAAGCTGGCAGGGGTGAGGAGGAGCGTGGGACCGGAGGAGGAGGAGGAGGAGG	1717	Qy	2720	CATTTTCCAGGTGCTGCCAGACATGACAACTGTGTGACCCAGGCAAGAGAGTGGACA	2779
Db	10604	ATGAGGCTGCTGCTAAATTTTCTTTTAAATAATTAATAAATAATTTTAAAGAAAGTTTTT	10545	Db	9528	CTATGAC- - -TTAAAAATATCTTGTACAAAGCTTGTGAGGTAGTCTAGAGCGGACAAA	9473
Qy	1718	- -TGTCCTCCGGGTGCTGGCAGACCGATTTGAATCTCTGGCTATGCTCTTGTGAGTGGCC	1775	Qy	2780	GCTGTAAATTTCTGTGGACAMMCGTACACCCACACCTTATTCATCTCTGCTGCTGCTGCTG	2839
Db	10544	AAAGATGGCTGGGCACAGTGAATCAGCCTGTAAATCCCAACTTTTGGGAGCGGAGACG	10485	Db	9472	GCCAGAAATACCTGCTTGACAA-----AGACAGATCTCATGACACAATTTGTTTGGC-	9421
Qy	1776	GCCGCGMCAAGCGCATCAGCCCTCGGCCGTGTGGCAGTTCCGCAAAATGATCAAGTGC	1835	Qy	2840	CGGCAATCACCTGTAGCAGTAGTGTATCCCTTCTGACCTTATGAAATTTCTAGTTGGTTTC	2899
Db	10484	GGTGGATCACTGAGGTGAGGTTTGTAGAG- -CAGCCTGGCCAACTGTTGAACTGGCC	10426	Db	9420	-----AATTTTGTGTTTTTCTTCTTCTTATTTTAAAAAGGTCAAAATCCCA	9375
Qy	1836	GTGATCCCGGGAGTACCCCTTCTTGGAAATACAACTACCGCTGCTACTGTGGCTTG	1895	Qy	2900	TCAGTAGCCGGGGGAAATAATAGTAAACAGCCATGATTTAGTTTAAATTTCTTGG	2959
				Db	9374	GGGTCTTGATATCTGGCAGTTGGTTTTCAGCAGTGTGCTGAGACAGTTACTTATCTTCTGT	9315

QY 3166 TGCACCATAGGTCACCTGACGCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGC 3225
Db 11280 CTTGATCTCAACTACTGCGGCTCAACCTCCAGGCTCAAGCAATCTCCACCTTAGT 11339
QY 3226 CTCCTAGTACTGGGACTACGAGCGTGACACCGCTCGCTGCTAA-TTAAAAAATTT 3284
Db 11340 CACCTGAGTAGCGGACACAGCGGTGCGCCACACACCTGCTGCTAAATTTTGTATTTT 11399
QY 3285 TTTTGTAGAGCTGGGTCTTACTAGCTTGGCCAGGCTTG-TCTTAACTCTCGGCTTCAA 3343
Db 11400 TTTTGTGAGACAGGGTTTCAACACGTTGCCAGGCTGGCTCTTGAACCTCTGGACTTAA 11459
QY 3344 GCAATCTCTACTCTGGCATCCAAAGTCTCGGATTACAGGGTGAGCCACCATGTGC 3403
Db 11460 ACGATCTCTCTGCTCGGCTCCAAAGTCTGGGATTACAGGCGTGAGTACCAACCT 11519
QY 3404 GGCTACTTATTTCTTACATTCCTCTTTCCAAATAGAAATGAATCCACAGAACAGGA 3463
Db 11520 GGCACCTGACTATTCCTCTTTTCTTTT----- 11547
QY 3464 TTACTGCTATTTTCTTCTCTTTCTTTTGTGAGACAGTCTCACTTCATCAGCTCAACCT 3523
Db 11548 TTTTCTGAGACAGTTTCTCTCTTTTCTCTTTTGTGCCAGGCTGGAGTGCAATGCGCT 11607
QY 3524 CCGTTGAGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTCCTGCTCAAGCCTC 3583
Db 11608 GATCTGAGTCACTGCGAGCTCCCTCTCGGTTCAAGTGATCTCTGCTCAGCCTC 11667
QY 3584 CTGAGTACTGGAATTAACAAGCGTGACACCACTGCTTGGCTAAATTTTGTATTTTATAG 3643
Db 11668 CTGAGTACTGGGATTACAGCATGTACCAACCATCCAGCTAA--TTTGTATTTTATAG 11725
QY 3644 CAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAACCTCTGACCTCAAGTGATC 3703
Db 11726 TAGAGACGGAGTTTCTTCATGTTGGTCAAGCTGGTCTTGAACCTCTGACCTCAGGTGATC 11785
QY 3704 TGCTGCTCAGTCTCCCAAGTCTGGAATTAAGCGTGAGTCACTGTGCTGCGCCGA 3763
Db 11786 CACCTACCTCAGCTCCCAAGTCTGGGATTAAGGTGAGCCACAGCGCCGCCAA 11845
QY 3764 TTA-----CTGCTCATTTTCTTTATTCCTAT 3789
Db 11846 CTATTCATTTTGTGCGAGATTTTGTGTTTGTGTTTGTGTTTAAATCTTCTCTC 11905
QY 3790 ATCCCCAGATCTAGACAGTGTCTGACATATAGTGTCTCAATAAATTAATGATGAAT 3849
Db 11906 TTAGGAGCTGTAAGACTATTACAGAGAGTTCAGAAAGGCACAAAATGGAAGTAAATGGCT 11965
QY 3850 GCACAGCTAGATATAAATTTCT-----TTTTCTTTTAAACAATC 3894
Db 11966 TCCACTCTTCTCTTAAGAACTACTAAATACAGTGTCTGGGTATTTTCTAAAGTTT 12025
QY 3895 TTGACAACTTTGCAGATAAATAACAATCTTGCAATCTGCTTTTTCATCTATCACTTGT 3954
Db 12026 TTAATAAATGAAATTAATTTGCAATTTGTTCACTTGTAAATTTTGGAGTCACTCATC 12085
QY 3955 ATGACTTTTTCATATTGCTCAACCTTATTTGTTACTGTTTTCATTTGTTACTATTTT 4014
Db 12086 AGTATATTTATCTTCGATGTTTTTCTAGGAGTTATGTTGTTTACATTTGTAAAGAACTT 12145
QY 4015 AGTCACCTGAATAATATGCTTAAATTTGTTATACATCTCTCTCCACTTTTAGAAGGC 4074
Db 12146 TAGAAAAATACATTTAGCCAGTCTCTGTAACACTGAATTTGATACTAGTTTGTAGTGACA 12205
QY 4075 AAAATTTTCAAAATCTGATGAAGCTATGAAC---CTCTCCCCAGAGAAATACACACAC 4131
Db 12206 TAAGCAGTGTGTCAGTCCCTTTATATGATACCTATTGTTGTAGGTACAACTGGTCCCTGGC 12265
QY 4132 ACACACTCACACAGTTTTTTTTTAAATGTTTGAACCTAAGACAAAGAACTCGA--- 4188
Db 12266 TTATGAAGTTTGACCTGAATTTTTTTCGACTTTTCAATGGTGTATAACCATCTATTGAGCA 12325

QY 4189 -TTAGAGGATGTTTGTTCATATTAATTAATA-----TAAGTCAAGTGGCAGAGTGA 4240
Db 12326 CTCACACGTTGTTTTTTTTTTTCTTTTAAAGACAGGGTCTCTTGGCTGGGAGCAGTGG 12385
QY 4241 CTCGAAGCTGTAAACACAGTACTTTTGAAGTCCAAGTGGGTGGATCACTTGAAGTGAGA 4300
Db 12386 CTCAGCCTGTAAATCCCAACACTTTTGAAGGGCCAGGGT-GGCGGATCACTTGAAGCTCAGG 12444
QY 4301 AGTTCCAGACACGCTGCTCAATATGTTGAAACCTTATCTACTTAAAAATCAAAAAAT 4360
Db 12445 GGTTTGAGAACAGCTGGGCAACATAGTGAGACCTTGTCTTAAAAAACACA-AAAAAT 12503
QY 4361 AGCTGGGTGATGATGCTGCTAGTCCAGCTACTCTGGGAGGCTGAGGCAAGAGAA 4420
Db 12504 AGCTGGGTGATGCGACCGACCTGTGTGCCAGGTACTCAGGAGGCTGAGGTGGAGAG 12563
QY 4421 TTGCTTGAACCTGGGAGGACAGGTTGAGTGAGCGGAGATCCCACTGCACTCCAGC 4480
Db 12564 TAACTTGAGCCTTAGGAGGTGGAGGCTACAGTGGGCGACAGTCAATGCCACTACACTTAGC 12623
QY 4481 CTGGCGGACACAGCAGACTCTATCTCAAAAAATAAATAAATAAATAAG 4532
Db 12624 CTGGGTGACAGAGTAAGACCCCATCTCAAAAAATAAATAAATAAAG 12675

RESULT 32
US-09-949-016-13968
; Sequence 13968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13968
; LENGTH: 68444
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(68444)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13968

Query Match 8.1%; Score 402.6; DB 3; Length 68444;
Best Local Similarity 58.9%; Pred. No. 1.2e-81;
Matches 886; Conservative 1; Mismatches 555; Indels 61; Gaps 9;

QY 3098 TTTGGGTTTTTTTTTGTGTTTGTAGACAGGCTTTGCTGTCAAGGATGAG 3157
Db 10528 TATTAGGTATATCTTTTTTTTTTTTGTGACAGAGTCTGCTGTGCGCCAGGCTGGAG 10587
QY 3158 CACAGTGGTGAACCATAGGTCACTGAGCCTCAACCTCTGAGCTCAAGGATCTGCTG 3217
Db 10588 TGCAGTGGCGCTATCTTGGCTCAGTCAAGCTCTCGCTTCTGGTTTACACCAITCTCT 10647
QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCACTGCGCTGGCTAAATAA 3277
Db 10648 GCCTCAGCCTCCGAGTGGCTGGGACTACAGSGCGCCCGCCACCACTGCGCTAAATTTT 10707
QY 3278 AAAATTTTTTTGTAGAGTCTGGTCTTACTAGTTGGCAGGCTTGTCTTAACTCTCTGG 3337
Db 10708 TGTA-TTTTGTAGAGACGGGGTTTCCCGTGTGAGCCAGGATGGTCTCGATCTCTCTGA 10766

QY 3338 CTTCAAGCAATCCTCTACCTTGGCATCCAAAGTCTGGGATTACAGGGGTGAGCCACC 3397
Db 10767 CCTC--GTGATGGCCCTCTCGGCTCCAAAGTCTGGGATTACAGGGGTGAGCCACC 10824
QY 3398 ATGTGGGCTACTATTTCTTTACATTCCTCTTCCAAATAGAAATGAAGATCCACAGAA 3457
Db 10825 GGGCCGGGCTTTATTTATGTATATCTTTAAACCAATATACAGTACATTTTGTATTTGT 10884
QY 3458 CAGGGATCTGCCTATTTCTCTCTTTCTTTTGGAGACAGTCTCACTTCATCACT 3517
Db 10885 GTTGTGTTTGTATTTTAAAGACAGTCTTGTCTTAATCTCCGGGCTGGAGTCAATGGCGT 10944
QY 3518 CAACCTCCGTCAGCTCACTGCAACCTCTGCTCTCCGGGCTTCAAGYGATTTCTCTGCCTA 3577
Db 10945 GATC-----TCGGCTCACCGCACTCTCGGCTCTCGGATTCAGGATTCCTCTACCTC 10998
QY 3578 AGCTCTCAGTAGCTGGAATTAAGAGTGCACACCACTGCTTGGCTAAATTTTGTAT 3637
Db 10999 AGCTCTCCCAAGTCTGGAATTAAGGCGCACTACCAAGGCTGAGTGTGAGCCACGTCCT 11058
QY 3638 TTTTAGCAGATGGGTTTACCATTGTTGCCAGGCTGCTCAAACTCCTGACTCAA 3697
Db 11059 TTTTAGTAGATGGGTTTCCACATGTTGGCAGGCTGCTCGAACTCCTGACTC-- 11116
QY 3698 GTGATCTGCTGCTCAGTCTCCAAAGTCTGGAATTAAGCGTGAAGTCACTGTGCCT 3757
Db 11117 GTGATCCACCGCTTGGCTCCCAAGTCTAGGATTAAGGTTGAGCCACGTCCTGCC 11176
QY 3758 GGCCGATTAAGTCTATTTCTTTATTTGCTATATATCCCAAGTCTAGA----- 3804
Db 11177 AGCTGCATGGTTTATAACTTATATATGACATCTTACTATATGCTATTTGTCATC 11236
QY 3805 -----GCAGTCTGACATATAGTATGCTTGTTCATGTTGTAATTTAA 3840
Db 11237 CTTATGTTGTTTCACTTTCTGCAAGTGTGTTAACTTTGTTCAATGTTGAAATTTAA 11296
QY 3841 TTGATCAATGACAGCTAGATATAAATTTCTTTCTTTT-----TAAACAA 3892
Db 11297 ATATAAATTTAGAAATAAACAATTTGTAAGTTTAACTTTGCTGTGGAGTAGCA 11356
QY 3893 TCTTGACAACTTTGACAGATAAATAACAATCTTTGCAATCTGCTTTTCACTTATCACTTG 3952
Db 11357 TGATGAAATCTTGTCTCGTCCCACTGTGTCAGCCCTGGATGTTAATCACTTTCTTTGCCCA 11416
QY 3953 TTATGATTTTTCATATTCCTCAACCTTTATTTGTTACTGTTTTCATTTCTTACTATT 4012
Db 11417 GCATATCTACGCTGTATATGCTACCTACCTGTTAGTGCAC--TTAGTAGCTTGTAGTCA 11474
QY 4013 TTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCTCTCTGCCACTTTAGAAG 4072
Db 11475 TTAGTAGCCATCTTGGGTGTTTATCGGATCACTCTTATGGTATGAGTGTATTATG 11534
QY 4073 CCAATTTTACAACTGATGAAGCTATGAACCTCTCCCAAGAGAAATACACACACA 4132
Db 11535 TCAAGTGACTTTATTTACTTAATAATGACCCAAAGCAAGAGTAGTAATGCTGGCA 11594
QY 4133 CACACTACACACAGTTTTTTTTTAAATGTTTGCNACTAAGACAAACCTGATGAG 4192
Db 11595 TATTGTTACTTGTTTTATTTTATTAATGTTTGTAAATTTCTTACTGTGCTTAAATTTATA 11654
QY 4193 AGGATGTTTGTTCATATTAATAAATAAATCACTAGTTGGGCAAGTCAAGCTGTA 4252
Db 11655 AATTACATTTTATCATAGATAGTATAGGAGCAAGCAGGTGCTCAGGCTGTAT 11714
QY 4253 ACACAGTACTTTGGAAGTCCAAGTGGGTGATCATCTTGAAGTGAAGATTCGAGACCA 4312
Db 11715 ATCCAGCCCTTTGGGAGGAGAGGTGGGGGATCA--TGAGTCAGGAGATCAAGACCA 11772
QY 4313 GCCTGTCAATAGGTGAACCTTATCTCTACTAAAAATACAAAATTAAGTGGGTGAG 4372
Db 11773 TCCTGCCCAACATGGTGAACCTGTCTCTACTAAAAATACAAAATTAAGTGGGTGAG 11832

RESULT 33

US-09-949-016-14293/c
; Sequence 14293, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14293
; LENGTH: 101128
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(101128)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14293

Query Match 8.1%; Score 402.6; DB 3; Length 101128;

Best Local Similarity 60.2%; Pred. No. 1.4e-81;

Matches 844; Conservative 1; Mismatches 510; Indels 46; Gaps 9;

QY 3133 TCTTGCTCTGTCCACCAGGCATGACACAGTGGTGCAACCATAGGTCACTGCAGCTCAA 3192
Db 24048 TTTTCTCTGTCGCCAGCTGGAGTGCAGTGGCAACCTCGGCTCAGTGCACCTCA 23989
QY 3193 CTTCTGAGCTCAAGGGATCTGTGACCTCAGCCTCCCAAGTAGCTGGGACTACAGGCT 3252
Db 23988 CTTCCACGTTCAAGCAATCTCTG-CCTCAGCCTCCGAGTAGCTGGATTACAGGCGC 23930
QY 3253 GCACCAACGCTGGCTGCTAAATAAATAATTTTTTTAGAGACTGGGTCTTACTAGCT 3312
Db 23929 CCACCACACGCTTGGCTTAATTTTGTGA--TTTTTAGTAGAGCGGGTTTCCACATGTT 23872
QY 3313 GGCAAGGCTGTCTTAAACTCTGCTTCAAGCAATCTCTACCTCGCATCCCAAGT 3372
Db 23871 GGCAAGGCTGTCTGAACTCTGACCTCTG-TATCCCTTCTGCTCGGCTCCCAAGT 23813
QY 3373 GCTGGATTACAGGGGTGAGCCACCATGCGGGCTACTTATTTCTTTACATTTCCATCTTT 3432
Db 23812 GTTGGATTACAGGTGTGAGCCACTGCACCGGCTTTTTTTTAAATTAATTTATTATT 23753
QY 3433 CCAATAGAATGAAGATCCACAGAAACAGGATTAAGTCTGCTATTTCTTCTCTTTT 3492
Db 23752 ATTAT-----TTTGACAGGGTCTCGCTCTGTCCACCAGGCTGGAGCGTA 23707

QY 3493 GAGACAGAGTCTCATTCTCATCACTCAACCTCCGTTTCAGCTCTCACTGCAACCTCTGCCTCC 3552
Db 23706 GTGCACAATC-----TCGGCTCACTGCAACCTCCGGCTCC 23671
QY 3553 CGGGTTCAAGYGATCTCTCGCTCAAGCCTCTGAGTAGCTGGAATTTACAAGCGTGACCC 3612
Db 23670 CAGGTTCAAGCAAGTCT-CTGCTCAGCCCTCTGAGTAGCTGGATTTACAGCATGTGCC 23612
QY 3613 ACCATGCTGGCTAAATTTTGTGATTTTATAGCAGAGATGGGTTTACCAATGTTGCCAG 3672
Db 23611 ACCACACTGGCTAGTTTTTGTATTTTTTTGTAGACAGAGTTTTGCCATATTTGCCAG 23552
QY 3673 GCTGCTCAAACTCCCTGACCTCAAGTGATCTGCTGCCTCAGTCTCCAAAGTGCTGGA 3732
Db 23551 GCTGCTCAAACTCCCTGAGCTCAAGTGATCCAGCTGCTCAGTCTCCCAAGTGCTGG 23492
QY 3733 ATTATAGCGTGAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTTTATTTGCTATATC 3792
Db 23491 ATT-CAGGTGTGAGCCACACACCTGGCCGCAATTTTCTTTATTTGTGTAATAATATACCTA 23433
QY 3793 CCNAGATCTAGACAGTGTCTGACATATAGTAGTGTCTCAATAAATAATTGATGAATGCA 3852
Db 23432 ACAATATTTATCATTTTACTATTTCTTAAATATGCAATTCAGTTGCAATTAATAATAATCA 23373
QY 3853 CA-GCCTAGATATAAACTTTCTTTTCTTTTAAACAATCTTGACAACTTTTGAGAA 3911
Db 23372 CATTCGTGTGTAAGTACGACCTTTCTATAACCCAAATGTTTATTCATACCCAGCAAA 23313
QY 3912 TAAATACAATCTTGCAATCTGCTTTTTCACCTATACCTTTGTTA-TGACTTTTTTCATATT 3970
Db 23312 ACTCTGTAACCATTAACAATAATTTCCCTTCCCACTTTCCACAGCCTCTGTTATCT 23253
QY 3971 GCCTCAAACTTTATGTTACTGTTTTTTCATTTGTTACTATTTTATGCTGATGAATAT 4030
Db 23252 ACTTTCTGCTCATGAATGACTATTTGTAGTACCTCAACAAGTGGGAATCACAACAG 23193
QY 4031 GGCTTAATTTGTTATACATCTCTGCTCCCTTTAGAGGCGCAATTTTACAAATCTGA 4090
Db 23192 TTGCTCTCTGTCTGGCTTATTTATGAAGCGGAATGTTTCAAGGTCATATGGTA 23133
QY 4091 TGAAGCTATGAACCTCTCTCCAGAGAAATACACACACACACACACTCACACACAGT 4150
Db 23132 TATAGCATATATCAAGACTGCCCTCTTTTAAAGCCGAGTAATTTCCATTATATGTATA 23073
QY 4151 TTTTTTTTAAATGTTGCACTAGACAGAAACCTGCATTAGAGGATGTTTGTTCATATT 4210
Db 23072 TACACCATTTTGTATTCTCTGTTGATGGACACTTGGGTTGTTCCACCTTTGGCTATT 23013
QY 4211 AATTAAAAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACACACAGTACTTTGGAAG 4270
Db 23012 GAGNATAGTCTGCTGATCAGCGCAGTGCTAATGCTGTATCCAGCACTTTGGGAG 22953
QY 4271 TCCAAGTGGGTGATCACTTTGAGGTGAGAAGTTTCAGACACAGCCTGGTCAATATCGTA 4330
Db 22952 GTTGAAGTGGGCAGATCACCTGAGGTGAGAGTTTCGAGACAGCCTGGCCAAACATGGTGA 22893
QY 4331 AACCTTACTCTACTAAAAATACAAAATTTAGCTGGGTGAGTGATGTCATGCCCTGATGC 4390
Db 22892 AACCCGCTCTCTACTAAAAATACAAAATTTAGCTGGGTGAGTGATGTCATGCCCTTTAGTC 22833
QY 4391 CCAGCTACTCGGAGGCTGAGGCAAGAAATTCCTGTAACCTGGGAGGAGAGTTGCGAG 4450
Db 22832 CCAGCTACTTTGGAGTCTGAGGCAAGAAATCTCTGAACTGGGAGGAGGTTGTAG 22773
QY 4451 TGAGCCGAGATCCACACACTGCACTCCAGCTGGGCGACACAGCAGACTCTATCTCAAA 4510
Db 22772 AGGCTGAGATCACACCAATGCACTCCAGCTGGTGCAGAGAATGGGACTCTGTCTCAAA 22713
QY 4511 AAATAAATAAATAAATAAA 4531
Db 22712 AAAAAAACAACAAAAAACAA 22692

RESULT 34
US-09-949-016-15700/c
; Sequence 15700, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15700
; LENGTH: 38983
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15700

Query Match 8.0%; Score 397.6; DB 3; Length 38983;
Best Local Similarity 60.4%; Pred. No. 1.3e-80; Indels 116; Gaps 11;
Matches 911; Conservative 1; Mismatches 480;

QY 3093 GACAGTGTGGGTTTTTTTTTTTGTGTTTGTAGACAGGGTCTTGCTCTGTCAACCCAGGC 3152
Db 4746 GATTCCTTTTTTTTTTTTTTTTTTTTGTAGATGAAGTCTGCTGTGTGCCAGGC 4687
QY 3153 ATGACACAGTGGTGCAACCATAGTCTACTGACAGCCTCAACCTCTCTGAGCTCAAGGGATC 3212
Db 4686 TGGAGTGCAGTAGCGCATCTAGGCTCACTGCAACTTCTGCTCCGGGTTCAAGCGATT 4627
QY 3213 TCCTGACCTCAGCTCCCAAGTCTGGAGCTACGAGCGTGCACACACAGCCTCGCTAA 3272
Db 4626 CTCCTGCTCAGCTCCCTGCGTAGCTGGGATTACAGGCATGTACCAACACACCCAGCTAA 4567
QY 3273 TTAATAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTGTGGCCAGGCTTGCTTTAAACT 3332
Db 4566 TTTTCTTA--TTTTAGTACAGATGGGGTTTTGCCATGTTGSCCAGGCTGTCTTGAAC 4509
QY 3333 CTTGCTTCAAGCAATCTCTTACCTTGGCATCCCAAGTCTGGGATTTACAGGGGTGAG 3392
Db 4508 CTTGACCTCAGGTGATCCACCCACCTTGACCTACCAAAAGTGTGGGATTACACGGTGAG 4449
QY 3393 CCACCATGTGGGCTACTTATTTCTTT-----ACATTCCATCTT 3431
Db 4448 CGACTGCAACCCAGCCAGAGAAATTTTTTATTAGGAAGAAGAGACTAACTTTTAAACAGT 4389
QY 3432 TCCAAATAGAATGTAAAGATCCACAGAACAGGGATTACTGCCTATTTTCTTCTTTCTTTT 3491
Db 4388 GGTACAGCACTTTTATATACACTTAGGGGAAAATGTTTTTACCCCTTTTTTTTATTTTTT 4329
QY 3492 TGAGACAGAGTCTCACTTCAATCACTCAACCTCCCTTCTAG-----CTCACT 3537
Db 4328 TGAGACAGAGTCTGCTCTGTGCCCGAGGCTGGGTGCGATCTTTGACTCACT 4269
QY 3538 GCAACCTCTGCTCCCGGGTTCAAGYGATTTCTCTGCTTAAGCCCTTCTGAGTAGCTGGA 3597
Db 4268 GCAACCTCACTCCCAAGTTCAAGCATTTCTCTGCTCAGCCTCCCGAGTAGCTGGA 4209
QY 3598 TTACAAGGCTGCACCAACCATGCTTGGCTAAATTTTTTGTATTTTATAGCAGAGATGGGTTT 3657
Db 4208 CTACAGGCGTGGCCATCAGCGCCAGCTAA--TTTTTGTATTTTATAGTAGACAGAGGTTT 4150
QY 3658 TACCATGTTGCCAGGCTGGTCTCAAACTCTGACCTCAAGTGATCTGCCTGCCTCAGTC 3717
Db 4149 CACCATGTTGCCAGGATGGTCTCAATCTCTTGAACCTC--GTGATCCGCGCCCTCGTCC 4092

Db 88148 GTTCATCCATTTTATCTGCTCTTTTCTTGTAATTTCTTTTAAATATTTTAAATATTTTATCACTGTTACCT 88089
Qy 3058 -----GCTATTTGCCCAAGATCACACAGCTGTGTAAGTGTGACAGTTTGGGTTTTTTTTT 3111
Db 88088 AAAAACTTTGTCTMACTTAATTTCAACAGTAGGTGTTCTGTGGTCTGGTTTTTTTTGTGTT 88029
Qy 3112 TGTGTTGTTTGTAGAGACAGGGTCTTGCTCTGTCTGCTCACCCAGGCATGAGCACAGTGGTCAAC 3171
Db 88028 TGTGTTGTTTGTAGATGGGGTCTCACTCTGTCTCACCCAGGC- TGAGTGCAATGGTGGAT 87970
Qy 3172 CATAGTCACTGACGCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCA 3231
Db 87969 CTCAGCTCACTGCAACCTCCACCTCCAGGCTCAAGCGATTTCTGCTCAGCCTCCTG 87910
Qy 3232 AGTAGCTGGGACTACGAGCTGACACACAGCGCTGCTAATTTAAAAATTTTTTGTGA 3291
Db 87909 CGTAGCTGGGATTACAGGCACCCACAGCACACTGGCTTAACTTTTGTGA- TTGTGATG 87851
Qy 3292 GAGACTGGGTCTTACTACGTGTCAGGCTTGCTTAAACTCTGCTTCAAGCAATCCT 3351
Db 87850 GAGACCGGGTTTCAACATGTTGGCCAGGCTGGTTTCGAACCTCTCCACCTGAAGTGATCG 87791
Qy 3352 CTACCTTGGGATCCCAAGTGTGGGATTTACAGGGGTGAGCCACATGTGCGG----- 3405
Db 87790 TCCTCTTGGCTTCCCAAGTGTGGGATTTACAGGCATGAGCCACCATACCCAGCCTACG 87731
Qy 3406 -----CTACTATTTCTTACATTCCTCTTTCCATAGATGTAAGATCCACAGA 3456
Db 87730 GGTCTATTTCTTATGATGTTGTTTCTCCCTCTTGATTAAGGGTCACATTTGCTGCTT 87671
Qy 3457 ACAGGATTAATGCTAT-----TTTCTCTCTTTTCTTTTGTAGACAGAGTCTCACT 3508
Db 87670 CTTTGCACTGCTCATGATGATTATCATTTATTTTATTTTGTAGCGGACTCTCACT 87611
Qy 3509 TCATCACTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCTCCCG 3554
Db 87610 CCATTGCCAGGCTGGCGTGCAATGGCACGATCTTGCTCACTGCAACCTCCGCTCCTG 87551
Qy 3555 GGTTCAGYCATCTCTGCTAGCTCTGAGCTCTGAGTGGTGAATTAACAGCGTGACAC 3614
Db 87550 GGTTCAGGCAATCTCCCACTCAGCTCTCCAGTAGTAGTGAATTAACAGCACCTGCCAT 87491
Qy 3615 CATGCTTGGCTAAATTTTGTATTTTGTAGCAGATGGGTTTACCATGTTTCCCGAGGC 3674
Db 87490 CATGCTTGGCTAAATTTT--GTATTTTGTAGACAGAGGTTTCAACATGTTGCCAGGC 87433
Qy 3675 TGGTCTCAAACTCTGACCTCAAGTATCTGCTGCTCAGTCTCCCAAGTGTGGAAT 3734
Db 87432 TGGTCTTGAACCTCTGACCTCAGGTGATCTCCCATCTCGGCTCCCAAGTGTGGAAT 87373
Qy 3735 TATAGCGTCACTGCTGCTGCGCGGATTAAGTCTATTTTCTTATTTGCTATATCCC 3794
Db 87372 TGTAGGATGAGGCACCATGCCGCTCAATGATGATCTCTGTCGCCAGCATTAAGA 87313
Qy 3795 CAGATCTAGACAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCAC- 3853
Db 87312 TAAAGAAGACAGAGATTGAATTCATATAAACACCCCAAGAGGCTTGCACTTC 87253
Qy 3854 -----AGCCTAGATATAAACTTTCTTTTCTTTTAAAAAATCTTGACAA 3901
Db 87252 CTTGTGTCAGGTAGCCAGGATGTGAGGCTGTTCTTCTTAAGCTAATCAGGAGTGGCT 87193
Qy 3902 CTTTGCAGATAAATAAATCTTGCATCTGCTTTTCACTTATCACTTGTATCACTT 3961
Db 87192 GGGTGTGAGGTTTGTGTTTGTGTTTATCTTGTGTTTCAAAATCTTGAATGTGAGAT 87133
Qy 3962 TTTTCAATTCCTCAAACTTTTATTTGTTTACTGTTTTTTCATTTGTTTACTATTTTAGTCACT 4021
Db 87132 CAGGTCACTAGCTCAGCTAGCATGGCTTTGGAACTTAATCAACCAACTAGATGTTGCCT 87073
Qy 4022 GAATAATATGGCTTAATTTGCT-----TATACATCTCTGCTCCACTTTAGA 4069
Db 87072 GTAAGATCTCTGCTTTTTCATCTCCCTGCCCCAGTTCCTCCAACTGCTGCTCAGTCAGAA 87013

Qy 4070 AGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAG-----AGA 4118
Db 87012 AGCCCATGCTGTGACAGTCTTTCTCCAGCCTGCTTGGGCCCAAGGAAATGAAATTTGA 86953
Qy 4119 AATACACACACACACACACTCAACACAGTTTTTTTTTAAATGTTTGAACATAAGACAA 4178
Db 86952 ATGAAAGTAGTCTATCTAGGAACGGCTTATGCTCTCTCGGAATTTAGTTTCATTTAGTCAA 86893
Qy 4179 GAAACCTCATAGAGGATGTTTGT-----C 4205
Db 86892 GTGCTGCTCGATAGAAATATAAAGTGAGCCACATACGTAATTTTAAATTTTCTAGTAGC 86833
Qy 4206 ATATTAAATTAATAAATACTCAGTTGGGCACAGTACTCAAGCCTGTAAACACAGTACTTT 4265
Db 86832 ACATTTAAAGATAAAGAGAGTCCAGGCACAGTGGCTCATGCCAATAATCTTAGCACTTT 86773
Qy 4266 GGAATCCAAAGTGGGTGGATCACTTGAGGTGAGAAGTTTCGAGACAGCCTGGTCAATAT 4325
Db 86772 GGGAGGCCAAGG-CAGTGGATCACCTGAGTTCAGGAGTTTCGAGACAGCCTGTTCAACAT 86714
Qy 4326 GGTGAAACCTTATCTCTACTAAATAACAAATTTAGCTGGGTGATGATCATGCTGCTG 4385
Db 86713 GGGGAAACCTTGTCTCTACTAAACCAAAAAATTTAGCCAGGCTTGGTGGCTTGTGCCCTA 86654
Qy 4386 TAGTCCAGCTACTCGGAGGCTGAGGCAAGAGAAATTTGTTGAACTTGGGAGGCAGAGT 4445
Db 86653 TAATCCAGCTACTCAGGATGCTGAGGCAGGAGAAATTTGTTGAACTTGGGAGGCAGAGT 86594
Qy 4446 TCACTGAGCCAGATCCCACTGCACTTCAGCCTGGGCGACACAGGAGACTCTATC 4505
Db 86593 GGCAGTGTGCCAGATGTTGCCACTTCACTCCAGCCTGGGTGACAGAGCTGAACACTGTC 86534
Qy 4506 TCAAAAAAATAAATAAATAATA 4529
Db 86533 TCAAAAGAAAAAAGATAAA 86510

RESULT 36
US-09-949-016-15970/c
; Sequence 15970, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15970
; LENGTH: 181251
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15970

Query Match 7.9%; Score 397.2; DB 3; Length 181251;
Best Local Similarity 56.9%; Pred. No. 3.1e-80;
Matches 927; Conservative 2; Mismatches 645; Indels 54; Gaps 9;
Qy 3087 AGTGTGACAGTTTGGGTTTTTTTTTGTGTTTGTAGACAGAGGCTCTGTCTGTCTAC 3146
Db 112220 AGAGTGAAGTCTGAGTTGTTTTTTTTTTTGTGACACACAGTCTCACTCTGTTGC 112161
Qy 3147 CCAGGCATGAGCACAGTGTGCAACATAGGTCACTGAGCCCTCAACCTCTGAGCTCAA 3206

Db 15435 AGTGAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCCCTCCGGGTTCATGCAATCTC 15494
Qy 3216 TGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACACAGCGCTGCTAATTA 3275
Db 15495 CTGCCTCAGCCTCCTGAGTAGCTGGGACTACAGCGCCCGACACACAGCGCGCTAATTT 15554
Qy 3276 AAAAAATTTTTT--GTAGAGACTGGTCTTACTACTGTGGCCAGCGTGTCTTAAACT 3332
Db 15555 TTTTGTGTTTTTTTTCAGTAGAGCGGGTTTTCACTGTGTAGCCAGATGGTCTCAATCT 15614
Qy 3333 CTGCGCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTCTGGGATACAGGGGTGAG 3392
Db 15615 CTTGACCTC--GTGATCTGCCCGCTTGGCTCCCAAGTGTCTGGGATACAGCGGTGAG 15672
Qy 3393 CCACCATGCGGCTACTATTCTTTACATCCATCTTTTCCAAATGAAATGTAAGATCCA 3452
Db 15673 CCACCGTGGCCAGCTGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 15712
Qy 3453 CAGAACAGGGATTACTGCCTATTCTTCTCTCTTTTGTGAGACAGAGTCTCACTTCAT 3512
Db 15713 -----TTTTTTGAGACAGTGTTCACCTTTGGCACCCAGGCTCCAGGCTGGAG 15761
Qy 3513 CACCTCAACCTCGGTTGAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYGAATCTCCT 3572
Db 15762 TGCAGTGGCACAATCTGAGCTCACTGCAACCTCTGCTCCAGGTTCAAGCGATTCTCCT 15821
Qy 3573 GCCTAGCCTCTGAGTAGCTGGAATTAAGCGGTGCACACCATGCTTGGCT--AATTT 3630
Db 15822 GTCTCAGCCTCTGAGTAGCTGGGATTACAGGTGTGCTCCAAATATGCTGGCTACATTT 15881
Qy 3631 TTTGTATTTTTAGCAGAGATGGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTTG 3690
Db 15882 TTTGTATTTTTAGGAGCGGGTTTTGCCATGTTGGCGGCTGGTCTCAAGCTCTTA 15941
Qy 3691 ACCTCAAGTAGTCTGCTGCTCAGTCTCCCAAAGTCTGGAATTAAGCGTAGCTAC 3750
Db 15942 ACCTCAGGTGATCCACCTGCTCGGTCTCCCAAAGTCTGGGATTACAGGTGAGCCAC 16001
Qy 3751 TGTGCTGGCGGATTACTGCTATTCTTTATTGCTATATCCAGATCTAGAGCAGTG 3810
Db 16002 TGGCCCCAGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGACA-GTCTTGCTCTGTCGCCAG 16060
Qy 3811 TCTGACATATAGTAGGTGCTCAATAATAATTGATGAATGCACAGCTAGATAAACTT 3870
Db 16061 GCTGGAGTGAGTGGCACCATCACGCTCACTCAGCATTAACCTCTGGCTCAA--- 16117
Qy 3871 TCTTTTTCTTTTTTAAAAAATCTTTGACAACCTTTGAGAAATAAATACAACTTTGATTC 3930
Db 16118 ---TGATCCTCCCAACCCAGCCTCCCAACTAGCTGGGACTACAGTTGCAAAACCAACCATAC 16174
Qy 3931 TGCTTTTTCATTTATCACCTTGTTATGACTTTTTTCATATTGCTCAAACTTTATTGTTA 3990
Db 16175 CTGGCTAAATTTGTTTTTTTGTATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 16234
Qy 3991 CTGTTTTTTCATTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTATACAT 4050
Db 16235 ACCATATGGCTCAGACTGGTCTCAAACTCTCGGCTCAAGCAGTCTCCCTCTCGGCT 16294
Qy 4051 CTTCTGCTCCATTTTAGAAGGCCAAATTTACAAATCTGATGAAGATGAAACCTCTC 4110
Db 16295 CCGAAGCGTGGGATTACAAAGTGTAGGCAATTACACCCAGCCCAACCTCTAGCTGAATA 16354
Qy 4111 CCAGAGAAATACACACACACACACACTCACACAGTTTTTTTTTTTTTTTAAATGTTG--- 4166
Db 16355 GGCAGAGAAATAGGTCCCTGACATCTTTGTTCTCCCAACCTCAGTTTATCCCGTCTGACA 16414
Qy 4167 -----CAACTAAGACAAAGAAACCTGCATTATAGGAGTGTGTTTCAT 4207
Db 16415 ATGGTTGTCCATGAGCCTCCACCTGGCCCCCTTAGCTTGTCTCCATCTGCATCTGGGT 16474
Qy 4208 ATTAATTAATAATAAATCTCAGTTGGGCACAGTGAATCAAGCCTGTATACACAGTACTTGG 4267
Db 16475 TCAACATAGGTCTCTCCACGGCTGGGATGTTGGCTCACACCTGTCTATCCAGCACTTGG 16534

Qy 4268 AAGTCCAAG-----GTGGGTGGATCACTTGAAGTGAAGTTTCGAGACGAGCCTGGTCAAT 4323
Db 16535 GAGGCGGAGCCGAGGCGGGCATGAGAGTCAGAGATCAGAGACCATCTTGCCCAAC 16594
Qy 4324 ATGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAAGCTGGGTGTAGTGATGCATGCC 4383
Db 16595 ATGGTGAACCCCATCTTTCTAAAAATACAAAAATTAAGCTGGGTGTGGGCATC 16654
Qy 4384 TGTAGTCCAGCTACTTCGGAGGCTGAGCAAGAAATTTGTTGAACCTGGGAGGCAGAG 4443
Db 16655 TGTAAATCTTAGCTACTTCGGAGGCTGAGCGAGGAATCGCTTGAACCCGGAGGTGGAG 16714
Qy 4444 GTTCAGTGAAGCGAGATCCCACTCACTCCAGCTTGGGCG-ACACAGCGAGACTCT 4502
Db 16715 GTTCAGTGGGCGGAGATTGCGCCACTGCATCCAGCCTTAGCGTTAAGAGCAAGACTCC 16774
Qy 4503 ATCTCAAAAAATAAATAAATAAATAA 4530
Db 16775 GTCTCAAAAAAATAAATAAATAAATAA 16802

RESULT 38
US-09-949-016-13725
; Sequence 13725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13725
; LENGTH: 100468
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(100468)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13725

Query Match 7.9%; Score 396.4; DB 3; Length 100468;
Best Local Similarity 59.4%; Pred. No. 3.7e-80;
Matches 872; Conservative 1; Mismatches 522; Indels 73; Gaps 9;
Qy 3096 AGTTTGGGTTTTTTTTTTTGTGTTTGTAGACAGGGTCTTCTCTGTCAACCCAGGCATG 3155
Db 15375 AGTTTGTGTTTGTGTTTGTGTTTGTGATGAGTCTTCTCTGTGCGCCAGGCTG 15434
Qy 3156 AGCAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGGATCTGC 3215
Db 15435 AGTGAGTGGGCAATCTCGGCTCACTGCAAGCTCCGCTCCCGGTTTCATGCCAATCTC 15494
Qy 3216 TGACCTCAGCTCCCAAGTAGCTGGGACTACAGGCTGCACCAACCGCTGGCTAATTA 3275
Db 15495 CTGCTCAGCTCTCTGAGTAGCTGGGACTACAGGCGCCGACACCAACCGCTAATTT 15554
Qy 3276 AAAAAATTTTTT---GTAGAGACTGGGTCTTACTACTGTGGCCAGGCTTGTCTTAAACT 3332
Db 15555 TTTTGTGTTTTTTCAGTAGAGACGGGTTTCACTGTGTGTAGCAGGATGGTCTCAATCT 15614
Qy 3333 CTGCGCTCAAGCAATCTCTTCACTTGGCATCCCAAAGTGTGGATTACAGGGGTGAG 3392

Db 6814 CAGCACACGACTCTCGGAGAGAGCTGCTCCGGGC -CTTGTGCAATAAGGTGAGGCTGG 6872
Qy 2767 AAGAGCTGACAGCTGTAATTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATAC 2826
Db 6873 AATGTGGGGCGGCGACGAGAGCATTTCCCAAGGTGTTTCAGGCACCAAGCTCTCTCTTT 6932
Qy 2827 TCGTCTCTCGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTTCCTTGACCTATGAA 2886
Db 6933 TCAGTTTGGATTAATTTCTACTGACCTGTCTTTGCCCTTACAGATTCTTTCTCTGTTGT 6992
Qy 2887 TTCTAGTTGGTTCTCAGTAGGCGGGGGAATAATAGTAGAACACAGCCATGATTTAGTG 2946
Db 6993 GCCAAATGTCTAATAAGCCCATCAATACATCTCTTTGTTGGAGATATGATTTTTCAGCT 7052
Qy 2947 TTAATTTTCTGTTCTGGGCGAGTCTCTTTAATCCTCAGAACACACTATGGGATAG 3006
Db 7053 CTGGAAATTCATTTGGTTGTTTTTAGAATTTCCACTCTCTGTATGAAATTCACCATCT 7112
Qy 3007 GTACAATTTATCCTCACTTAACAGATAAGAAACCTGAGGCTCAGAAGGCTGA----- 3057
Db 7113 GTTCATCCATTTATCTGTCTTTCTGTAAATTTCTTAACATATTTATCACTGTACCT 7172
Qy 3058 -----GCTATTTGCCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGGTTTTTTT 3111
Db 7173 AAAAAATCTTTGTCAACTAATTTCAACACGTAGGTGTTCTGTGGGTCTGGTTTTTTTGT 7232
Qy 3112 TGTGTGTTTGTAGACAGGTTCTGCTCTGTCACCCAGGCATGACAGAGTGGTCAAC 3171
Db 7233 TGTGTTGTTTTGAGATGGGGTCTCACTCTGTCAACCCAGGC -TGAGTCAATGGTGGAT 7291
Qy 3172 CATAGGTCACCTGAGCCTCAACTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCA 3231
Db 7292 CTGAGCTCACTGCAACTCACTCCAGCTCAAGGATCTCTGCTCAGCCTCCTG 7351
Qy 3232 AGTAGTGGGACTACGAGCGTGACACACCGCTCGCTGCTTAATTAATAAATTTTGTGA 3291
Db 7352 CGTAGCTGGGATTAACAGCACCCACAGCACACTGGCTAACTTTTGTGA -TTTGTAGTG 7410
Qy 3292 GAGACTGGGCTTACTAGCTTGCCAGGCTGCTTAACCTCTGCTTCAAGCAATCTCT 3351
Db 7411 GAGACCAAGTTTCAACCATGTTGCGCAGGCTGTTTCAACTCTCCACCTGGAAGTGA 7470
Qy 3352 CCTACCTTGGCATCCCAAGTGTGGGATTAACAGGGGTGAGCCACCATGTGCGG----- 3405
Db 7471 TCCTCTTGGCTTCCCAAGTGTGGATTAACAGGCATGAGCCACCATACCCAGCCTAG 7530
Qy 3406 -----CTACTAATTTCTTACATTCATCTTCCAAATAGATGTGAATPCCACA 3456
Db 7531 GGTCTATTTCTATTGATTGTTGTTTCTCCCTCTTGATTATGGGTCACATTTGCTGCTT 7590
Qy 3457 ACAGGATTAATGCCTAT-----TTTCTCTCTTTCTTTTGTGACAGAGTCTCACT 3508
Db 7591 CTTTGATGTCTCATGATGATTATCATTAATTTTATTTTGTGAGCGGACTCTCACT 7650
Qy 3509 TCATCACTCAACTCGGTTCA-----GCTCACTGCAACTCTGCTCTCCG 3554
Db 7651 CCATGGCCAGGCTGGCGTCAATGGCAGCATCTTGCTCACTGCAACTCCGCTCTG 7710
Qy 3555 GGTTCAGYGATTTCTCTGCTCAAGCTCTCTGATGAGTGGGAATTAACAAGGTGCAACAC 3614
Db 7711 GGTTCAGCGATTTCTCCCACTCAGCTCTCCCAAGTAGTAGAATTAACAGGCACCTGCCAT 7770
Qy 3615 CATGCTTGGCTAATTTTGTATTTTGTAGCAGAGTGGGTTTTTACCATGTTGCCAGGC 3674
Db 7771 CATGCTTGGCTAATTTTGTATTTTGTAGAGACAGGTTTTCACCATGTTGGCCAGGC 7828
Qy 3675 TGGTCTCAAACTCCTGACCTCAAGTGATCTGCTGCTCAGTCTCCCAAGTCTGGAAT 3734
Db 7829 TGGTCTTGAATCCTGACCTCAGTGATCTCCCACTCGGCTCTCCCAAGTCTGGAAT 7888
Qy 3735 TATAGGGTGAGTCACTGCTGCTGGCGGATTAATGCTATTTTCTTTATGCTATATCCC 3794
Db 7889 TGTAGGCATGAGCCACCATGCCCCGCTCATGTATGATCTCTGTGTGCCAGACATTATGA 7948

Qy 3795 CAGATCTAGACAGTGTCTGACATATAGTAGTGCTCAATAAATATTGATGAATGCAC- 3853
Db 7949 TAAAAAGAGAGCAGAGATTGAATTCATATAAACACCCCCAAGAAAGGGCTTGACATTC 8008
Qy 3854 -----AGCCTAGATATAAACTTTCTTTTCTTTTAAACAAATCTTGACAA 3901
Db 8009 CTTGTGTCAAGTAGCCAGGATGTGAGGCTGTCTCTCTTAAGCTAATCAGGAGGTGGCT 8068
Qy 3902 CTTTCAGAAATAAATACAAATCTTGCAATCTGCTGCTTTTTCACCTTATCCTTTGATGACTT 3961
Db 8069 GGGTTGCAAGTTTACTTGGTTTCAATTTTCTGTTTCAAAATATCTTGAATGTGAGAT 8128
Qy 3962 TTTTCATATTTGCTCAAACTTTTATTTTACTGTTTTCATTTGTTTACTATTTTACTCACT 4021
Db 8129 CAGGTCACTAGCTAGCTAGCTAGCATGGCTTGGAAATCTAATCAACCAACTACGATGTGCCT 8188
Qy 4022 GAATAATATGGCTTAATTTGCT-----TATACATCTCTCTGCTCCACCTTTAGA 4069
Db 8189 GTAAGATCTCTGCTTTTTCATCCCTGCCCGCTTCCAACTGCTGCTCAGTCAGAA 8248
Qy 4070 AGGCCAAATTTACAAATCTGATGAAAGCTATGAACCTCTCTCCAG-----AGA 4118
Db 8249 AGCCCATGCTGTGACAGTCTTTCTCCAGCCTGCTTGGGCCCAAGGAAATGGA 8308
Qy 4119 AATACACACACACACACACTCACACAGTTTTTTTTTAAATGTTTCAACTAAGACAA 4178
Db 8309 ATGAAAGTAGTCTATCTAGGAACGGCTTATGCTCTCTGGAAATTTAGTTTCATTTAGTCNA 8368
Qy 4179 GAAACCTGCTATTAGAGGATGTTTGT-----C 4205
Db 8369 GTGCTGTCCGATAGAAGTATAAAGTGAGCCACATACGTAATTTTAAATTTTCTAGTAGC 8428
Qy 4206 ATATTAAATTAATAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGTACTTT 4265
Db 8429 ACATTTAAAAAGTAAAAAGAGTCCAGGCACAGTGGCTCATGCAATAAATCCTTAGCATT 8488
Qy 4266 GGAAGTCCAAGTGGTGGATCATCTTGAAGTTGAGAAGTTTCAGACCCAGCCTGGTCAATAT 4325
Db 8489 GGGAGCCAGG- CAGTGGATCACTGAGGTGAGAGTTTCAGACCCAGCCTGGTCAACAT 8547
Qy 4326 GGTGAAACCTCTATCTACTAAAAATACAAAAATAGCTGGGTGATGATGCATGCTGCTG 4385
Db 8548 GGGGAAACCTTGTCTCTACTATAAACCAAAAAATTAGCCAGGCTTGGTGGCCTGTGCTTA 8607
Qy 4386 TAGTCCCAAGTACTCGGAGGCTGAGGCAAGAGATTCCTTGAACCTGGGAGGAGAGT 4445
Db 8608 TAATCCCAAGTACTCAGGATGCTGAGGAGGAGATTTGCTTTGAACCCAGGGGGCAAGTT 8667
Qy 4446 TGCAGTGAGCCGAGATCCACCACTGCACTCCAGCCTGGGCGACACAGCAGACTCTATC 4505
Db 8668 GGCAGTGTCCGAGATGCTGCCACTTCACTCCAGCTGGGTGACAGAGCTGAACACTGTC 8727
Qy 4506 TCAAAAAAATAAATAAATA 4529
Db 8728 TCAAAAAAATAAATAAATAAATA 8751

RESULT 40

US-08-814-095-7/c
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 3050 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills


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/ STATE: Michigan
/ COUNTRY: U.S.
/ ZIP: 48334
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/814,095
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Montgomery, Ilene N.
/ REGISTRATION NUMBER: 38,972
/ REFERENCE/DOCKET NUMBER: 2391.00066
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (248) 539-5050
/ TELEFAX: (248) 539-5055
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35060 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
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/ DESCRIPTION: promotor, ACHE gene and ARS gene"
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ POSITION IN GENOME:
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RESULT 45
US-09-949-016-12268/c
; Sequence 12268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12268
; LENGTH: 30536
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12268

Query Match 7.8%; Score 389.2; DB 3; Length 30536;
Best Local Similarity 53.6%; Pred. No. 9.6e-79;
Matches 1253; Conservative 3; Mismatches 936; Indels 144; Gaps 16;

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RESULT 4/
US-09-949-016-12232/c

US-09-949-016-12232/C
; Sequence 12232, Application US/09949016


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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12232
; LENGTH: 58593
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(58593)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12232

Query Match          7.8%; Score 389; DB 3; Length 58593;
Best Local Similarity 58.8%; Pred. No. 1.4e-78;
Matches 840; Conservative 1; Mismatches 516; Indels 72; Gaps 7;

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DB 28924 GCAGTGGCGCAATCTCGGCTCACTGCAACCTCCGCCCTCCGGGTTCAAGTGATTTCTCTG 28865
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DB 28864 CCTCAGCCTCCCAAGTAGCTGGAGTACGAGCGTGACACACCGCTCGCTAAATTTTG 28805
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DB 28667 -----TTTTTAGACAGAGTCTTTTCCCTGTCATCCAGGCTGGAGCGCAGT 28623
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QY 3699 TGATCTGCTGCTCAGTCTCCCAAGTGTGGAATTTAGGGGTGAGTCACTGTCCTG 3758
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QY 3759 GCCGATTACTGTCTATTTTCTTTATTTGCTATATCCCAGATCTAGAGCAGTGTCTGACAT 3818
DB 28385 GCCAATTATATTTGTTTCTGTTTGAATTAATTC---AGTTTGCCTTTATCTCTTAAT 28330
QY 3819 ATAGTAGGTGCTCAATAAATAATTAATGAATGACAGCCTAGATATAAACTTTCTTTTTC 3878
DB 28329 TTTTTCCTTTTGTCTTCTTTAGATTTTACCTTACTGTGACATTTTCCCTTTTAATTTCC 28270
QY 3879 TTTTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACATCTTGCAATCTGCTTTT 3938
DB 28269 TGCATTGTCTACTTTTGAATGAACCTTTTATCTCCTAAGCAATAACAGTGTTTACAGC 28210
QY 3939 CACTTATCACCTTGTATGACATTTTTCATATATGCTCAAACTTTATTTGTTACTGTTTTT 3998
DB 28209 CATGCATTTTCTTGTGAATACTACTTTTGGCTGC-----ATTTCATAAGTAGTGTTC 28157
QY 3999 TCATTGTTACTAATTTTAGTCACTGAATAATATGCGCTTAATTTGCTTATACATCTCTC 4058
DB 28156 TGAGTTATTTTAAATAAGCCTATAGTTCTGTTTAAAGCTTTGTATTGAAGTATGATAC 28097
QY 4059 TCCACTTTTAGAAGGCCAAATTTTACAAATCTGATGAAGCTATGAACCTCTCTCCAGAGA 4118
DB 28096 ACATACAGAAAAGCAACATATCAAAATATGTTCAAGTTTGGTGAATATTTCACAAATTC 28037
QY 4119 AATACACACACACACACACTCACACACAGTTTTTTTTTAAATGTTTGGCACTAAGACAA 4178
DB 28036 CACCCAGACTGAGAACACAGACATTTGCCAGTACCATAATTTGCAGGACCTAGTG 27977
QY 4179 GAAACCTGCATTTAGAGGATTTTGTTCATATTAATTAATAAATAAATACTAGTTGGGCA 4238
DB 27976 CAAATGAAATGCTCAGCCCTTTGGTCAATATCATTAACGACTTTGGCTGGTGCAGT 27917
QY 4239 GACTCAAGCCTGTACACAGTACTTTTGAAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGA 4298
DB 27916 GGCTCACCCCTGTAATCCAGAACTTTGGGAGCGCGGCGGCGGCGGCGGCGGCGGCGG 27857
QY 4299 GAAAGTTTCAGACACCGCTGGTCAATATGTTGTAACCCCTATCTCTACTAAAAATAACA 4358
DB 27856 GGAGTTTCAAGCAGCCCTGGCCACATGTTGTAACCCCTATCTCTACTAAAAATAACA 27797
QY 4359 TTAGTGGGTGTAGTGTGATGTCATGCTGTAGTCCCAGTACTCGGGAGGCTGAGGCAAGAG 4418
DB 27796 TTAGCAGGCGATGTTGGGCGACATGCTGTAATCCAGCTACTCGGAGGCTGAGGCAAGAG 27737
QY 4419 AATTCCTTGAACCTGGGAGGCGAGGTTGCGAGTGGCGAGATCCACACCTGCACTCCA 4478
DB 27736 AATCCTTTGAACCCCGGAGGTTGCGAGTGGCGAGATCGGCCATTTGCACTCCA 27677
QY 4479 GCCTGGGCGACACACGAGACTCTATCTCAAAAAATAAATAAATAAATAAATAAATAA 4527
DB 27676 GCCTGGGCGAATAGAGTGAGACTCCATCTCAATAATAATAATAATAATAATAATA 27628
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RESULT 48

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US-09-949-016-17611/c
; Sequence 17611, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
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Db 20464 -TAATTTGCTTTTACATTACTTACATGATATTTTTTGTAGTTGTAACCAAGCCTCTATT 20522
QY 3877 TCCTTTTAAACAATCTTGACAACTTTGCAGAAATAAATACAACTTGCATTCGCTTT 3936
Db 20523 AAATCTAGAAATCACTCTTCTGCTGCTCTAATAATATTGGAATATTTAGGCGTTT 20582
QY 3937 TTCACCTATCACCTTGTATGACTTTTTCATATTTGCTCAAACTTTTATGTTTACTGTTT 3996
Db 20583 CTTGAGGAAGTCACATCTTTAAACAATTAATCTTGAATGATGACTGCTAACTCTTTT 20642
QY 3997 TTTCACTTTTACTATTTTACTCTACTGAATAATATGGCTTAATTTGCTTATACATCTCTCT 4056
Db 20643 TCCATATAACAGTATAATAAAGAAATAGAGCCCTATCGCACATCAGACACAAAATC 20702
QY 4057 GCTCCACTTAGAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGA 4116
Db 20703 AATCCTGGACAGATTGAAGAACTAAGTACAAAGAGCAAACTTTAAAGTTAGAAAAATA 20762
QY 4117 GAAATACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCMACTAAGAC 4176
Db 20763 CAGGAGAACCATGCAACCTCAGAGTAGAGAAGAAATTTTTTCCCGAGTCTTTAATAC 20822
QY 4177 AAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAATACTCAGTTGGGCACA 4236
Db 20823 TTG-ACTGTATTGAGGCGATCTTTTACAAAACCTACAGTACAATTTATCAGGCTGGGCACA 20881
QY 4237 GTGACTCAGCCTGTAAACACAGTACTTTGGAAGTCCAGGTGGGTGGATCACTTGAGCT 4296
Db 20882 GTGGCTCACACCTGTAATCCAGCACTTCGGGAGGCCAAGTGGGCGGATCAC--GAGGT 20939
QY 4297 GAGAAGTTCCAGACCACTGCTCAATATGTTGAAACCCCTATCTCTACTAAAAATAC-AA 4355
Db 20940 CAGGAGATCAAGACCATCTCTGGCTAACACGGTGAACCCCGTCTCTACTAAAAATACAA 20999
QY 4356 AAATTAGCTGGGTGTAGTATGATGATGCTGTAGTCCAGTACTCGGAGGCTGAGGCAA 4415
Db 21000 AAATTAGCCGGCGTGTGGTGGTGCCTGTAGTCCAGTACTTGGGAGGCTGAGGCAG 21059
QY 4416 GAGAATGCTTGAACCTGGGAGGACAGGTTGCAAGTGGCCGAGATCCCAACACTGCAT 4475
Db 21060 GAGAATGGCATGAACCCGGAGGACAGCTTGCAGTGAGCAAGATCGCACCACTGCAT 21119
QY 4476 CCAGCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531
Db 21120 CCAGCTGGGCGACAGAGTGAGACTCTGTCTCAAAAAATAAATAAATAAATAA 21175

RESULT 53

US-09-949-016-14878/c
; Sequence 14878, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14878
; LENGTH: 17704
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(17704)

OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14878

Query Match 7.7%; Score 384.8; DB 3; Length 17704;
Best Local Similarity 59.7%; Pred. No. 7.7e-78;
Matches 888; Conservative 1; Mismatches 538; Indels 61; Gaps 12;
QY 3099 TTGGGTTTTTTTTTCTGTTTGTAGACAGAGGTTCTTGCTC-TGTCACCCAGGATAG 3157
Db 4293 TTTTCTTAAATTTTTTTTTTTTGGACCAAGTTTGTCTTGTTCACCCAGGCTGGAG 4234
QY 3158 CACAGTGGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGATCTGTG 3217
Db 4233 TGCATATTACAGCATCTTGGCTCACTGCAACCTCCACCTCCAGGTTCAACCGATTCTCT 4174
QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACCACACAGCCTGGCTTAATAA 3277
Db 4173 GCCTCAGCCTCCGAGTAGTTGGGACTACAGCACCCACCATCATGCCCGGCTAATTTT 4114
QY 3278 AAAATTTTTTGTAGACTGGGTCTTACTAGTTTGGCCAGGCTTGTCTTAACTCCTGG 3337
Db 4113 GTA--TTTTTAGTAGACAGGTTTCCACATGTTTGGCCAGGCTGGT-TTGAATCTCTGA 4057
QY 3338 CTTCAAGCAATCCTCTACCTTGGCATCCAAAGTGTCTGGGATTACAGGGGTGAGCCAC 3397
Db 4056 CCTCAAGTGATCCACCCGCTCAGCCTTCCAAAGTGTGGGATTACAGGCATGAGCCACT 3997
QY 3398 ATGTCGGCTACTTATTTCTTTTACATTCATCTTTCCAAATGATGAATGCCAGAA 3457
Db 3996 GCGTTTGGCGCTGAGTCAGTGAATTTCTATAAAGGTGATTGCAATTATGCTATTTCCCTGTT 3937
QY 3458 CAGGATTAATCTTATTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACC- 3516
Db 3936 TAAAGATCTTAAAGAGTATTCCTTTTTTTTGGACAGAGTCTCACTCTGTCCCA 3877
QY 3517 -----TCAACCTCCGTTGAGTCACTGCAACCTCTGCTCCCGGTTTCAAGVG 3564
Db 3876 GGCTGGAGTGACGGGGCAATCTCAGCTCACTGACGCCCGCTCTCTGGGTTCAAGCG 3817
QY 3565 ATCTCTCGCTTAAGCTCTGAGTAGCTGGAAATTAAGCGTGACCACTGCTTTGGC 3624
Db 3816 ATCTCTCGCTTAAGCTCTGAGTAGCTGCGAGTACGGGACAAAGCCACAGCCAGC 3757
QY 3625 TAAATTTTTTGTATTTTACAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAA 3684
Db 3756 TAAAT-TTTGTATTTTAGTAAAGACAGGTTTACCATAATTGGCCAGGCTGCTCGAA 3698
QY 3685 CTCTGACCTCAAGTGATCTGCTGCTCAGTCTCCAAAGTGTGGAAATTAAGCGCTG 3744
Db 3697 CTCTGACCTC--GTGATCTGCCCGCTCAGCCTCCCAAGTGTGGAAATTAAGGCATA 3640
QY 3745 AGTCACTGTGCTGGCGGATTAATCTCTATTTTCTTATTTGCTATATCCCAGATCTAGA 3804
Db 3639 AGCCACCGCGCCGCGCAAGTGTAACTTTTAAAGATGACATCAAAAGCCCTGCATGACCT 3580
QY 3805 G-----CAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTA 3844
Db 3579 GGGCCTTCTCTCTCTCTAGCCTTACTGTGATTTGATGTAACCATTTCTAGCATTTGA 3520
QY 3845 TGAATGCACAGCCTAGATATAAATCTTCTTTTCTTTTAAAC-AACTTGACAACCT 3903
Db 3519 AGTATTTGGCAAGTTTTTTTTTAACTGTCAAGTGAGGATACTAATGTAATAGGGGAGA 3460
QY 3904 TTGCAGATAAATAACATCTTCATTTCTGCTT--TTTCACTTATCACCTTGTATTGACTT 3961
Db 3459 TAACAGCATATAAAGTGCCCAAGCACTACTGCTGGCTTAGCGTTAAACAATAATTTGGCT 3400
QY 3962 TTTTCATTTGCTCAAAACCTTTTATTTGTTACTGTTTTTTTCACTTACTTATTTAGTCACT 4021
Db 3399 ATTGTGGAAGAGCAACATTTATTCATGTAATTTTTCAGTCTCTACTCTGTCTCAAGA 3340
QY 4022 GAATAATATGGCTTAATTTTGTCTTATACATCTCTGCTCCTCACTTTTGAAGGCCAAATTTA 4081


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Db 9821 C--AAGTCAAGAGATCCAGACCATCTCGCTAAACAGTGAAACCCCGTCTCTACTAAA 9878
Qy 4349 AATAC--AAAAATAGCTGGGTAGTGATGCATGCTGTAGTCCAGCTACTCGGAGG 4406
Db 9879 AATACGAAAAAATAGCTGGCGTGGTGGCGGTGCTGTAGTCCAGCTACTCGGAGG 9938
Qy 4407 CTGAGGCAAGAGAAATCTTTGAACCTGGGAGGAGAGGTTGTCAGTGGAGCCGAGATCCAC 4466
Db 9939 CTGAGGCAGAGAAATGCGGTGAACCCGGGAGGAGAGCTTGCAGTGAGCCGAGATTGCGC 9998
Qy 4467 CACTGCATCTCCAGCTGGGCGCACAGCGAGACTCTATCTCAAAAAATAAATAAATAA 4526
Db 9999 CACTGCCCTCCAGCTGGGTGACAGAACGATACTCCGTCTCAAAAAATAAATAAATAA 10058
Qy 4527 ATAAAGGAT 4535
Db 10059 AAAAGAGAT 10067

RESULT 55
US-09-949-016-14172/c
; Sequence 14172, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14172
; LENGTH: 194933
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(194933)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-14172

Query Match 7.7%; Score 383.4; DB 3; Length 194933;
Best Local Similarity 59.6%; Pred. No. 4.7e-77;
Matches 859; Conservative 1; Mismatches 487; Indels 94; Gaps 9;

Qy 3098 TTTGGGTTTTTTTTTTTGTGTTTGTAGACAGGGTCTGCTGTGCACCCAGGATGAG 3157
Db 4948 TTTTGTGTTTTTTTTTTTTTTTTTGTAGACAGAGTCTGCTGTGCACCCAGGCTGGAG 4889
Qy 3158 CACAGTGGTCACCATAGCTCACTGAGCCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217
Db 4888 TGCAGTGGCAATCTCAGCTCACTGCAAGCTCTGCGCTCCCGGGTTAAGGGATCTCCT 4829
Qy 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACAGAGCGTGACCAACACGCTGGCTAAATAA 3277
Db 4828 GCCTCAGCCTCCCAATAGCTGGGACTACAGGTGCCCCCAACACGCTGCTCAATTTT 4769
Qy 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTGGCCAGGCTTGTCTTAAACTCCTGG 3337
Db 4768 TTGTATATTTAGTAGAGATGGGTTTTCAACCATGTTGGCCAGGCTGTCTCAAAAC----- 4715
Qy 3338 CTTCAAGCAATCTCTTACCTTGGCATCCCAAGTGTGGATTACAGGGGTGAGCCACC 3397
Db 4714 --TCAGGCAATTTGGCCACCTCAGCCTCCCAAGTGTGGGATTACAGGATGAGCCACT 4657
Qy 3398 ATGTGGGCTACTTATTTCTTTTACATTTCCATCTTTCCAATAGAATGTAGATCCACAGAA 3457
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Db 3654 GCATCCAGCCTGGGCAACAGAGCAAACTCCATCTCAAAAAAAAAAAGCATAGATTATC 3595
QY 4530 A 4530
Db 3594 A 3594
RESULT 56
US-09-949-016-13025
; Sequence 13025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13025
; LENGTH: 102053
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(102053)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-13025
Query Match 7.7%; Score 382.6; DB 3; Length 102053;
Best Local Similarity 57.3%; Pred. No. 5.3e-77;
Matches 858; Conservative 1; Mismatches 530; Indels 108; Gaps 5;
QY 3104 TTTTGTGTTGTTGTTTGTAGACAGAGGCTCTGCTCTGTCACCCAGGCTAGACAGT 3163
Db 40691 TTTTGTGTTGTTGTTTGTAGACAGAGTCTGCTCTGTCACCCAGGCTGGAGTGCAGT 40750
QY 3164 GGTGCAACCATAGTCACTGCAGCCTCAACCTCTCGAGCTCAAGGATCTGCTGACCTCA 3223
Db 40751 GGGCAATCCCACTCAGTCAACCTCCGGCTCCAGGTTCAAGAGTTCTCTTGCTCA 40810
QY 3224 GCTCCCAAGTAGCTGGGACTACGAGCGTGCACACACCGCTGGCTTAATTAATAAAT 3283
Db 40811 GCCTCCGAGTAGCTGGGATTACAGGTGCCGCCACCATGCTAAAGTTTGTGAT 40870
QY 3284 TTTTGTAGAGTGGGTCTTACTAGTTGGCCAGGCTGTCTTAACCTCTGGCTCAA 3343
Db 40871 TTTTAATAGAGACGGGCTTCAACAGGTTACCCAGGCTGCTCGAACCCCTGACCTCAG 40930
QY 3344 GCAATCCTCTACTTTGGCATCCAAAGTCTGGGATTACAGGGTGAGCCACCATGTGC 3403
Db 40931 GTGATCACTGCTCGGCTCCAAAGTCTGGGATTACAGCGTGAGCCACCATGCC 40990
QY 3404 GGCTACTATTCTTTACATTCATCTTTCCAAATAGAATGTAAAGTCCACAGAACAGGA 3463
Db 40991 GGCCTTCCAAACATATTGAATCACTCTCTTTTGTGTTAATTAAGAAATCAATTG 41050
QY 3464 TTTACTGCTATTTCTCTCTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCT 3523
Db 41051 ATACAGTTACAGTCAATTTATGTTGTTTTCAGTTTGGGTTCTCTTTCCCATCTCTGT 41110
QY 3524 CCCT-----TCAGCTCACTGCAACCT 3544
Db 41111 TGATTTATTTATATGCCAGGCTGGAGTGCAGTGGTGAATCTAGTTGACCTGCAACCT 41170
QY 3545 CTGCCTCCCGGTTCAAGYGATTCTCTCTGCCTAAGCCTCCTGAGTAGCTGGAATACAA 3604

Db 41171 CTGCCTCTGGGTTCACTGATTTCTCTGCTTAGCTCCCAAGTAGCTGGTACTACAGG 41230
QY 3605 CGTGCAACCATGCTTGGCTAAATTTTGTATTTTGTAGCAGAGATGGGTTTACCATTG 3664
Db 41231 CACGTGCTGCCACGCCAGGCTAA-TTTTGTATTTTGTAGTAGAGTGGGTTTACCATTG 41289
QY 3665 TTGCCAGGCTGCTCAAACTCCTGACCTCAAGTGATCTGCTGCTCAGTCTCCCAAA 3724
Db 41290 TTGGTCAGGCTGCTCGAATCTTGAGCTCAGGCAATCCGCTGCTGGGCTTCCAA 41349
QY 3725 GTGCTGGAATTATAGGCTGAGTCACTGTGCTGCGCCGATTAATCTATTTTCTTTAT 3784
Db 41350 GTGCTGAAATTACAGGCTGAGCCACTACCCAGCC--TCCATCCTTGTGATTAAT 41407
QY 3785 GCTATATCCCAGATCTAGAGCAGTGTGACATATAGTAGTGTCAATAAATAATGA 3844
Db 41408 ACTAATATCCGTAATAGTCAATGTTTGTGAAACACATTTAGAGAGGAGATGGGCCGA 41467
QY 3845 TGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAATCTTTGACAACT 3904
Db 41468 CG-----TGTTGGCTCATG 41481
QY 3905 TGCAGAATAAATACAACTCTTGCAATCTGCTTTTCTCATTATCACCTTGTATTGACTTTT 3964
Db 41482 CCTATAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATCACTTGAGCTCAGGAGTTG 41541
QY 3965 CATATTGCTCAAACTTTTATTTGTTACTGTGTTTTCATTGTTACTATTTTACTCACTGA 4024
Db 41542 AGACCAGCTTAGGCAATATAGTGAGACCTGTCTCTATTTACTGAAAAAACAAGTTTAA 41601
QY 4025 TAATATGGCTTAATTTGCTTATACATCTCTCTGCTCCACTTTTGAAGGCCAAATTTACAA 4084
Db 41602 TTTAAAAAATGAGAGAAAAAATGTGTATC-----CATGGTCCC 41641
QY 4085 ATCTGATGAAAGCTATGAACCCCTCTCCCAAGAGAAATACACACACACACACTCACA 4144
Db 41642 TTATAGTGGAAAGAGAGGTGAATGAGCTTTAATGATTGAGGGAAGCCCAACTAGTT 41701
QY 4145 CACAGTTTTTTTAAATGTTTGCACACTAAGACAAGAAACCTGTCATTAGAGGATGTTGT 4204
Db 41702 TGTTTTCTGTTTTCAACCAAGTTTTTAATTTCTTTTCCATTCTGAACCTAGCCTTTTA 41761
QY 4205 CATATTAATTAATAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGTACTT 4264
Db 41762 ACATTTAGATAGATGTTGGGCTGGGTTCGATGGCTCACACCTGTAAATCCAGCACTT 41821
QY 4265 TGGAAAGTCAAAGGTGGGTGGATCACTTGAGGTGAGAAGTTGAGACCAAGCCTGGTCAATA 4324
Db 41822 TGGGATGCCAAGGTGGGTGGATCACTTGAGGTGAGGAGTTGAGACCCGCTGACCAACA 41881
QY 4325 TGGTGAACCCCTATCTCTACTAAAAAATACAAAAATAGCTGGGTAGTGTGATGCTGCT 4384
Db 41882 TGGTGAACCCCTGCTCTCTACTAAAAAATACAAAAATAGCTGGGTGGGTGGGCTCT 41941
QY 4385 GTAGTCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATGCTTGAACCTGGGAGGAGAG 4444
Db 41942 GTAATCCCAGCTACTTGGGAGGCTGAGGAGGAGATCACTTGAACCTGGGAGGTGAGG 42001
QY 4445 TTGAGTGAAGGAGATCCCACCTGCACTGCTGGGCGACACAGCGAGAGCTCTAT 4504
Db 42002 TTGAGTGAAGTGAATTTGCGCCATTGCACTCCAGCTGGGTAAACGAGCAACTACATCT 42061
QY 4505 CTCAAAAAATAAATAAATAAAGATCGGAGAGAAACAAAACTAATAAGATT 4561
Db 42062 CAAAAAATAAATAAATAAAGAGAAATTTGGAACCTAAGAGGATTTCTTAAATTTCTT 42118

RESULT 57

US-09-949-016-15786/C

; Sequence 15786, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

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; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15786
; LENGTH: 35629
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(35629)
; OTHER INFORMATION: n = A,T,C or G
; US-09-949-016-15786

Query Match          7.6%   Score 382.2;   DB 3;   Length 35629;
Best Local Similarity 59.7%   Pred. No. 4.1e-77;
Matches 870;   Conservative 1;   Mismatches 494;   Indels 92;   Gaps 10;

QY 3110 TTTGTTGTTTGTAGACAGGGTCTTGTCTCTGTCACCCAGGATGAGCACAGTGTGCA 3169
DB 8198 TTTTGTGTTTGTGACGGAGTCTGTCTGTCTCCCGAGGCTGGAGTGCAGTGGCGTG 8139

QY 3170 ACCATAGGTCACTGCACGCTCAACCTCCTAGCTCAAGGATCTGTGACCTCAGCTCC 3229
DB 8138 ATCTCGGCTCACTGCAACCTCTCGCTCCCTGGTTTCAGGAGATTCTCTCGCTCAACCTCC 8079

QY 3230 CAAGTAGCTGGGACTACGAGCTGCACACACGCTGGCTAATTAATAAAATTTTGTG 3289
DB 8078 CGAGTAGCTGGGACCAAGGCTGTGTCACACGCTGGCTAATTTTATA--TTTGTAG 8021

QY 3290 TAGAGACTGGGTCTTACTAGTTGGGAGCTTGTCTTAACTCTCGGTTTCAAGCAATC 3349
DB 8020 TAGAGATAGGGTTTCAACATGTTGGCCAGGCTGTCTCAAACTCTTGACCTCAAGTGATC 7961

QY 3350 CTCTACTTTGGATCCCAAGTCTGGGATACAGGGTGAGCCACCATGCGGCTAC 3409
DB 7960 CGCCCGCTTTGGGCTCTCAAGTCTGGGATACAGGCATGAGCCACCATGCGTGGCCCA 7901

QY 3410 TTATTTCTTTACATTCATCTTTTCCAATAGAATGTAAGATCCACAGAACAGGGATTACTG 3469
DB 7900 ACATGTTATCTTT----- 7886

QY 3470 CCTATTTTCTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATCATCACTCAACCTCGTTC 3529
DB 7885 ----TATTTTATTTATTTTATTTTGTAGACGGAGTCTCACTCTGTCACCTGGACTGGAGTGC 7830

QY 3530 A-----GCTCACTGCAACCTCTGCTCCCGGTTTCAAGYATTCTCTCTGCC 3575
DB 7829 AGTGGTTTGAATCTTGGCTCACTGCAAGCTCCGCTCCAGGTTTCAACCAATCTCTCTGCC 7770

QY 3576 TAAGCCTCTCTGAGTAGTGGAAATTACAAGCGTGCACCCACCATGCTTGGCTAA----TTTT 3631
DB 7769 TCAGCCTCCCAATTAGCTGGGATTACAGGCGCCGCGCATCACGCCAGCTAATTTT 7710

QY 3632 TTGTATTTTGTAGCAGAGATGGGTTTTCATGTTGCCAGGCTGGTCTCAAACTCCTGA 3691
DB 7709 TTGTATTTTGTAGACAGGGGTTTCACTGTTGTAGCCAGGACGGTCTCAATCTCCTGA 7650

QY 3692 CCTCAAGTGATCTGCTGCTCAGTCTCCCAAGTCTGGAAATTATAGGCTGAGTCACT 3751
DB 7649 CCTC--GTGATCCGCTGCTCGGCTTACCAAGTCTGGGATTACAGGATGAGCCACC 7592

QY 3752 GTGCTGGCCGATTAATCTGTCTATTTTCTTTTATTTGCTATATATCCCCAGATCTAGACAGTGT 3811
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DB 7591 ACACCTGGCCGA-----TCCTTAATCCTCTTAATAAACCTCAACGGTAGGTAC 7544
QY 3812 CTGACATATAGTAGTGTCTCAATAAATAATTAATGATGAATGCACAGCTAGATATAAATTT 3871
DB 7543 TACAGCTATCCCCCTTTTTCAGGCAAAAGAAATCAAGTGACGGGGACCTTTAAAGAGTTGT 7484
QY 3872 CTTTTTCTTTTTTAAACAATCTTTGACAACTTTTCAGAAATAAATACAATCTTGCAATCT 3931
DB 7483 CAAAGTCAATGACCAAACTGCAGCAATTAATTCAGCCACACACCCGCTCTTCTGGG 7424
QY 3932 GCTTTTTCATCTTATCACCTTGTATGACTTTTTCATATTTGCTCAAACTTTATTTGTTAC 3991
DB 7423 ATTGCTCCATTTCTTAATGCTATCAGCGCGCAAGGAATGACAAAAAGCCCTCTGAG 7364
QY 3992 TGTTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGCTTAATTTGCTTTATA-CAT 4050
DB 7363 AGGAGCTACTCTAAACACAGGCAACGAAACAAATAAAAAATCAAGTGACTATAAAGACAGCAT 7304
QY 4051 CCTCTGCTCCACTTTTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCTCTC 4110
DB 7303 CAAACAGCAGCAAAACAAAAATCTTAGCAGAAATTTATAGCATCAGGCTGGGTGCGATGGC 7244
QY 4111 CCCAGAGAAATACACACACACACACACTCTCACACACAGTTTTTTTTTAATGTTGCAAC 4170
DB 7243 TCACGTCTGTAAATCACAGTACTCTGGAGGCCAAGCGCAGGCGGATCACTTGAGGTCAGGA 7184
QY 4171 TAAGACAAAGAACCTGCAATTAGAGGATGTTTGTTCATATTAATTAANAAT-----AACTC 4225
DB 7183 GTTGAGAGCCAGCTGCCCCAACATGTTGAGACCTCATCTGCTAAAAATACAAAAAAT 7124
QY 4226 AGTTGGGCACAGTACTCAAGCTCTAAAGCTCTAAACACAGTACTTTTGAAGTCCAAGGTGGTGA 4285
DB 7123 GTTCAGGTGCGCGCTCACGCTGTATCCAGCACATTTGGGAGGCTCAGCGCGGCGGA 7064
QY 4286 TCACCTTGAGGTGAGAAGTTTCGAGACACGCTGCTCAATATGTTGTAACCTATCTCTACT 4345
DB 7063 TCA--TGAGGTGAGGAGCTCAAGACCATCTCTGGCTAAACACGGTGAAACCCCTCTCTACT 7006
QY 4346 AAAAAATACA-AAAAATAGTGGTGTAGTGTAGTGCATGCTGTAGTCCAGCTACTCGGGA 4404
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QY 4405 GGCTCAGGCAAGAGAAATGCTTGAACCTGGGAGGAGAGTTGCAGTGAGCCGAGATCCC 4464
DB 6945 GGCTGAGGCAAGAGAAATGCTTGAACCCGGAGGAGAGCTTGCACTGAGCCGAGATGCC 6886
QY 4465 ACCACTGCACTCCAGCTGGCGCACACAGCGAGACTTATCTCAAAAAAATAAATAAATA 4524
DB 6885 GCCACTGCACTCCAGCTGGCGCACACAGCGAGACTCTGTCTCAAAAAAATAAATAAATA 6826
QY 4525 AATAAAGATCGGAGA 4541
DB 6825 AAGGAAAGAAAAAGAAA 6809

RESULT 58
US-09-949-016-12153
; Sequence 12153, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12153
; LENGTH: 23569
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(23569)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12153

Query Match 7.6%; Score 381; DB 3; Length 23569;
Best Local Similarity 60.3%; Pred. No. 6.5e-77;
Matches 902; Conservative 1; Mismatches 476; Indels 116; Gaps 12;

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DB 7092 AGTGCAGTGTGCAAAATCATAGTTCACTGCAGCCTTGAACCTCTGGACTCAGGAGTCT 7151
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DB 7152 CCCTGCTCAGCCTCCCAAGTAGTGGGACTACAGGTGCTCACCACCATGCTGGCTAAT 7211
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DB 7272 CAATTTCTGGGCTCAAGCAA-----TCTACTCTGTCTCCAAAGTGTGAGATGACAGG 7328
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DB 7389 TGTGCAGACAACTTTGGGTAAGTCTGACATAGGCATTTTTTAAAAAACTCCCTGATTTT 7448
QY 3474 -----TTTTCTCTCTTTTGTAGACAGAGTCTCACTTCATCACTCAAC 3521
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DB 7509 TGGGGTGCACTGGCGGATCTGGCTCACTGCAAGCTCCACCTCCCGGTTTATGCAATT 7568
QY 3568 CTCCTGCTAAGCCTCTGAGTAGCTGGAATTAACAAGCTGACACCACTGCTTGCTAA 3627
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DB 7629 TTTTGTATTTTGTAGCAGGAGTTTACCCGTTGTTAGCCGGATGCTCTGATCTC 7688
QY 3688 CTGACCTCAAGTATGCTGCTGCTCAGTCTCCCAAAGTCTGGAATTAAGCGCTGAGT 3747
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QY 3748 CACTGCTGCTGGCGGATTAAGTCTATTTCTTTTATTTGCTATATCCAGATCTAGAGCA 3807
DB 7747 CACTGCTGCGAGCAACTCCCTGATTTT-----AATGTGAGGC 7786
QY 3808 GTGCTGTGACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGCTAGATATAA 3867
DB 7787 AGGATTGAGACTAAGTACTACTAGTCTAAATGGTTCTGAAAGCTTGAGCAGGCTTCAAAATCA 7846
QY 3868 CTTTCTTTTCTTTTAAAAACAATCTTGACAACCTTTGACAATTAATACAAATCTTGCA 3927

DB 7847 C--TTGGAGCCCTTGTGTTGAAACTCAAGTTTCAAGTGTGGCTGCAATTCACAGAGTTCTGA 7905
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DB 7906 TTGAG---TAGGTCTTTGGGAGCGGAGCTGTGAATTTGCAATTTCTAGCTAGTCTTTAAG 7962
QY 3988 TTACTGTTTTTTTCAATTTGTTACTATTATTTAGTCACTGAATAATATGCTTTAAATTTGCTTATA 4047
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RESULT 59

US-09-949-016-15351
; Sequence 15351, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15351
; LENGTH: 23574
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(23574)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15351

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Db	46090	GTGATCTCTCCGCGCTTGGCCCTCCCAAAGTGTGGGATTACAGCGGTGAGCCACCGACCC	46149
Qy	3404	GGCTACTTATTT-----CTTTACATTCCTATCTTTCCCAATAGAAATGTAAGAT	3449
Db	46150	AGAAAAGAACTTTACAGAGAGAAAACATATTTCTAGACCCCTGAAGATATACAGTTAACT	46209
Qy	3450	CCACAGAACAGGGAATTACTGCCTATT-----TTC	3478
Db	46210	CTCGAACATGGGGTTTATGGGGTGTGACCCCTTAAAGTCAAAATATTTCCCATATAAATT	46269
Qy	3479	TTCCCTTCTTTTTTGAGACAGAGCTCACTTCATCACTCAACCTCCGT-----	3527
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Qy	3528	---TCAGCTCACTGCAACCTCTGCCTCCGGGTTCAAGYGAATCTCTGCCTCAAGCCCTCC	3584
Db	46330	ATCTCAGCTCACTGCGAGCTTCATCTCTTAGGTTTAAGGTATTTCTCTGCCTCAGCCTCC	46389
Qy	3585	TGAGTAGCTGGAATTAACAAGCTGCACCACTGCTTGCTGAATTTTTTGTATTTTTTAGC	3644
Db	46390	TGAGTAGCTAGGATTACAGGTGTATGCCGCACCGCTAGCT-ACTTTTTGTATTTTTTAGT	46448
Qy	3645	AGAGATGGGGTTTTACCATGTTGCCCAGCGTGTCTCAAACTCCTGACCTCAAGTGATCT	3704
Db	46449	AGAGATGGGGTTTCAACATGTTGGCCAGCGTGTCTCGAACTCTCTGACTTTCAAGTAAATCC	46508
Qy	3705	GCCTGCCTCAGTCTCCCAAAGTCTCGAAATTAAGCGGTGAGTCACTGTGCCTCGCCCGAT	3764
Db	46509	ACCTGCCTTGGCCTCCCAAAGTCTGGGATTACAGGCATAAGCCACTGTGCCCGGCC---	46565
Qy	3765	TACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTAGACAGTGTCTGACATATAGTA	3824
Db	46566	----TCATATAAGTTTTTGACGCCCTCCACCCCAAATTTAACTACTGATAGCTACCATT	46621
Qy	3825	GGTGCTCAATAAATATTTGATGAATGCAAGCTAGATATAAATTCTTTTCTTTTTT	3884
Db	46622	GACCAAAGCCTTACTGATAAACAGTTGATTCACATATATTTTGTGTATATATCTGTAT	46681
Qy	3885	TAAACAATCTTGACAACATTTGCAGATAAATAACAATCTTGCAATCTGCTTTTCACTTA	3944
Db	46682	TCITTACAGTAAGGTATGGTAGAGAAAGGAAATATTAAGAAATCAGGCCAGATCCAGTG	46741
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Db	46742	GCTCATGCCGTAACTCTAGCACTTTTGGGAAAGTTGAGGAGGGGGATCACTTGAGCTCAG	46801
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Qy	4125	CACACACACACACTCACACAGTTTTTTTTTAATGTTTGCACCTAAGACAAGAAACC	4184
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Qy	4305	CGAGACCAGCCTGGTCAATATGTTGAAACCTCTATCTACTAAAAATAAAAAATTAGCT	4364

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16948.836 Million cell updates/sec

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Scoring table: IDENTITY_NUC
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Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	474.8	9.5	US-10-741-600-17681 Sequence 17681, A
3	456.6	9.1	US-10-322-281-618 Sequence 618, Appl
4	444.4	8.9	US-10-717-597-68 Sequence 68, Appl
5	438	8.8	US-10-017-161-1659 Sequence 1659, Ap
6	434.2	8.7	US-10-322-281-676 Sequence 676, App
7	434.2	8.7	US-10-087-192-100 Sequence 100, App
8	433.2	8.7	US-10-087-192-844 Sequence 844, Appl
9	429.8	8.6	US-10-723-681-1 Sequence 1, Appli
10	425.4	8.5	US-10-322-281-448 Sequence 448, App
11	416	8.3	US-09-920-671-11 Sequence 11, Appl
12	414.6	8.3	US-10-719-993-6883 Sequence 6883, Ap
13	414.2	8.3	US-10-087-192-484 Sequence 484, App
14	413.6	8.3	US-10-317-500-4 Sequence 4, Appli
15	412.4	8.3	US-10-085-117-328 Sequence 328, App
16	405.8	8.1	US-10-322-281-314 Sequence 314, App
17	403.6	8.1	US-09-740-043-3 Sequence 3, Appli
18	402	8.0	US-10-981-277-44 Sequence 44, Appl
19	401.8	8.0	US-10-756-149-2307 Sequence 2307, Ap
20	400.4	8.0	US-09-764-864-1644 Sequence 1644, Ap
21	400.4	8.0	US-10-484-577-660 Sequence 660, App
22	400	8.0	US-10-741-600-17664 Sequence 17664, A
23	399	8.0	US-10-087-192-1978 Sequence 1978, Ap

24	398.6	8.0	174448	5	US-10-087-192-148	Sequence 148, App
c 25	398.4	8.0	167343	3	US-09-962-436-281	Sequence 281, App
c 26	398.4	8.0	167343	3	US-09-964-824A-273	Sequence 273, App
c 27	398.4	8.0	167343	9	US-10-843-641A-2740	Sequence 2740, Ap
c 28	398.4	8.0	167343	9	US-10-843-641A-5576	Sequence 5576, Ap
c 29	398.4	8.0	201143	7	US-10-240-425-1099	Sequence 1099, Ap
c 30	396	7.9	76798	3	US-09-880-107-3949	Sequence 3949, Ap
31	394.6	7.9	19300	7	US-10-317-271A-4	Sequence 4, Appli
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33	391.4	7.8	1980090	8	US-10-741-600-17676	Sequence 17676, A
34	390.8	7.8	15000	3	US-09-954-531-175	Sequence 175, App
35	390.8	7.8	15000	9	US-10-843-641A-1242	Sequence 1242, Ap
c 36	390	7.8	13224	3	US-09-764-853-897	Sequence 897, App
c 37	389.6	7.8	23456	7	US-10-322-281-64	Sequence 64, Appl
c 38	389.6	7.8	60057	5	US-10-087-192-700	Sequence 700, App
c 39	389	7.8	62555	9	US-10-741-600-17630	Sequence 17630, A
c 40	389	7.8	120955	9	US-10-756-149-4579	Sequence 4579, Ap
c 41	388.8	7.8	150275	9	US-10-981-277-55	Sequence 55, Appl
c 42	388	7.8	75252	5	US-10-087-192-904	Sequence 904, App
c 43	387.8	7.8	48001	7	US-10-304-107-4	Sequence 4, Appli
c 44	387.8	7.8	300000	6	US-10-262-552-33	Sequence 33, Appl
c 45	387.8	7.8	300000	7	US-10-703-210-33	Sequence 33, Appl
c 46	386.4	7.7	304905	7	US-10-271-416-1	Sequence 1, Appli
c 47	385.2	7.7	61103	5	US-10-087-192-58	Sequence 58, Appl
c 48	385	7.7	114411	8	US-10-482-065-22	Sequence 22, Appl
c 49	384.8	7.7	73237	7	US-10-723-860-3910	Sequence 3910, Ap
c 50	384.2	7.7	73237	7	US-10-741-601-5712	Sequence 5712, Ap
c 51	383.4	7.7	96594	3	US-09-997-722-22	Sequence 22, Appl
c 52	383.4	7.7	227246	7	US-10-322-281-314	Sequence 314, App
c 53	382.2	7.6	6892	3	US-09-764-877-3770	Sequence 3770, Ap
c 54	382.2	7.6	6892	6	US-10-242-515-3770	Sequence 3770, Ap
c 55	382	7.6	47219	7	US-10-699-941-10	Sequence 10, Appl
c 56	382	7.6	59884	9	US-10-699-941-11	Sequence 11, Appl
c 57	381	7.6	57759	9	US-10-783-271-108	Sequence 108, App
c 58	380.8	7.6	32193	3	US-09-764-877-2623	Sequence 2623, Ap
c 59	380.8	7.6	32193	6	US-10-216-464-37	Sequence 37, Appl
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c 61	380.4	7.6	183610	8	US-10-484-577-664	Sequence 664, App
c 62	380	7.6	75252	5	US-10-087-192-904	Sequence 904, App
c 63	379.8	7.6	72604	8	US-10-162-497-7	Sequence 7, Appli
c 64	379.8	7.6	72604	8	US-10-623-313-7	Sequence 7, Appli
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c 66	379.6	7.6	256493	5	US-10-087-192-1000	Sequence 1000, Ap
c 67	379.4	7.6	3239	5	US-10-027-632-114978	Sequence 114978, A
c 68	379.4	7.6	3239	6	US-10-027-632-114978	Sequence 114978, A
c 69	379	7.6	276276	5	US-10-087-192-754	Sequence 754, App
c 70	378.4	7.6	32204	3	US-09-764-855-327	Sequence 327, App
c 71	378.4	7.6	32204	3	US-09-764-872-517	Sequence 517, App
c 72	378.4	7.6	32204	5	US-10-072-349-327	Sequence 327, App
c 73	377.6	7.6	48509	7	US-10-322-281-510	Sequence 510, App
c 74	376.8	7.5	72691	8	US-10-741-600-17712	Sequence 17712, A
c 75	376.6	7.5	48069	8	US-10-719-993-6756	Sequence 6756, Ap
c 76	375.6	7.5	221600	9	US-10-840-590-1	Sequence 1, Appli
c 77	375.4	7.5	103574	9	US-10-756-149-2307	Sequence 2307, Ap
c 78	374.2	7.5	12683	5	US-10-242-355-703	Sequence 703, App
c 79	374.2	7.5	58845	5	US-10-087-192-40	Sequence 40, Appl
c 80	374	7.5	96592	3	US-09-997-722-88	Sequence 88, Appl
c 81	374	7.5	160552	8	US-10-697-828-11	Sequence 11, Appl
c 82	373.4	7.5	42794	8	US-10-741-600-17670	Sequence 17670, A
c 83	372.8	7.5	52677	5	US-10-087-192-130	Sequence 130, App
c 84	372.2	7.4	32152	3	US-09-764-855-328	Sequence 328, App
c 85	372.2	7.4	32152	3	US-09-764-872-518	Sequence 518, App
c 86	372.2	7.4	32152	5	US-10-072-349-328	Sequence 328, App
c 87	371	7.4	13264	3	US-09-764-853-897	Sequence 897, App
c 88	370.8	7.4	143671	6	US-10-236-031B-53	Sequence 53, Appl
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c 91	368.6	7.4	108111	8	US-10-719-993-6843	Sequence 6843, Ap
c 92	368.6	7.4	202814	8	US-10-719-993-6812	Sequence 6812, Ap
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98 366.8 7.3 8807 3 US-09-764-869-1415 Sequence 1415, Ap
99 366.8 7.3 8807 5 US-10-091-504-1415 Sequence 1415, Ap
100 366.8 7.3 8807 6 US-10-227-577-1415 Sequence 1415, Ap
101 366.6 7.3 24801 9 US-10-684-042-18 Sequence 18, Appl
102 366.6 7.3 25301 7 US-10-671-007-3 Sequence 3, Appl
103 366.2 7.3 12744 6 US-10-242-355-702 Sequence 702, App
104 366 7.3 27681 3 US-09-764-869-1997 Sequence 1997, Ap
105 366 7.3 27681 3 US-09-764-869-1998 Sequence 1998, Ap
106 366 7.3 27681 5 US-10-091-504-1997 Sequence 1997, Ap
107 366 7.3 27681 5 US-10-091-504-1998 Sequence 1998, Ap
108 366 7.3 27681 6 US-10-227-577-1997 Sequence 1997, Ap
109 366 7.3 27681 6 US-10-227-577-1998 Sequence 1998, Ap
110 366 7.3 64921 6 US-10-085-117-70 Sequence 70, Appl
111 365.8 7.3 39768 5 US-10-087-192-1030 Sequence 1030, Ap
112 365.8 7.3 47219 7 US-10-699-941-10 Sequence 10, Appl
113 365.8 7.3 59804 7 US-10-699-941-11 Sequence 11, Appl
114 365.4 7.3 31853 6 US-10-242-355-757 Sequence 757, App
115 365.4 7.3 243390 7 US-10-322-281-462 Sequence 462, App
116 365.2 7.3 31277 5 US-10-087-192-1510 Sequence 1510, Ap
117 365.2 7.3 62134 8 US-10-417-375-82 Sequence 82, Appl
118 364.4 7.3 485237 3 US-09-933-267A-1 Sequence 1, Appl
119 363.4 7.3 52216 3 US-09-747-810-1 Sequence 1, Appl
120 363.4 7.3 75327 8 US-10-719-993-6912 Sequence 6912, Ap
121 363.4 7.3 75327 8 US-10-741-600-17832 Sequence 17832, A
122 363.4 7.3 100762 7 US-10-322-696-154 Sequence 154, App
123 363.2 7.3 32194 3 US-09-764-891-7028 Sequence 7028, Ap
124 363.2 7.3 141121 8 US-10-741-600-17651 Sequence 17651, A
125 363.2 7.3 210204 9 US-10-723-860-1746 Sequence 1746, Ap
126 363.2 7.3 210204 9 US-10-756-149-1685 Sequence 1685, Ap
127 362.4 7.3 13409 3 US-09-764-891-9601 Sequence 9601, Ap
128 362.4 7.3 13409 5 US-10-205-428-930 Sequence 930, App
129 361.8 7.2 26928 3 US-09-880-107-2278 Sequence 2278, Ap
130 361.8 7.2 26928 5 US-10-020-141-7 Sequence 7, Appl
131 361.8 7.2 26928 5 US-10-017-631-1 Sequence 1, Appl
132 361.8 7.2 26928 7 US-10-235-192A-34 Sequence 34, Appl
133 361.8 7.2 106707 7 US-10-694-685-8 Sequence 8, Appl
134 361.6 7.2 35962 8 US-10-775-169-234 Sequence 234, App
135 361.6 7.2 35962 8 US-10-473-126-2 Sequence 2, Appl
136 361.6 7.2 175737 8 US-10-723-860-1753 Sequence 1753, Ap
137 361.6 7.2 175737 9 US-10-783-271-34 Sequence 34, Appl
138 361.6 7.2 175737 8 US-10-719-993-6817 Sequence 6817, Ap
139 361.4 7.2 169739 7 US-10-450-826-93 Sequence 93, Appl
140 360.8 7.2 57457 8 US-10-741-600-17639 Sequence 17639, A
141 360.6 7.2 148935 8 US-10-741-600-17708 Sequence 17708, A
142 360.2 7.2 14176 3 US-09-764-864-1644 Sequence 1644, Ap
143 360.2 7.2 177531 8 US-10-484-577-660 Sequence 660, App
144 360 7.2 9968 3 US-09-764-856-100 Sequence 100, App
145 360 7.2 9968 3 US-09-764-856-100 Sequence 100, App
146 360 7.2 9968 5 US-10-102-627-100 Sequence 100, App
147 359.6 7.2 4863 8 US-10-278-698-56 Sequence 56, Appl
148 359.6 7.2 4863 8 US-10-278-698-570 Sequence 570, App
149 359.4 7.2 130320 6 US-10-408-168-1 Sequence 1, Appl
150 359 7.2 22161 3 US-09-764-847-1020 Sequence 1020, Ap

ALIGNMENTS

RESULT 1
US-10-607-806-1
; Sequence 1, Application US/10607806
; Publication No. US2005004159A1
; GENERAL INFORMATION:
; APPLICANT: Adam, Gail Isabel Reid
; APPLICANT: Langdown, Maria L.
; APPLICANT: Denissenko, Mikhaili F.
; APPLICANT: Dennis, Edward
; APPLICANT: Cantor, Charles
; APPLICANT: Rubin, Byron
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR REDUCING FAT
; TITLE OF INVENTION: DEPOSITION AND TREATING ASSOCIATED CONDITIONS
; FILE REFERENCE: 524592003200

Query Match 100.0%; Score 4997.8; DB 8; Length 12174;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5000; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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US-10-607-806-1
; CURRENT APPLICATION NUMBER: US/10/607,806
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392,362
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 12174
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; ORGANISM: Homo sapiens
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; OTHER INFORMATION: y = C or T
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: m = A or C
; FEATURE:
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; OTHER INFORMATION: y = C or T
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: k = G or T
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; NAME/KEY: misc_feature
; LOCATION: (11649)...(11649)
; OTHER INFORMATION: m = A or C
; US-10-607-806-1

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Qy 241 GCTGGCACTTTTTCACACCTGCAAGTCTGAACCTCAGATTGGCTCAGCTAAAGAAAGCTTGCC 300
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Db 5040 TGATCTCAGATCACTACACCTCCATCTCTGGGTTCAATATTTCTTGCTCAGCCT 5099
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Db 6180 GAGGAGCGTGGGACCCCGAGGAGCAGGAAGCAGTGTGTCCCGGGGTGCTGGCAGACC 6239
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Db	6900	CTGCTCTACTA	AAAAAATACAAAAAT	TAGCCGACATGGTGGCGAGCGCT	GTAAACCCCA	6959
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Db	8340	TTGATGAAT	GTGCAACGCTAGATATA	AAATCTTTCTTTTCTTTT	TTTAAACAATCTTGACA	8399
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QY	3961	TTTTCATAT	TGCTCAAACTTTATTTG	TACTGTTTTTTTCA	TGTTTATGATCAC	4020
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QY	4021	TGAATAAT	TAGGCTTAAATTTGCTT	ATACATCTCTGCTCCA	CTTTAGAGGCCAAATTT	4080
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Db	8760	ACTTTGGA	AGTCCAAAGGTGGTGGAT	CACTTCAGGTGAGAA	GTTCGAGACCAAGCCTGGTC	8819
QY	4321	AAATATGGT	GAACCCCTATCTCTA	CTAATAAATAA	CTAGCTGGGTGTAGTGATG	4380
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QY	4381	GCCTGTAGT	CCAGCTACTCTGGGAG	CTGAGCAAGAGAA	TTGCTTGAACCTGGGAGGCA	4440
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QY	4441	GAGGTTGCA	GTGAGCGGAGATCC	CACTCCAGCTCCAG	CTGGGCGCACACAGCAGACT	4500
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QY	4501	CTATCTCA	AAAAATAAATAAATAA	ATAAAGATCGGAG	AGAAACAAACTAATAAGAT	4560

[illegible]

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RESULT 2
US-10-741-600-17681/c
; Sequence 17681, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 17681
; LENGTH: 333811
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(333811)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Table)
US-10-741-600-17681

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	Query Match	9.5%;	Score 474.8;	DB 8;	Length 333811;
	Best Local Similarity	50.9%;	Pred. No. 1.8e-97;		
	Matches 1926;	Conservative	3;	Mismatches 1650;	Indels 203; Gaps 26;
Qy	794	ACATTTATTATTATCTTATTATTATGTAGACAGAGCTCTTGCTTTGTCGCCAAGGCTGA	853		
Db	10492	AAAACTTTTTTGTGGTTGTGTTTGGATGGAGTCTCACTCTCTGCACCAGGCTGA	10433		
Qy	854	GTCAGTGGTGCAGATCTCGGCTCAGTCGAAGCTCCACCTGCTGGGTTCAGCCCATTTCTCC	913		
Db	10432	GTACAGTGGTGCAAATCTCGGCTCAGTCGAACCTCCACCTCCTGGTTCAGTGATTCTCC	10373		
Qy	914	CGCCTTAGCCCTCCCAGTAGCTGGGACTAAAGGGGCGCTGCCACCAGCCCGCGTAATTTT	973		

10372	Db	TGCCTCAGCCTCCGCGAGTAGCTAGGATTACAGGTGCACGCCACCGTCTCGGCTAA---TT	10311
974	Qy	TTTGTATTTTAAATAAGACGGGGTTTCATCGGTGTTAGCCAGGATGGTCTCGATCTCATG	1033
10315	Db	TTTGTATTTTAAAGACAGAGGTTTACTCCATGTTGGTCAGGCTGTCCTAAATTCCTG	10256
1034	Qy	ACCTTGATGTCGGCTCGCTCGGCTCCCAAAGTGTCTGGATTTACAGGCATGAGCCA---	1090
10255	Db	ACCTCGTGAGCCACCGCTCAGCCTCCCAAAGTGTAGGATTTACAGGCGTGAGCCACGG	10196
1091	Qy	CCGTGCCGGGCTTATCACAATTTATTATTATTGTTTTCTCTCCCACTAGGTTGTAAGC	1150
10195	Db	CCGGCCAGGGCAAAAATCTTTATAACCTTGATAGCAAGATTTCTTACATGGAACAC	10136
1151	Qy	TCCATGAGTTAGAGATTATTATTATTATT-----ATTATTATTATTATTATTATT	1196
10135	Db	AAAGGCACAAAATCATTTAGAAAACAAAATTGGAGCGGCGGTGCTCACGCGCTGTA	10076
1197	Qy	TTATTATTATTATTATCTGTTCACTGCTGTATCTTAGCTCTTAGGACAGAGCCTGGC	1256
10075	Db	ATCCAGCAGCTTTGGGAGCGCGAGACAGACGGAACACGAGGTGAGAGAAACGAGACC	10011
1257	Qy	ACATAGTAAGTGCTCAA-----TAAATATTCACTGGATATAAACAGTGCAGATA	1303
10015	Db	CTGGCTAACACGGTGAATCCTGCTCTACTAAATAACAAAAATTAGCCGGGCATGGT	9956
1304	Qy	GTTTAAAACTATCTGAC-----CTAGGAGGCTGAGGCAGGAGAAATGCGGTGAAC	1356
9955	Db	GGTGGGCGCTGTAGTCCAGCTACTTTGGAGGCTGAGCAGGAGAAATGGTGTGAAC	9896
1357	Qy	GGAAAGCAGATTTGCATGAGCTGAAATCGTGTCATGCACTCCAACTTGGGCAACAG	1416
9895	Db	GGAGCGGAGCTTGCAGTGAGCGAGATAGTGCACTGCACTCCGCGCTGGACAAAGAG	9836
1417	Qy	CAGACTCCATCTCAAAAAAATAAAAAAATACTCAGGCCTAGCTGGTGGCACATGCCT	1476
9835	Db	CGAGAGACTGTCTCAAAAAAATAAAAAAATAATGGATTGTATCAAAATATTAATCT	9776
1477	Qy	GTAATCTAGCTGAGGCGGTAGGCTCCCAAGAAAGAAAGAAAGAAAGAAAGAGATA	1536
9775	Db	CTTCAGAGGACAGTGTGTATATGAATATGAATGCCAGCTCACAGCTGAGAGAAAT	9716
1537	Qy	TATATATATATACACACACAAAGATATAAACTTTATATATAATAAGTTTTTCAT	1596
9715	Db	GAAGCCTGTCTAATAAAGGGCTTGTATTGAGATTATATAAAATATCTCACAACT	9656
1597	Qy	AAAAAATAAACCTCTACCACTTTACITTCACAGGTTCTTGGGTCCAAAGCTCTTCA	1656
9655	Db	AGACAACTCAATAAATAAGCAGAGATCTGAACAGCCACTTTTCCAAAGAGATACA	9596
1657	Qy	AGAGGAGAGCTGGCAGGGGTGAGGAGGAGCGGTGGGACCCGAGGAGCAGGAAGG	1716
9595	Db	TGGAAA-----ATAGGTACATGAAGAAGTCTCAACAGTCTGTTAAGAAAATG	9544
1717	Qy	GTGTCCCGGGGTCTGGCAGACCGATTGAACTCTGGGCTATGTCTTTTTCAGTGG	1776
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1777	Qy	CCGCCGACAGGCATCAGCCCTCGGGCGGTGGCAGTTCCGCAAAATGATCAAGTGG	1836
9495	Db	GCTGAGCGGGTGATACCTGAGGTGCGGAGTTCAAGACCACTGACCAACATGGTGA	9436
1837	Qy	TGATCCCGGGAGTGACCCCTTTTGGAAATACAACAATACAGGCTGCTACTGTGG	1896
9435	Db	AACCCCGTTTCCACTAAAATATACAAAAAATAATTAACCTATGCATGGTGGCT	9376
1997	Qy	GGGCTCAGGCAACCCCGTGGATGAATCGGAAGTAAAGTATCGCGCTCGAGGAAAA	1956
9375	Db	TAGTCCAGCTACATGGAGGCTG-----AGACAAGAGARCTGCTTTGAACCTGG	9324
1957	Qy	GGAGTGTCTCGCGGGCGGGTGCGCACACGCCAAGGATCTCAGCAGGCATACAAAG	2016
9323	Db	GTGAGGCTCGAGTGAGCCGAGATTGAGCCACTGCACTCCAGCCTGGGTGACACAGT	9264

Db 7220 CTTTCAATAATGTAATAAATCTCAAGGTGGTTTAAAGTGAATAATTTTAAATAGGTGAAT 7161
QY 4224 TCAGTTGGGCACAGTCACTCAAGCTGTAAACACAGTACTTTTGAAGTCCAGGTGGGTG 4283
Db 7160 TCAGCAGGACCGGTGGCTCAGATCTGTAAATCCACAGCACTTTGGAAGGCCGAGGCGGTG 7101
QY 4284 GATCACTTCAGGTGAGAAGTTCCAGACCAAGCTGGTCAATATAGTGAACCCCTCTCTA 4343
Db 7100 GATCAC--AAGGTCAAGACTGGGACCGTCTGGCTTAACAGATGAACCCCACTCTA 7043
QY 4344 CTAATAATAC--AAAAATAGCTGGGTGTAGTATGATGCATGCTGTAGTCCAGCTACTC 4400
Db 7042 TGAATAATACAAAAAATAGCACCGCTGGTGGTGGATGCTGTAGTCCAGCTACTC 6983
QY 4401 GGGAGCTGAGGCAAGAGATTGCTTGAACCTGGGAGGAGAGGTTGCAAGTGGCCGAGA 4460
Db 6982 GGGAGCTGAGGCAAGAGATTGCTTGAACCTGGGAGGAGAGGTTGCAAGTGGCCGAGA 6923
QY 4461 TCCACCACTGCACCTCCAGCTGGGCGACACAGCAGACTCTATCTCAAAAAAATAATA 4520
Db 6922 TGGCACCACTGCACCTCCAGCTGGGCGACAGAGTGAGACTCTGTCTCAAAAAAATAATA 6863
QY 4521 AA 4522
Db 6862 AA 6861
RESULT 3
US-10-322-281-618/c
; Sequence 618, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 618
; LENGTH: 42360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-618
Query Match 9.1%; Score 456.6; DB 7; Length 42360;
Best Local Similarity 99.8%; Pred. No. 8.7e-94;
Matches 456; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4545 ACAAACCTAATAAGATTCCTGAAGTAAAGCAGAGATACGTAAATATATATATATTAAGTT 4604
Db 42360 ACAAACCTAATAAGATTCCTGAAGTAAAGCAGAGATACGTAAATATATATATTAAGTT 42301
QY 4605 TAAATGCATTTTAACTGTAATCTTATTTGTTTATTTTGGTTATATAAAGTAAACAGCAAA 4664
Db 42300 TAAATGCATTTTAACTGTAATCTTATTTGTTTATTTTGGTTATATAAAGTAAACAGCAAA 42241
QY 4665 AGTAATGCAACTTCAAAKCTACATAAATATCTATTTATGGAAGTGGAAAGGCATCTATAA 4724
Db 42240 AGTAATGCAACTTCAAAKCTACATAAATATCTATTTATGGAAGTGGAAAGGCATCTATAA 42181
QY 4725 TCCCTACTACCAAGATAACCAAGTACATATCTCTCCAGATTTTGGGCGATACACTAGC 4784
Db 42180 TCCCTACTACCAAGATAACCAAGTACATATCTCTCCAGATTTTGGGCGATACACTAGC 42121
QY 4785 TTTTATTTTGGGAAATTTTCATGTGAGGATACCTAAATTTTCTAAATGTCTATGT 4844
Db 42120 TTTTATTTTGGGAAATTTTCATGTGAGGATACCTAAATTTTCTAAATGTCTATGT 42061
QY 4845 AGTATTTCCATTTAAGGATGTTCATATTTTAAAAATACATGCTTTAAAGTAGAGAACT 4904

Db 42060 AGTATTTCCATTTAAGGATGTTCCATAATTTTAAATAATACATGCTTTAAAGTAGAGAACT 42001
QY 4905 AGTTTGGGCATGGTGGCTCAGCCTGTATCCAGCACTTTTGGAGGCCGAGGCAATGGA 4964
Db 42000 AGTTTGGGCATGGTGGCTCAGCCTGTATCCAGCACTTTTGGAGGCCGAGGCAATGGA 41941
QY 4965 TCACCTTGAGGTCCGAGGTTTGAGACCAAGCCTGGACAA 5001
Db 41940 TCACCTTGAGGTCCGAGGTTTGAGACCAAGCCTGGACAA 41904
RESULT 4
US-10-717-597-68/c
; Sequence 68, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dörner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 126990
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-68
Query Match 8.9%; Score 444.4; DB 7; Length 126990;
Best Local Similarity 54.1%; Pred. No. 1.1e-90;
Matches 1225; Conservative 3; Mismatches 98; Indels 51; Gaps 14;
QY 2291 AGGCCAGGCGGCTGGCTCATGCTGTAAATCCAGCACTTTTGGAGGCCGAGGCGGCGG 2350
Db 28169 AGGCCAGGCGGCTGGCTCATGCTGTATCCAGCACTTTTGGAGGCCGAGGCGGCGG 28110
QY 2351 ATCACTTGAGGTGAGGTTTGAGACCAAGCCTGGCCAAACATGGTGAAACCCCTGTCTCTAC 2410
Db 28109 ATCACTTGAGGTGAGGTTTGAGAACAGCCTGGCCAAACATGATGAAACCTTTGTGCCAC 28050
QY 2411 TAAAAAATACAAAAATTAAGCCGACATGTTGGGAGCGCC-----TGTAAACCCAGCTAC 2465
Db 28049 T-AAAAATACAAAAATTAAGTGGCGCTAGTGGCAGACACCTATAGTCTAGCTAGCTAC 27991
QY 2466 TTGGGAGACTGAGTTGGAGGTTTCACTGAGCAAGCTGGTGTCTGTCTGTCTGTCTGTCTGT 2525
Db 27990 TTGGGAGCTGAGGCGGGAATCGTTTGAACCCGGAGGTAGAGGCTGAAGTGAAGTGAAG 27931
QY 2526 GTAAACAGAGCAACTCTGTCTCAAA-----AAAAAATATGCTTTTCAATATAATATATATA 2581
Db 27930 ATCACACCACTGCACCTCCAGCCTAGGTGACAGCAAGGCGCTCATCTCAAAAAAATAATG 27871
QY 2582 AAGGACTTATATTTTTCAGCCATAGGATCATTTCTCTGAGCATCTTGGGAGGCCAAGCGGCG 2641
Db 27870 GTGGGCCAGGCAAGCGGTGCTCAGCTCAGTAATATCCAGCACTTTTGGGAGGCCAAGCGGCG 27811
QY 2642 TCCCAACCTGTTTCCCTGAGAGTGGGCGAGGCTGAGCTGATTTCTCTCTCTCTCTCTCTCT 2701
Db 27810 AGATCATGAGGTGAGGATCAAGACCATCTCTGGCTAACCGGTGAACCCCGCTCTCTCTAC 27751
QY 2702 TATCTCAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2761

Db 27750 TAAAAATACAAAAAATTAGCCGGGCATCGTGGTGGCGCGCTGTAATCCCGAGCTACTTTGGG 27691
Qy 2762 AGCCCAAGAGCTGGACAGCTGTAATTTCTGCTGGACAMMCGGTACACCCACACCTATT 2821
Db 27690 AGGCTGAGGCGGAGAAATAGCGGTGAACCCGGGAGGCGGAGCTTGGCAGGAGCGGAGATCG 27631
Qy 2822 CATATCGTCTCTCGGCTCGGCAATCACCTGTAGCAGTAGGTTTATTCCTCTCCCTTGCACCT 2881
Db 27630 CACTGTCGCGCTCAATTCAGCCTCGGAGACAGAGTGAGACTCCATCTCAAAACAAAACA 27571
Qy 2882 ATGAATTTCTAGTTGTTCTCAGTAGCCGGGGGAAATAATAGTAAC-----AACAG 2933
Db 27570 AAACAAAACAAAACAAAGTGGTGGGCGATGCCCTCTAATCCTAGCTACTTTGGAAGGCTGAG 27511
Qy 2934 CCATGATTTAGTTAATTTCTTGTTCTGGGCGAGTGCTCCTTTAATCCTCAGAACAA 2993
Db 27510 GCAGGAGAATCGGTTGAACCCCGGAAGCAGAGAGCTCGAGTGACCAAGATCACACCACTG 27451
Qy 2994 CACTATGGGATAGGT-ACAATTTATCCTCACTTAACAGATAAGAAAACTGAGGCTCAGAAG 3052
Db 27450 TACTCCAGCCTGGTGACGAACGAGACTCTCCATAGTTTCATGAAATACCAACAT 27391
Qy 3053 GCTGAGCTATTTCGCCAAGATCACACAGCTTGTAGTGGTGACAGTTGGGTTTTTTTT 3112
Db 27390 TCTAATCCGACACCGCAAGATTTACTCTAGCCTTCACCATGTCCATATCTTTAACTCCTT 27331
Qy 3113 GTTGTGTTTATAGACAGGGTCTTGCTCTGTCAACCCAGGACATGACAGTGGTGAACC 3172
Db 27330 TCTCTAATGTGAGATGGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAAGTGGTGATC 27271
Qy 3173 ATAGGTCAGTCGACGCTCAACCTCCTGAGCTCAAGGATCTGTGACCTCAGCCTCCCAA 3232
Db 27270 TCA-----CCTCCACCTCCAGGTTCAAGCGATCTCTCGCTCAGCCTCC- TG 27223
Qy 3233 GTAGCTGGGACTAGAGCTGCACCAACAGCCTCGCTAATTAATAAAAAATTTTTTTGTAG 3292
Db 27222 GTAGCTGGGAATACAGCGGTGCACCAACCATGCCCGCTAATTTTATA--TTTTCAGTAG 27165
Qy 3293 AGACTGGGTCTTACTAGTTGGCCAGGCTTGCTTAACTCCCTGGCTTCAAGCAATCCTC 3352
Db 27164 AGTCGCAAGTTTCAACATGTTTCCAGGCTGGTCTCAAACTCCCTGAACCTCAAGTGATCCAC 27105
Qy 3353 CTACCTTGGCATCCAAAGTCTGGGATTAACAGGGGTGAGCCACCATGTGCGGCTACTTA 3412
Db 27104 CCGCGCAGCTCCCAACGTCTGGGATATAGGGGTGAGCCACTGCACCTGGCCTTTCT 27045
Qy 3413 TTTCTTTTACATTCATCTTTTCCAAATAGAATGTAAAGATCCACAAACAGGGATTAAGCTT 3472
Db 27044 GTACTCTTTATTTCACTGGTCTGTTCTTTTGGTTTCAGTATCATAGTACTTTTG 26985
Qy 3473 ATTTTCTTCTTCTTTTGTGACAGAGTCTCACTTCATCATCCTCAACCTCGTTTCAGC 3532
Db 26984 TTTCTGTAGCTTAAAAAT--ATATATTTTAAAGACTGGAATGAGTGGCATGATCTCAGC 26927
Qy 3533 TCACTGCAACTCTGCTCCCGGGTTCAAGYGATTTCTCTGCTTAAGCCTCCTGAGTAGC 3592
Db 26926 TCACTGCAACTCCACCTCCAGGCTCAATATTCTGTGACTCAGCCTCCTGAGTAGC 26867
Qy 3593 TGGAAATTAAGCGGTGCACCAATGCTTGGCTAAATTTTTTGTATTTTTTAGCAGAGATGG 3652
Db 26866 TGGGATTTACAGGAGGAGCACCACCATGCCCACTAA-TTTTTGTATTTTTCAGTAGATGGA 26808
Qy 3653 GGTTTTACCATGTTGCCAGGCTGTTCTCAAACTCTGACCTCAAGTGATCTGCCGCT 3712
Db 26807 AGTTTACCATGTTTCTTAGGCTGATCTTAACTCTCTGACCTCGAGTGATCCGCCGCT 26748
Qy 3713 CAGTCTCCCAAGTGTGGAAATATAGGCGTGAGTCACTGTGCTGGCGGATTAAGTGTCT 3772
Db 26747 CAGCTCCCAAGTGTGGGATAACAGGCATAGCTGCTGCGTGACGCTTTCTGTATTC 26688
Qy 3773 ATTTTCTTTATGCTATATCCAGATCTAGAGCAGTGTCTGACATATAGTAGTGCTCA 3832
Db 26687 TTTATTCTGTTTCAATTGATCTGTTCTCTTTTGGTTTCAGTATCATACTATTTTGTGTTGT 26628

Qy 3833 ATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAACAA 3892
Db 26627 TTCTATAGCTTAAAAATATGTAATTTT---TTTGTAGATAGGCTCTCACTGTGTCACCCAG 26571
Qy 3893 TCTTGACAACTTTTGAGAAATAAATCTTTGCAATCTTTGCAATCTTGCTTTTCACTTATCACTTTG 3952
Db 26570 GCTGGAGTGACTGGTGTGATCATGGCTCACTGTCATCTCAACCTCTTATACTCA-ATTG 26512
Qy 3953 TTATGACATTTTTCATATTTGCTCAAAACCTTTTATGTTTACTGTTTTCATTGTTTACTATT 4012
Db 26511 ATCTCTCCCACTCACTCCCAAGTAGTGCACCAACCATGTTTGGCTAAATTTTAAATTT 26452
Qy 4013 TTAGTCACTGATATATATGGCTTAATTTGCTTTATACATCTCTCTCCCTTTTGAAGG 4072
Db 26451 TTTGTAGAAAACAGAGCTTTGCCATGTCACCCAGGCTGGTCTTGAACCTCTGGGCTGAAG- 26393
Qy 4073 CCAAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCAAGAGAAATACACACACA 4132
Db 26392 --AGATCCGCTGACCTCATCTCTCCCAAAGTGTGGAATTTACAGGTGTGCACCACTTTGCC 26335
Qy 4133 CACACACTCACACAGATTTTTTTTTTAAATGTTTGGCAACTAAGACAAGAA-----ACC 4184
Db 26334 CAGCCAAAAATATGTTTTTGGCAGATCACCTGAGGTGGGAGTTTCAAGACCAGCCTGGCC 26275
Qy 4185 TGCATTAGAGGATGTTTGTTCATATTAATTTAAAAATAACTCAGTTGGGCACAGTGACTCA 4244
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Qy 4245 AGCCTGTAAACCACTACTTTTGGAAAGTCCAAAGTGGGTGGATCACTTGAAGTGAAGATT 4304
Db 26214 TGTCTGTAATCCAGTACTCTGGAAGGCCAAGGAGGTGGATCACCTGAGGTGAGGATT 26155
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Db 26154 TAAAGACCAAGCCTGGCCAACTGGTGAACCCCTGCTCTACTAAAAATACAAAAATAGCT 26095
Qy 4365 GGGTCTAGTGTGATGCTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTGC 4424
Db 26094 GGGCGTGTGACCGGTGCTGTAAATCCAGCTACTCAGGAGGCTGAGGCGAGAGATCAC 26035
Qy 4425 TTGAACCTGGGAGGAGGTTGCAAGTGGCGAGATCCCACCTGCACTCCAGCTCGG 4484
Db 26034 TTGAACCTGGGAGGTAGAGTTGCAAGTGGCGAGATCATGCCATTGCACTCTAGCCTGG 25975
Qy 4485 GCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA 4530
Db 25974 GTGACAGAGCGAGATTCTCTCAAAAAAGAAAAAGAAAAAAA 25929

RESULT 5

US-10-017-161-1659/c
; Sequence 1659, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1659
; LENGTH: 58448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source

QY 1457 TAGCTGGGTGGCACATGCCTGTGAATCCTAGCTGAGCGGTAGGTCCTCAGAGAAGAAGA 1516
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QY 1517 AGAAGAAAAAAGAAGATATATATATATATACACACACAAGAAGATATAAATTTATAT 1576
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QY 1577 ATATAAAGTTTTCATTAAAAAAMAAAAAACCTCTACCCACTTTCACCTTTACAGGTT 1636
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QY 1637 CTGGGTCACAGGTCCTTCAGAGGAGGAGCTGGCAGGGTCAGGAGGACGCTGGGACC 1696
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QY 1697 CGAGGGAGCAGGAAGGAGGTGTGTCCCGGGGTCTGGCAGACCGAATTTGAACTCTGGCT 1756
Db 35394 CAGTCTTTACAAAAACAAGGTTTAAAAATTTAGCCAGGTGTGATGGTGCATACCTGTAGTA 35335
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Db 35334 CCAGCTACTTTGGGAGGCTAAAGGGGGAGGAGAAATTCCTTGAGCTCAGGAGTTTGAGGT 35275
QY 1817 CCGAAAAATGATCAAGTCCG-TGATCCGGGGAGTGACCCCTTCTTGGAAATACAACAACT 1875
Db 35274 ACAGACAGTGGTGAAGGAAAAATCTCCAGTGGTGGAACTTTGGAGCAATACATCTGTG 35215
QY 1876 ACGGC-TGCTACTGTGCTTGGGGGCTCAGGCACCCCCGTGATGAATCGSACAAGTAA 1934
Db 35214 GATGCTTCTGTGAGGAAAGGTGGCCTAAAGGTACAGATTTACATGGACTGG----- 35163
QY 1935 GTGATCCGCCTGCAGGAAAAATTTGAGTGCCTGCGGGGGGGGGTGGGGCAGACGCAAG 1994
Db 35162 -----TGACGACATCTGTAGGCTGGCCAGCTGCAGAGACTTTGMAAGAGACACA 35113
QY 1995 GATCTCAGGGCATACAAGGGGACTTGCATATCTGCTAAGGATAACATATTTTCACCT 2054
Db 35112 ACTGGCAATCTGATGGCTTAGGAGACAGGACTGT----- 35079
QY 2055 CTTGTCAAAATAACAATAATGTTTCCAAAGAGACCTGTAGCGAACCGACCCGTTAGAGA 2114
Db 35078 -----GGCCAGCTCTCAAAATAGTCAAGGGTGGGAAGATTTCCATATGAAGT 35030
QY 2115 TGGNAACAATGACCGAGTCGNAACAAGTGGGAGTCTCCCTCCAGTGGCAGATGTA 2174
Db 35029 GCCCATCAGAGAGCCATCGGTGACAGACCCCTCGGTGATGAGATGGGATGACTCATGCTG 34970
QY 2175 GCAACAGTAAACATCAGACAACTATCCAGCTGTCTATTTTCTAGCAGTGGTTGTCAGTCG 2234
Db 34969 TAGATTGTGCAGCTCTTTACCTGGCCA-GACCCATGCTTTCTCAATGGTCCCATACAG 34911
QY 2235 ACCTTCTGAATACAGGATTTTACTGTATCTTGGCAACCATGTTTAAAAATCGCTTTCAGGC 2294
Db 34910 AGTGCTCCACCCAGATGTCTGGGTGTGTAGAAA-----ATGGCTGTGCTCAATTGGC 34856
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Db 34856 CGGCGGGTGGCTCAACCTGTAAATCCAGCACTTTGGGAGCGCGGAGGAGCAGCGATCA 34796
QY 2355 CTTGAGTTCAGGAGTTCGAGACCAAGCTGGCCAACTATGTTGAAACCTGTCTCTACTAA 2414
Db 34795 CTTGAGTTCAGGAGTTCGAGACCACTTTGGCTAACCGGTGAAATCTGTCTCTACCAA 34736
QY 2415 AA-----ATACAAAAATTAGCCGGACATGTTGGCGAGCCCTGTAAACCCAGCTACTTGGGA 2471
Db 34735 AAAATACAAAAAATTAGCTAGGCTAGTGGCGGGCCCTGTAGTCCAGCTACTCGGGA 34676
QY 2472 GACT-----GAGTTGGAGGTTTCAGTGAGCCCAAGTTCGT 2505
Db 34675 GGCTGAGGAGGAGAAATCCCTTTGAACTGGGAGGTGGAGGTTGAGGTGAGCCAGATCGT 34616
QY 2506 GTCACTGCTGTCCAGCCTGGGTAAACAGA--GCAACTCTGTCTCAAAAAAATAAATGCTTT 2563

Db 34615 GTCACTGCACCTAGCTGGGCGACAGAAAGAACTCGTCTCAAAAAAATAAATAAATAA 34556
QY 2564 TCAATAAATATATGATAAAGGACTTATATATTTTTTCAAGCCATAGATCATTTCTCCTGA 2623
Db 34555 AAGAAAGAAAAAAGAAATGGCTGTCTCAGGCCAGGCACAGTAGCTCATGCCATATA 34496
QY 2624 AGC-----ATCTTGGCGAAGTCATCCCCACACCTGTTCTCTGAGAGTGGCAGGTGAGG 2674
Db 34495 ATCCAGCTACTCGGGAGGCTGAGGAGGAGAACTTGAACCTTGGGAGGAGGTTGAG 34436
QY 2675 GCTGACCTATTCTCTGCACCTTACTCTATCTCAGCTGTCCCTCCCACTTTCCAGGT--- 2731
Db 34435 TGAGCCAAAGATCGCATCATTTCCAGCTGGGCAACAAAAAGTGAAACTCTATCTCAA 34376
QY 2732 ----GCTGCCACACATGACAACTGCTAYGACCAGGCCAAGAGCTGACAGCTGTAA 2787
Db 34375 AAAGGAAAAAAGAAATGCTTGTCTATGTTTTTATACAGTGTCTTTAAATTTCAATTCA 34316
QY 2788 TTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATCTCGTGTCT-----GGCT 2839
Db 34315 GTTTTTCTAAGTTTTTTTTTTTTTTTCCGAGACAGAGTCTTGTCTGTCAACCAGGT 34256
QY 2840 CGSCAATCACCTGTAGCAGTAGTATTATCCCTTCTTGTGACCTATGAATTTCTAGTTGGTT 2899
Db 34255 GGAGTGCAGTGGCAGATCTTGGCTTACTATAAACCCTCCACCTTCTGGGATCAAGCAGTT 34196
QY 2900 TCAGTAGGCG-----GGGGGAAATAATAGTAACAACAGCCATGATTTAGTGT 2948
Db 34195 TCAGGTCTCAGCTCTCTGAATAGCTGGGACTACAGGCTCCCAACCACCTGCCAGCTGCA 34136
QY 2949 AATTTCTTGGTTCTGGGCACT-----GTCTCTTTAATCTCAGAACACATATGG 3002
Db 34135 TTTTGTGTTTTGTTTTGTTTTTATGTTTATGAGTAGTAGGTTTTTGTCTATATATGGCGGGCTGG 34076
QY 3003 ATAGTTACAATTTATCTCTCACTTAAACAGATAAGAAAACTGAGGCTCAGAAAGGCTGAGCTAT 3062
Db 34075 TCTCGGATTACTAGCTCAAGTGATTCACTCCCTCGGCTCCCAAGTTCTAGGATTAT 34016
QY 3063 TTGCCCAAGATCAGACAGCTTGTAGTGTGACAGTTTGGGTTTTTTTTTGTGTGTTT 3122
Db 34015 AGGCAATGAGCCACCATGCGGCTTTTCTTTTATGTTTTTAAAAATAAAAATAAATATATG 33956
QY 3123 AGAGACAGGT-----CTTGCTCTGTCAACCAGCATGAGCAGAGTGG 3165
Db 33955 CCAGTCTTGGTGGCTACAGCTGTAAATCCAGCACTGTGCCCAGGCTGGAGTGAGTGG 33896
QY 3166 TGCAACCATAGTCTACTGAGCCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAGC 3225
Db 33895 CACCATGTCGGCTCACTGCAACCTCCGCTCCAGGATCAAGCGATTCTCCACCTTGGC 33836
QY 3226 CTCCCAAGTAGCTGGAGCTACAGCGTGCACCAACCGCTGGCTAAATTAATAAATAAATTT 3285
Db 33835 CTCCCAAGTAGCTGGATTTAGAGCACCGCCGACCAACCCAGCTAAATTTTGTGA---TTT 33778
QY 3286 TTTGTAGACATGGGTCTTACTACGTGTGGCCAGGCTTGTCTTAAACTCTCGGCTTCAAGC 3345
Db 33777 TTAGTAGACAGAGGTTTCCACCATGTTGGCCAGACTGGTCTCGAACTCTGACCTCAGT 33718
QY 3346 AATCTCTCTACTTGGCATCCAAAAGTGTGGATTTACAGGGGTGAGCCCAATGTGCGG 3405
Db 33717 GATCTCTCTGCTCAGCTCCCAAGTTCTGGATTTACAGTCTGAGCCACCAACCGCCAG 33658
QY 3406 CTACTTATTTCTTTACATTCATCTTTCCAAATAGATGTAAAGATCCACAGAACAGGAT 3465
Db 33657 ---CCTGCGCTGCCACATTTTTTAAATTTATTTATATATTTTTTTGAGCGGAGTCTC 33601
QY 3466 ACTGCTATTTTCTCTCTTTTCTTTTGGAGACAGAGTCTCACTTTCATCACTCAACCTCC 3525
Db 33600 GCTCTGT-----TACCCAGGCTGGAGTGCAGTGGCGCCA 33567
QY 3526 GTTAGCTCAGTGCAGAACCTCTCGCTCCCGGTTCAAGYATTTCTCTGCTAAGCTCTCT 3585

Db 33566 TCTCGGCTCACTGCAAGCTCCGCTCCCGGGTTACGCCATTCTCTGCTCAGCCTCCC 33507
QY 3586 GAGTAGCTGGAATTTACAAGCGTGCACACCATCTCTGGCTAAATTTTGTATTTTATGCA 3645
Db 33506 AAGTAAGTGGACTACAGGCGCCGCCACACCGCGCTAAATTTTGTGATTTTATGAT 33447
QY 3646 GAGATGGGGTTTACCAGTGTGCCCCAGGCTGGTCTCAAACTCTGACCTCAAGTATCTG 3705
Db 33446 GAGATGGGGTTTACCAGTGTGCCCCAGGCTGGTCTCAAACTCTGACCTCAAGTATCTG 33389
QY 3706 CTTGCTCAGTCTCCCAAGTGTGGAATATATAGGCGTGAAGTCACTGTGCGTGGCGGAT 3765
Db 33388 CCACCTCGGCTCCCAAGTGTGGAATATATAGGCGTGAAGTCACTGTGCGTGGCGGAT 33331
QY 3766 ACTGTCTATTCTTTTATTGCTATATCCCGAGATCTAGAGCAGTGTCTGACATATAGTAG 3825
Db 33330 CTTGGCCAGTTTTTAA--ACATTTCAAGTGAGTGTCTTTGTTGAATAAGGCAAA 33274
QY 3826 GTGCTCAATAAATAATGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT 3885
Db 33273 CGTTTTGCTCCATCAATTTTTCATCTCCAAGAGTTTCTGACACAGTGCCTCTCTGTG 33214
QY 3886 AATAAATCTTGACAACTTTTGGAATAAATAAATAAATAAATAAATAAATAAATAA 3945
Db 33213 AATAAAGCAGTGTGTTGACAACTCAAGTTTTTGTGTTGTTGTTGTTGTTGTTGTT 33154
QY 3946 CACTTTGTTATGACTTTTTCATATTCGCTCAAACTTTTATGTTACTGTTTTTCTATTCT 4005
Db 33153 AACAGTAAATTTCTTATGAGCTAACCACTGATTTGAACCATGAGTATAAATGCCAAG 33094
QY 4006 TACTATTTAGTCACTGAATAATATGGCTTAATTTGCTTTATATCATCTCTGCTCCACT 4065
Db 33093 TAGTTCTTCCAAGACAGACTTTTGTGATGATCTCTGATATGAATGACATTAATCTATCT 33034
QY 4066 TAGAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCGAGAGAAATACAC 4125
Db 33033 TGGCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 32980
QY 4126 ACACACACACACTCACACAGTTTTTTTTTTAAATGTTTGAACCTTAACAGAAACCT 4185
Db 32979 -----CATTTACAGATCTTACTAGTCTATGGGCTGTAAGCATTCACCATTTTATGTT 32925
QY 4186 G-CATTAGAGGATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4244
Db 32924 GAAATAAGTTGACTCATCAGCAGGATAAAGATTATGTTGTCGCGGGTGTGGTGCCTCA 32865
QY 4245 AGCTGTACACAGTACTTTGGAAGTCCAAGTGGGTGATCACTTTGAGGTGAGAGTT 4304
Db 32864 CGCTGTAAATCCAGACACTTTGGGAGGCTGAGCGGGCGGATCAC--GAGGTGAGAGAT 32807
QY 4305 CGAGACAGCTGCTCAATATGTTGTAACCCCTATCTCTACTATAAATAAC-AAAAATTAGC 4363
Db 32806 CAAGACATCTCTGGCTAAACATGTTGAACCCCATCTCTACTATAATAAATAAATTAGC 32747
QY 4364 TGGGTGTAGTATGATGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAAATTG 4423
Db 32746 CGGGCTGTGTGGCGGCTTCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAAATTG 32687
QY 4424 CTTGAACCTGGAGGAGAGGTTGCACTGAGCGGAGATCCACCACTGCACTCCAGCCTG 4483
Db 32686 CTTGAACCCAGAGGAGG-GGCATTTGCACTGAGCCAGATCGCGCACTGCACTCCAGCCTG 32628
QY 4484 GCGCACACAGCAGACTCTATCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 4543
Db 32627 GCGCACAGAGGAGACTCTGTCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 32568
QY 4544 AACAAATAAATAAGATTCCTGAAGGTAAGCAGAGATACGTAAATATATGTAATAAGT 4603
Db 32567 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 32508
QY 4604 TTAATGCAATTTAACTGTAATCTTATGTTATTTTG 4641
Db 32507 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 32470

RESULT 6

US-10-322-281-676
; Sequence 676, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 676
; LENGTH: 93544
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-322-281-676

Query Match 8.7%; Score 434.2; DB 7; Length 93544;
Best Local Similarity 59.7%; Pred. No. 2.1e-88;
Matches 861; Conservative 1; Mismatches 559; Indels 22; Gaps 7;
QY 3104 TTTTTTTTGTGTTGTTTGTAGACAGAGGTCTGTCTGTCTCAACCCAGGCGATGAGCACAGT 3163
Db 18099 TTTTTTTTGTGTTGTTTGTAGAGATGGAGTCTTAGCCCTGTTGCCAGGCTGGAGTGCAGT 18158
QY 3164 GGTGCAACATAGTCTACTGTCAGCTCAACCTCTCTGAGCTCAAGGATCTGCTGACCTCA 3223
Db 18159 GGCACCATCTGGGTCACTGCAACCTCCACCATGTGGGTTCAAGAGATTCTACTGCTCA 18218
QY 3224 GCCTCCCAAGTAGCTGGGACTAGGAGCGTGCACACACAGCGCTGCTAATTAATAAATTT 3283
Db 18219 ACCTCCCAAGTAGCTGGGAAATTACAGGCTGTGTCACACACACCTTGTCTAATT--TTTGTGT 18276
QY 3284 TTTTGTAGAGACTGGGTCTTACTAGCTTGGCAGGCTGTCTAAACTCTCTGGCTTCAA 3343
Db 18277 TTTTATTAGACAGAGGTTTCCGCATGTTGGCAGGCTGATCTCAACTCTCTGGCTCAA 18336
QY 3344 GCAATCTCTACTTGGCTCCCAAGTGTGGGATTAAGGGGTGAGCCACCAATGTGC 3403
Db 18337 CTGATCCGCTCGCTCCGCTCCCAAGTGTGGGATTAAGGTGTGAGCCACCAATGCCT 18396
QY 3404 GGTACTTATTCTTTTATCTTCAATCTCTTCCATAGATGTAAGATCCACAGAAACAGGA 3463
Db 18397 GGCACCAACAGGCTTTTATTACAGGTTGCCTCATTAACCTGAATTTCTCTCTCCAAATTC 18456
QY 3464 TTACTGCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACCTTCATCACTCA---A 3520
Db 18457 TTGTTACCAACACAGGAACATGAGATGGAGTCTCGCTCCGTCGCCAGTCTGGAGTGC 18516
QY 3521 CTTCCGTTTCACTCACTCAACCTCTGCTCCCGGGTTCAAGYGAATTTCTCTGCTTAAGC 3580
Db 18517 AGTGTATCTCAGCTCACTCAACCTCTGCTCTCGGGTTCAAGTGTATTTCTCTGCTCAGC 18576
QY 3581 CTCCTGAGTGTGGAATTAAGGCTGCACACCATGCTTGGCTAAATTTTGTATTTT 3640
Db 18577 CTCCCAAGTAGCTGGGACTACAGGATGGCCACCCACCTGGGTAA--TTTTTGTATTTT 18635
QY 3641 TAGCAGAGATGGGGTTTATACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTCAAGTG 3700
Db 18636 TAGTAGACAGGGGTTTACCATGCTGGCAGGCTGGTCTCGAATCTCTGACCTC--GTG 18693
QY 3701 ATCTGCTGCTCAGTCTCCCAAGTGTGGAATATATAGGCGTGAAGTCACTGTGCTGCG 3760
Db 18694 ATCCACCCGCTCAGCTTCCCAAGTGTGGGATTAAGGATGAGCCACCAATACCTGCG 18753
QY 3761 CGATTACTGTCTATTTT-----CTTTATTTCTATATCCCGAGATCTAGAGCAGTGTCTG 3814
Db 18754 CAGGAACATAGACAGTTTATGAGACATCTTTCTGAAATAGGGCTGGTGGCCCTCATTTATTC 18813

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QY 3815 ACATAGTAGGTCTCAATAAATTTGATGAATGCACAGCCTAGATATAAATTTCTT 3874
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 18814 ATTAATGCTATTTTCTCCAAAACCCGGGAACCAAAATAGATGTGATAGCATCCCTC 18873
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3875 TTTCTTTTTTAAACAACCTTGACAACTTTGCAGAAATAAATAACAATCTTGCAATCTGCT 3934
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 18874 ATGATCTGAAGTTACTGCTCGTAACCTGCGGTCCCATCGATTTGGGATTTGGGGATGCC 18933
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3935 TTTTCTACTTAACA-CCTTGTTATGACTTTTTTCATATATGCTCAAACTTTATTTGTTACTG 3993
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 18934 TGCACGTGTCTGTGTCATGTGTCATGTCTGCGGTGCCATCAGTCTGTGAGCTCCCTCT 18993
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3994 TTTTTCATGTTACTATTTTACTGACTGAATAATATGCTTAATTTGCTTATACATCCT 4053
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 18994 GGGCTGCGTCCGTTTTTCTATCTTCTGTTGATATCTCAGCAGCTTTGTACAATACCTGGC 19053
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4054 CTTGCTCCACTTTAGAGGGCAAAATTTACAAATCTGATGAAGCTATGAACCCCTCTCCCC 4113
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19054 ACTCAATGAATTAATAAATAATCTGAAGCGGGGTGGGGGAGCTTGTCAATATAGCCCC 19113
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4114 AGAGAAATACACACACACACACTCACACAGCTTTTATTTTAAATGTTGCAACTAA 4173
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19114 ACCTTGTTTTGCCCTTGGACTTGATAAAGCCGTTTGTGCTATGCTATGTCTCATCTCT 19173
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4174 GACAAGAACTCTGATTTAGAGGATGTTTGTTCATATTAATTAABAAATACTCA- 4226
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19174 TTCTAGACAATGATTTACTTTGGATGAATAGGCAGATCTCTTGGTTAAACCATAAAGACAG 19233
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4227 GTTGGGCACAGTGAACCCCTGTAAACACAGTACTTTTGGAAAGTCCAAGGTGGGTGGAT 4286
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19234 GCTGGGCGCGTGCACATCTGTAATCCAGCAGCTTTGAGAGCGCGAGGCGGCAGAT 19293
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4287 CACTTGAGGTGAGAAGTTGAGACACAGCCTGGTGCATATATGGTGAACCCCTATCTCTACTA 4346
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19294 CACTTGAGGTGAGAAGTTGATACACAGCCTGGCACAACATGGTGAACCCCAATCTCTACTA 19353
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4347 AAAATACAAAATTAGCTGGGTGATGATGATGCTGCTGAGTCCAGCTACTCGGGAGG 4406
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19354 AAAATACAAAATTAGCCGAGTGGGTGGCGCATGCTGTAATCTCTAGCTACTTTGGAGG 19413
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4407 CTGAGGCAAGAGAATTTCTTGAACCTTGGGAGGAGAGGTTGCACTGAGCGCAGATCCAC 4466
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19414 CTGAGGCAAGAGAATCGTTGAACCCGGAGGTTGAAGCTTTCAGTGAGCGCAGATTTGTC 19473
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4467 CACTGCACTCCAGCTGGGCGACACAGCGAGTCTATCTCAAAAAAATAAATAAATAA 4526
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19474 CATTTACACTCCAGCTGGGCAACAGAGCGAGACTGTGTCTCAAAAATGAAAAACCCATAAG 19533
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4527 ATA 4529
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 19534 ACA 19536
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 7

```
US-10-087-192-100/c
; Sequence 100, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: CANCER
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 160482
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(160482)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-100
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Query Match 8.7%; Score 434.2; DB 5; Length 160482;

Best Local Similarity 60.2%; Pred. No. 2.8e-88;
Matches 888; Conservative 1; Mismatches 525; Indels 61; Gaps 8;

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QY 3106 TTTTTTTGTTGTTTGTAGAGACAGGCTCTGCTGTCCACCCAGCATGAGCACAGTGG 3165
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5181 TGTTTTTTTTTTCTCTCGATACGGAGTCTTCTCTGTGGCCAGGCTGGAGTGCAGTGG 5122
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3166 TGCACACCATAGTCTACTGCAGGCTCAACCTCTCTAGCTCAAGGGATCTCTGCTGACCTCAGC 3225
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5121 CATGATCTCGGCTCACTGAAACCTCTGCTCTCTGGGTTACAGTGATTTCTCTGCCTCAGA 5062
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3226 CTCCCAAGTAGCTGGGACTACGAGGCTGCACACACACGCTGG--CTAATTAATAAAAAATT 3283
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5061 CTCCCAAGTAGCTGGGATTTACAGGCTGAGCCACCATGCTGGCCCTAAATGTTTGTGATTT 5002
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3284 TTTTTGTAGAGACTGGGTCTTACTAGTTGGCAGGCTTGTCTTAAACTCTCTGGCTTCAA 3343
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 5001 TTTTGTAGTAGAC-AGTTTTCGTACATTTGTCAGGCTAGTCTCAAACTCTCTGACCTCAA 4943
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3344 GCAATCCTCTCACTTGGCATCCCAAGGTGCTGGGATTAACAGGGTGAGCCACCATGTGC 3403
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4942 GTGATCCGCTCGCTTGATGTACCAAGGTCTGGGATTTACAGATGTGAGCCACCCGCC 4883
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3404 GGCTACTTATTTCTTTACATTCATCTTTTCCAAATAGATGTAAGTCCACAGAACAGGA 3463
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4882 GGCCAGTCAATTCATCTCTCTTTTTTTTTTTTTTTTGTAGACAGAGTCTCATTTCTGTC 4823
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3464 TTACTGCTCTATTTCTTCTCTTTTTTTTGTAGACAGAGTCTCACTTCACTCACTCAACCT 3523
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4822 ATCCAGGCTGGAGTGT-----AGTGGCAC 4799
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3524 CGTTTCACTCACTCAACCTCTGCTCCCGGTTTCAAGYGATTTCTCTGCTTAAGCCTTC 3583
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4798 GATCTCGGCTCACTTCACTTTTCACTCCCGGTTTCAAGTGATTTCTCTGCTCAGCCTC 4739
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3584 CTGAGTAGCTGAATTTACAGGCTGCACACCATGCTGGCTAAATTTTGTATTTTGTAG 3643
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4738 TTGAGTAGCTGGGATTTACAGGCATGCACACCGCACCGGCTAAATTTTATATTTTGG 4679
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3644 CAGAGATGGGTTTATACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTCAAGTGATC 3703
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4678 GAGAGATGGGTTTCAACATGTTAGACAGGCTGGTCTCAAACTCTCTGACCTCAAGCAATC 4619
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3704 TGCCTGCTCAGTCTCCCAAGTGTGGAAATTTATAGGCTGTAGTCACTGTGCTGCGCCGA 3763
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4618 TGTGCTGCTTGGCTCTTAAAGTGTGGGATTTACAGGCTGAGCCACACACCCGCCCAA 4559
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3764 TTACTGTCTATTTTCTTTATTTCTATATCCCGAGATCTAGAGCAGTGTCTGACATATAGT 3823
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4558 --ATCATTTCACTTTTACAAAGTTCTGTCTGTATGCCAAATGAATCTCTCAGGACTGACT 4501
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3824 AGGTGCTCAATAAATAATTTGATGAATGCACAGCCTAGATATAAACTTTCTTTTTTTTT 3883
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4500 TCTAGCTCTAACCTCTAAACATATATTTAAGTGTCTTTTAAAGCCAGGACTTAGATTCCT 4441
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3884 TTAAAAAATCTTGACAACTTTTGCAGATAAATAACATCTTGCAATCTCTGCTTTTTCACCT 3943
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4440 CAGAAATCTCAAAATCAACAAATCCAAATTTCAACATATATTTTCCCTAAATTTCTGCCCT 4381
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3944 ATCAGCTTGTTA-----TGACTTTTTCATATTTGCTCAAACTTTATTTGTTACTGTTT 3997
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 4380 TTCTCTGTATTTCTCTAGTTTGTCTTAATAGTATCACCCTTAATTCAGGAAGAAATTTCAA 4321
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3998 TTCAITGTTTACTATTTTACTCACTGAAT--AATATGGCTTAAATTTTGTCTTATACATCCTCC 4055
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 4320 GTCACTTCAATTTTCTCTCTCAAGGCAATAAAGCACTAATCTCTAGAGCTCAACC 4261
Qy 4056 TGCTCCACTTTAGAGGCCAAATTTACAATCTGATGAAGCTATGAACCTCTCCCCAG 4115
Db 4260 TTAACAGTCTCTGGAATGAGATGAAGGTTAAGCTTACTGAACACAGACCAAACTAG 4201
Qy 4116 AGAAATACACACACACACACACTCACACACAGTTTTTTTTTTAATGTTTGCAACTAAGA 4175
Db 4200 GCACAGCAGCAGGGTTGTTCAATTGAATTCATCTCTCAGAGCCCTAAGGAATAGCT 4141
Qy 4176 CAAGAAACCTGCATTTAGAGATGTTTGTTCATATTAATTAATAAT-----AACTCAGTT 4229
Db 4140 CCAATTTTATAGAGGAAGAAACTGAGGTTCCAAAGAAAGTAAGAAATTCACACAGGAGGCT 4081
Qy 4230 GGSCACAGTACTCAAGCCTGTAAACACACAGTACTTTTGGAGTCCAAAGTGGGTGATCAC 4289
Db 4080 GGGTGGTGGGCTCAGCCCTGTAATCCTAGCACTTTTGGAGGCCAAAGGGGGCAGATCAC 4021
Qy 4290 TTGAGGTGAGAACTTCGAGACCAAGCCTGTGTAATATGTTGAAACCTCTCTACTAAAA 4349
Db 4020 CTGAGGTCAAGACTCGAGACCAAGCCTGACAAACATGTTGAAACCCATCTCTACTAAAA 3961
Qy 4350 ATCAAAAAATTAGCTGGGTAGTATGATGATGCTGTAGTCCAGTACTTCGGAGGCTG 4409
Db 3960 ATCAAAAAATTACCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3901
Qy 4410 AGCAGAGAAATGCTTGAACCTGGGAGGAGGAGGTTGCAAGTCC-----GAGATCC 4463
Db 3900 ACCGAGAGAAATGTTTGAACCCAGAGGCGGAGGTTGCAAGTCC-----GAGATCC 3841
Qy 4464 CACCACTGCACTCAGCCTGGGCGACACAGCAGACTCTATCTCAAAAAATAATAAT 4523
Db 3840 TGCCACTGCACTCAGCCTGGGCGACACAGCAGACTCTGCTCCAAAAAATAATAAT 3781

RESULT 8

US-10-087-192-844/c
; Sequence 844, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 844
; LENGTH: 91760
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(91760)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-844

Query Match 8.7%; Score 433.2; DB 5; Length 91760;
Best Local Similarity 61.6%; Pred. No. 3.5e-88;
Matches 906; Conservative 1; Mismatches 474; Indels 89; Gaps 10;
Qy 3106 TTTTGTGTTTGTAGAGACAGGGTCTGTCTGTCCACCAGGCATGAGCAGAGTGG 3165

Db 5566 TTTTGTGTTTAAATTTAGAGACTGGTGTGCTCTGTGCGCCAGGATGAGTGCAGTGG 5507
Qy 3166 TGCACACATAGTCTACTGACGCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGC 3225
Db 5506 CATGATCATGGCTCTACTCAACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5447
Qy 3226 CTCCCAAGTAGCTGGGACTTACGAGCGTGCACCAACGCTGGCTAAATTTAAAAAAT-TT 3284
Db 5446 CT-CCGAGTAGTGGAACTACAGGTGAGCACACACACCTGGCTAATTTATTTTATTT 5388
Qy 3285 TTTGTAGAGACTGGGTCTTACTAGTGGCGAGGCTTGTCTTTAAACTCCTGGCTCAAG 3344
Db 5387 TGTGTGTAGAGAGGGTCTCGCTATGT-----GGCTGGTCTTGAACCTCTGGGCTCAAG 5334
Qy 3345 CAATCCTCTACTTGGCATCCAAAGTCTGGGATTAAGGGGTGAGCGACCAATGCTGCG 3404
Db 5333 TGATCCTCCACCTCGGCTCTCAAGGCGCTGGGATTCAGGTGTCAGCTCTACACCCA 5274
Qy 3405 GCTACTTATTTCTTT-----ACATTCATCTTTCC 3434
Db 5273 GCTATAATACTTTTAAATACCAGATAATCTGTGCTGCTGGCCAAAGAAACAATTTT 5214
Qy 3435 AATAGAAATGAAGATCCACAGAACAGGATTAATCTCTCTTTCTTTCTTTCTTTCTTTCT 3494
Db 5213 ACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5157
Qy 3495 GACAGAGTCTCACTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 3540
Db 5156 GGTGAGTATTTGTTCTGTGCGCTAGGCTTGAGTGCAGTGGTGTGATCTTTGACTCACTG 5097
Qy 3541 ACCTCTGCTCTCCGGGTTCAAGYGATTTCTCTGCTTAAGCCCTCTGAGTAGCTGGAATTA 3600
Db 5096 ACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5037
Qy 3601 CAAGCGTGACACCACTGCTGGCTTAAATTTTGTATTTTGTAGCAGAGATGGGTTTATC 3660
Db 5036 CAGGTGCGCTCCACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4977
Qy 3661 CATGTGCGCAGGCTGCTCAAACTCTGACCTCAAGTATCTGCTGCTGCTGCTGCTGCTGCT 3720
Db 4976 CACTTTGGCCAGGCTGGTCTGAACTCTGACCTCAAGTGATCCACCTGCTGCTGCTGCTG 4917
Qy 3721 CAAAGTGTGGAATTTATAGGCGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3780
Db 4916 CAAAGCGCTGGGATTTATAGGCATGAGCAATGCACTCTGGCTGAAAGGATAAATCTTCT 4857
Qy 3781 TATTCCTATATCCAGATCTTAGACAGTGTCTGACATATAGTAGGTGCTCAATAAATAA 3840
Db 4856 TTTTGTAGCATTTCTTCTGGTCAATTACAGCA-----TGCTGGTATACATA 4810
Qy 3841 TTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 3900
Db 4809 TGTTTTCTGGCTGATTTTGACCTGTGATTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 4750
Qy 3901 ACTTTGCAGAAATAAATAACAATCTGCAATCTGCTTTTCTTTTCTTTTCTTTTCTTTT 3960
Db 4749 CTTCCTCTCTCT-CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4692
Qy 3961 TTTTCATATGCTCAAAACCTTTATTTGTTTCTGTTTCTTTTCTTTTCTTTTCTTTTCT 4020
Db 4691 TTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4632
Qy 4021 TGAATAATATGGCTTAAATTTGCTTATACATCTCTGCTGCTGCTGCTGCTGCTGCTGCT 4080
Db 4631 CTTCCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4584
Qy 4081 ACAAAATCTGATGAAAGCTATGAACCTCTCCCAAGAGAAATACACACACACACACACT 4140
Db 4583 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4524
Qy 4141 CACACACAGTTTTTTTTAAATGTTTGTCAACTAAGAAACAAGAAACCTGCAATTAGAGAT 4200

Db	18422	TC--GTGATCCGGCTCGCTCGGCTCCCAAGAGTGTGGGATTCATTATTTTGTGTTTTTGT	18479
Qy	3754	GCCTGGCCGATTACTGCTCTATTTTCTTTATG--CTATATCCCCAGATCTAGACAGTGT	3811
Db	18480	AGACAGAGTTCTCACTGTGTTGCCCAGCGTGTCTTGAACCTCTGATCTCAAGTGATCT	18539
Qy	3812	CTGACATATAGTAGTGCTCAATAATAATATGATGATGACAGCTAGATATAAACTTT	3871
Db	18540	TCCACACTCAGTCTCTCAAAGGCTGGGATACAGGGGTGAGCCACTGCACCCCACTTC	18599
Qy	3872	CTTTTCTTTTTTTTAAACAACCTTGACAACTTTGCAGAAATAATACAACTCTTGCAATCT	3931
Db	18600	CCTCTACTTTT-----GACGGTTTCTCTGCTATGAATGT	18636
Qy	3932	GCTTTTCACTATACACTGTTATGACTTTTTTCATATATGCTCAAACTTTATGTGTAC	3991
Db	18637	GCATGTCCAGTTGCTGTCTTAGAACTTGATATTACCTTCTCATCATCA-----	18689
Qy	3992	TGTTTTTTCATTGTTACTATTTTAGTCACTGGAATAATATGGCTTAATTTGCTTATACATC	4051
Db	18690	-----GCCATTGGAGGAGACTGGGACCGCTCAGATTTATGATCTGACCCATT	18737
Qy	4052	CTCCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCCTCTCC	4111
Db	18738	CTTTTCGGCAGGGTTCTCTGTGSGCTGTCTCCATCACCAAACTGGAATCAGAAGAGTTT	18797
Qy	4112	CCAGAGAAATACACACACACACACACTCACACAGTTTTTTTTTAATGTTTGCACACT	4171
Db	18798	CCATAGCCCTTTTTTTTCCCCACATCTTTGCTGAAGCAGAGTTTTTGAA-----AAAC	18850
Qy	4172	AAGACAAGAAACCTGATTAGAGGATGTTTGTTCATTTAAATTAATAAATACTCAGTTGG	4231
Db	18851	AAAACCAAACTAAGCTATTCCCCAGAAGAAATCTGTAATCAAAGATAAGCTCTGCCGG	18910
Qy	4232	GCACAGTGACTCAAGCCTGTAAACCAAGTACTTTTGAAGTCCAAGGTGGGTGGATCACTT	4291
Db	18911	GCACAGTGGCTACGC-----CTTTTGGAGGCCAAGCGGGCGGATCACT	18956
Qy	4292	GAGGTGAGAGTTTCGAGACCGCTGGTCAATATGTTGAACCCCTACTCTACTATAAAAT	4351
Db	18957	GAGTCCAGGAGTTCTAGACTGCCAGGCCACATGTAACCTCATCTCTACTATAAAT	19016
Qy	4352	ACAAAATTAGCTGGGTGTAGTGAATCATGCCCTGTAGTCCCAGTACTCGGAGGCTGAG	4411
Db	19017	ACAAAATTAGCTAGATGTGGTGGTACCTGTAGTCTCAGCTACCTGGGAGGCTCAG	19076
Qy	4412	GCAAGAAATTGCTTGAACCTGGGAGCGAGGTTGCACTGAGCCGAGATCCCACCCTG	4471
Db	19077	GCAAGAAATCGCTTGAACCTGGGAAGTAGAGGTTGCACTGAGCCGAGATGTCACCACTG	19136
Qy	4472	CACCTCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA	4531
Db	19137	CACCTCAGCCTGGGCGAGGAGTGAGACGACCTCACAAAAATTTACATAAATAAATGAA	19196
Qy	4532	GGATCGGAGAGAAACAAA 4550	
Db	19197	AAGTAAAAATAAAAAATACAA 19215	

Db	Seq ID	Sequence
Db	34665	TGCTGGGATGACAGGTGTGAGCCACCACATCGGCGCTTTATTATTATATTTTCGAGACAGG 34606
Qy	3786	CTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTGAT 3845
Db	34605	GTATCTC-----TCTGTTGCCAGGCTGGAGTGCAGTGCAGCTCAGGCTGGTTGCA 34552
Qy	3846	GAATGCACAGCTAGATATAAATCTTTCTTTCTTTTAAAAAATCTTTGCAAACTTT 3905
Db	34551	GCCTCAAACTCCTGGGCTCCAGCA--ATTCTCCGCTCAGCCCTCTGGGTAGCTGGAAC 34494
Qy	3906	GCAGAATAAATAACAATCTTGCAATCTGCTTTTTCACCTTATCACCTTGTATTAGCTTTTTTC 3965
Db	34493	TACAGGTGCAAAATTTATCATGCTGGCTAAATTTTTTAAATTTTTTTCGAAATGGGGTCTCT 34434

QY 3428 TCTTTCCAAATAGATCCACAGAACAGGGATTACTGCATTATTTCTTCTTTCT 3487
Db |||||
QY 64516 TTTTGTGAGATCAGGTCTCACTCTGTGCCAGGGTGTAGTCAGTCGGCAATC----- 64570
Db |||||
QY 3488 TTTTGTGAGACAGATCTCACTTCATCACCTCAACCTCCGTTCCAGTCTCACTGCAACACCTCTG 3547
Db -----TCAGCTCACTGCAACCTCG 64590
QY 3548 CTTCCCGGGTTCAAGYGATTTCTCTCGCTTAAGCTCTCTGAGTAGCTGGAAATTACAAGCT 3607
Db |||||
QY 64591 CTTCCAGGTTTCAGGTGATTTCTCTGCCCTCAGCCTCCCAAGCAGGTGGGATTTCAAGCAT 64650
QY 3608 GCACCAACCATGCTTGGCTAATTTTGTATTTTACAGAGATGGGGTTTTACCATGTG 3667
Db |||||
QY 64651 ACACCAACCATGCATGGCTCA-TTTTGTATTTTGTAGAGA-GGGGTTTCCATGTG 64708
QY 3668 CCAGGCTGGTCTCAAACTCTGACCTCAAGTGATCTGCTGCTCAGTCTCCCAAAGTG 3727
Db |||||
QY 64709 GCCAGGATGGTCGGAACCTCTGACCTCATGTGATCCACCGCATCAGCTCCCAAAGTG 64768
QY 3728 CTGGAATTATAGCGGTGAGTCACCTGCTGCTGGCGGATTACTGTCTATTTTCTTTATGCT 3787
Db |||||
QY 64769 CTGGGATTTAAGCGTGAATCACTGCACCTGGCTAGAAAATCTCTTAAAGCCTAATCTT 64828
QY 3788 ATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAATAATTGATCA 3847
Db |||||
QY 64829 TTTTCTTTTCCCTTATATAATTAGGTGACTATGTAACCCNAACACATAGGGTAGAA 64888
QY 3848 A-----TGCAAGCCTAGATATAAACTTTCTTTTCTTTTAAAAAATTTGACAAC 3903
Db |||||
QY 64889 ACTCGTGAATAATTTTGGAGATATCTTTGCAAGTGTGTGCTCAGGCTGGAT 64948
QY 3904 TTGCAGATAAATACAACTCTTGCAATCTGCTTTTCACTTATCACCTTGTATGACTTTT 3963
Db |||||
QY 64949 ATGGATGTGTGCTTAGTGTGAGTGCATAGATTTAGGATTTCCACACCTGATGTATGCTTT 65008
QY 3964 TCATATTGCTCAAACTTTATTTGTTACTGTTTTTTCATTTGTTA---CTATTTTAGTCAC 4020
Db |||||
QY 65009 TGGTGAATCTTTTAGCGGATATGCTCTCATGTTCAAGGATTAATGGCATACTGGTTTAT 65068
QY 4021 TGAATAATATGGCTTAATTTGCTTTATACATCTCTGCTGCTCCACTTTTGAAGGCAAAATTT 4080
Db |||||
QY 65069 TTAACCCCATGTTTAACTTAATTTAAGACCGATTTACTTCTCTTGGAGCTAATTTCT 65128
QY 4081 ACAAATCTGATGAAGCTATGAACCTCTCCCAAGAGAAATACACACACACACACT 4140
Db |||||
QY 65129 TAACTTTTCTGATGATGTTTTGTTGCTTAAGTTAAGACTAATATAACACAGAAGTCTTA 65188
QY 4141 CACACACAGTTTTTTTTTAAATGTTTGAACACTAAGACAAGAAACCTGCATTAGAGGATGTT 4200
Db |||||
QY 65189 CTATCTTTTTCATATTAGAGATTTTGGTTTATTAATCTAGTGGAAATTTTAAATATCAT 65248
QY 4201 TGTTCATATTAAATTAATAAATCA-----GTTGGGCACAGTGAACCTG 4250
Db |||||
QY 65249 TTTACATGTTTACTCTCAAGATCTGATGATTGACTGACTGGGTGCAGTGGATCACAACCTG 65308
QY 4251 TAACCAAGTACTTTGGAAGTCCAAGTGGGTGGATCACTTTGAGTGAAGATTTCCAGAC 4310
Db |||||
QY 65309 TAATCTCAGACACTTTGGGAGGCCAAGCGGGCAGATCACTTTGAGTTCAGAGCTCAGAG 65368
QY 4311 CAGCTGGTCAATATGTTGAAACCTTATCTCTACTAAAAATAAAAAATTTAGCTGGGTGT 4370
Db |||||
QY 65369 CAGCTTGGCTTAAATGGTGAACCTCTCTGTAGTAAATAACAAAATTTAGCCGACTT 65428
QY 4371 AGTGATGATCTGCTGATGCCAGTACTCGGAGGCTGAGGCAAGAGAAATTTGCTTTGAAC 4430
Db |||||
QY 65429 GGTGGTGGCTGCTGTAATCCAGCTACTTGGGAGACAGAGGTGAGAGAAATCACTTTGAAC 65488
QY 4431 CTGGGAGGCAGAGGTTCAGTGAAGCCGAGATCCACACTGCACTCCAGCTGGGGCACA 4490
Db |||||
QY 65489 CCAGAGGGCGAGGTTCAGTGAAGCCATGATCACTCCATTTGCACTCCAGCTGGGGCACA 65548
QY 4491 CAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAG 4532

Db 65549 GAGTGAGACTCGTCTCAAAAAAATAAATAAATAAAG 65590

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RESULT 12

US-10-719-993-6883/c

; Sequence 6883, Application US/10719993

; Publication No. US20040265849A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; FILE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001496

; CURRENT APPLICATION NUMBER: US/10/719,993

; CURRENT FILING DATE: 2003-11-24

; NUMBER OF SEQ ID NOS: 55342

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6883

; LENGTH: 187844

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)..(187844)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;

US-10-719-993-6883

Query Match

Best Local Similarity 8.3%; Score 414.6; DB 8; Length 187844;

Matches 868; Conservative 3; Mismatches 462; Indels 98; Gaps

QY 3105 TTTTTTTTGTGTTGTTGTTAGAGACAGGGTCTTGTCTGTCAACCAGGATGAGCACAGTG 3164

Db |||||

QY 94170 TTCAATTCATTTATTCATTCGAGATGGGTCTTGTCTGTGTCAGGCTGGAGTGAATG 94111

Db |||||

QY 3165 GTGCAACCATAGGTCACCTGCAGCCTCAACCTCTCAGCTCAAGGGATCTGTGACCTCAG 3224

Db |||||

QY 94110 GTGCAATCTCGCTCACTGCAACCTCCACCTCCAGGATTCAGTGATTCCTCGCTCAG 94051

QY 3225 CTTCCAAAGTAGCTGGGACTACGAGCTGCACCAACCGCTGGCTTAATAAAAAATTT 3284

Db |||||

QY 94050 CTTCTGATGTAACCTGGGATTCAGACMCCTGTCACCAACCGGCTAATTTTGTGA--TT 93993

QY 3285 TTTTGTAGAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAAACTCTCGCTTCAAG 3344

Db |||||

QY 93992 TTTAGTAGAGATGGAGTTTACCATTGTTGGCAGGCTGGTCTCAAACTCTGACCTCAA 93933

QY 3345 CAATCCTCCTACCTTGGCATCCAAAGTGTGGGATTCAGGGGTGAGCCACATGTGCG 3404

Db |||||

QY 93932 GGATCCACCCACCTTGGCTCCCAAAGTCTGGGATTACAGGCATGAGCCACTGGCCCA 93873

QY 3405 GCTACTTATTTCTTTACATTCATCTTTTCCAAATAGATGTAAGATCCACAGACAGGAT 3464

Db |||||

QY 93872 GCCATGTACATTTAATTTGTAATACTATATCTCTTTGGT-----CACCATCTTGTCT 93822

QY 3465 TACTGCCTATTCTTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATCACCTCAACCTC 3524

Db |||||

QY 93821 TTTTCTTTTCTTTTCTTTTCTTTTGTAGACAGAGTCTGCTCTGTGCGCCAGGCTGG 93762

QY 3525 CGT-----TCAGCTCACTGCAACCTCTGCTCTCCGGGTTTCAAGYATTCTC 3570

Db |||||

QY 93761 AGTGAGTGGCGCATCTCGGCTCACTGCAAGCTCCGCTCCCTGGCTCACGCCATTCTC 93702

QY 3571 CTGCTTAAGCTCTCTGAGTAGCTGGAATTAAGCGTGCACCAACCATGCTTGGCTAATTT 3630

Db |||||

QY 93701 CTGCTCAAGCTTCCAGAGTAGCTGGGACTACATGTGCCACCAACCGCCCGGAGAAATTT 93642

QY 3631 TTTGTATTTTACAGAGATGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTG 3690

Db |||||

QY 93641 TTTGTATTTTAAATCGAGACGGGGTTTCAACGTTGACCGAGATGGTCTCGATCTCTCTG 93582

QY 3691 ACCTCAAGTGATCTCGCTGCTCAGTCTCCCAAAGTGTGGAAATTTATAGCGGTGAGTCA 3750

Db |||||

Db 68040 GGGCATGGTGATGTAAGTCTGTAGTCCAGCTACTCAGGAGGCTGAGGTAGGACAATCAC 67981
Qy 4425 TTGAACCTGGAGGAGAGGTTGCAGTGAGCGAGATCCACACTGCACTCCAGCCTGG 4484
Db 67980 TTGAACCCAGGAGCGGAGGTTGCAGTGAGCTGAGATTGTGCACCTGCACTCCAGCCTGC 67921
Qy 4485 GCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATAAAGATCGGAGAGAA 4544
Db 67920 GCGACAGGTGAGACTCCATCTCAAAAAAATAAATAAATAAATAAATAAAGAGAGAA 67861
RESULT 15
US-10-085-117-328
; Sequence 328, Application US/10085117
; Publication No. US20030232334A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: 529452000121
; CURRENT APPLICATION NUMBER: US/10/085,117
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 45367
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-085-117-328

Query Match 8.3%; Score 412.4; DB 6; Length 45367;
Best local Similarity 54.4%; Pred. No. 1.5e-83;
Matches 1322; Conservative 2; Mismatches 918; Indels 190; Gaps 17;
Qy 2279 AAAATCGCTTTTCAGGCGAGCGCGGTGGCTCATGCTGTAATCCAGCACTTTGGGAGGC 2338
Db 38718 AAAATGAAGTCAAGCGCGGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGC 38777
Qy 2339 CGAGCGCGGAGATCACTTGAAGTCAAGAGTTGAGACAGCAGCTGCGCAACATGGTGAAA 2398
Db 38778 TGAGGTGGCGAGATAACCTGAGTCAAGAGTTCAAGACAGCAGCTGCGCAACATGGCGAAA 38837
Qy 2399 CCTGTCTCTACTAAAAATACAAAATTAGCGGACATGGTGGCGAGCGCTGTAACCC 2458
Db 38838 CCTGTCTCTAC-CAAAAATACAAAATTAAGTGGGATGGTGGCCATGCTGTAAACCC 38896
Qy 2459 CAGCTACTTGGGAGACTGAG-----TTGGAGGTTTCAGT 2492
Db 38897 CAGCTACTCGCGGGCTGAGGCGAGGAGATCACTTGAACCCAGGATGTGGAGTTTCAGA 38956
Qy 2493 GAGCCAAAGTCTGTGCTGCTGTCAGCGCTGGGTAAACAGAGAACTGTGCTCAAAAAA 2552
Db 38957 GAGCCAGGCTTTGCGCACTGCACTTTCAGCGCTGGGTGACAGAGCAAGACTCTGTCTCAAAA 39016
Qy 2553 AAAAAATGCTTCAATAAATATATATAAAGGACTATATTTTTCAGCCATAGGATC 2612
Db 39017 AAAAAAAGTCAAGTGTCTCAAGGCCATTCGAACCTCAACATTT-CACTCGGGTC 39071
Qy 2613 ATTTCCTCTGAAGCATCTTTGGGGAAGTCACTCCCACTCTGCTGAGAGTGGGCGAGGTGA 2672
Db 39072 TTTTGATACCAAGCCAGGCGTGAATGATCAACTGTTT-TTAGATGGAGAACTGA 39129
Qy 2673 GGGCTGACCTATTGCTCTGCACTTACTCTATCTCAGCTGTGCTCCCACTTTCCAGGTG 2732
Db 39130 GGCATGGA--AGGGCAGTGTCTTCGACCACTGTCATGTGGGACTCACCTGGGGAACT 39187
Qy 2733 CTGCCAGACATGACAACTGCTAVGACCAGCGCAAGAGCTGGACAGCTGTAATTTCT 2792
Db 39188 GAGGAGGGAATTTGCTTGTG-----GGACTGGAGGAGCTGATGGATTTAAGAGCTTGTGG 39243

Qy 2793 GCTGACAMMCGGTACACCCACACCATATTATCTATCTGCTCTGCTCGGCAATCACCTG 2852
Db 39244 GCAGGACACCGTGTCTCACAGCTGGGCTGGGAGAGTAACACAGCTCTGCAATTC- 39299
Qy 2853 TAGCAGTAGGTTATCCCTTCTCTGACCTATGAATTTAGTTGGTTCTCAGTAGGCCGG 2912
Db 39300 -----AAAAAGCTTAG 39310
Qy 2913 GGGAAATAATAGTAACAAACAGCCATGATTTAGTGTAAATTTCTTGGTCTCTGGGAGTGT 2972
Db 39311 CCCAGTAGGACAAACAGCATCTACTTCTCTACTAGCTCCAGAGCAGAGGCTAACTA 39370
Qy 2973 CTCCTTTAATCCTCAGAAACAACTATCGGATAGGTACAAATATCTCTCACTTAAACAGATA 3032
Db 39371 AGCCTCAGCTTCTACTTCTGCGCATGAGAGTGAATAATCTAACTTCACTATGTCGTAA 39430
Qy 3033 AGAAAACCTGAGGCTCAGAGGCTGAGCTATTTGGCCCAAGATCACACAGCTTGTAGTGGT 3092
Db 39431 GGATGCCAATTGCAAGAGCCACTTGTCTTGTCCACTGTGGGGTGCAGTGTAAAGATAA 39490
Qy 3093 GACAGTTTGGGTTTTTTTTTTTGTGTGTAGAGACAGGCTTCTGCTCTGTCAACCCAGGC 3152
Db 39491 CAGAACTTTTTATCTTTTTTTTTTTTTTTTGTAGACGAGAGTCTGCTCTGTGCGCCAGGC 39550
Qy 3153 ATGACACAGTGGTGCAACCATAGTCACTGCGCTCAACCTCTCTGAGCTCAAGGGATC 3212
Db 39551 TGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAAGCTCTGCTCCAGGTTTCAACACCAT 39610
Qy 3213 TGCTGACCTCAGCCTCCCAAGTAGCTGGGACTAGCAGCGTGCACACACAGCCTGGCTAA 3272
Db 39611 CTCCTGCTTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCACACCATGCTC---CTAA 39667
Qy 3273 TTAATAAAATTTTTTTGTAGAGACTGGGTCTTACTTACCTTGGCCAGGCTGTGCTTAAACT 3332
Db 39668 TTTCTGTACTTTTTTAGTAAAGACAGGTTTACCATGTTAGCCAGGATGTTCTGCACT 39727
Qy 3333 CTGCTTTCAAGCAATCTCTCTTACCTTGGCATCCCAAGTCTGCGGATTTACAGGGGTGAG 3392
Db 39728 CTGACCTCATG--ATCCACTTGCCTCAGCTTCCCAAGTGTGGGATTTACAGGTGTGAG 39785
Qy 3393 CCACATGTGGCGTACTTATTTCTTTACATTCATCTTTCCAAATAGATGTAAGATCCA 3452
Db 39786 CCATGCGCTCGGCTTTTTTTTTTTTTTTTCTTTGAGA----- 39822
Qy 3453 CAGAACAGGATTAAGTCTTCTTCTTCTTCTTTTGTAGACAGAGTCTCACTTCAT 3512
Db 39823 -----CTGAGTCTGTTGTGTCGCCAGGCTGGAGTGAG 39857
Qy 3513 CACCTCAACCTCCGTTACGCTCAGTCAACCTCTGCTCCCGGTTCAAGYATTTCTCT 3572
Db 39858 TGGTCCAATC-----TTGGCTCACTGCAACCTCTGCTCTCTGGGTTCAACAGATTTCTCT 39912
Qy 3573 GCCTAAGCCTCTGAGTAGCTGGAATTAAGAGCTGCACACCATGCTTGGCTAATTTTT 3632
Db 39913 GCCTCAGACTCCCAAGTATCTGGGATTAAGCGGCTGCCACCATGCTTCAAGTGTGCTAA 39971
Qy 3633 TGTATTTTAGCAGAGTGGGTTTTTACCATGTTGCCAGGCTGTCTCTCAAACTCTGAC 3692
Db 39972 TGTATTTTAGAGAGAGCGGGTTTACCATGTTGGCCAGAGTGTGTCTCAAACTCCGAC 40031
Qy 3693 CTCAGTAGTCTGCTGCTCAGTCTCCCAAGTGTGGAATTAAGCGTGTGAGTCACTG 3752
Db 40032 CTCAGGTAATCCACTGCTTGGCTCCCAAGTGTGGGATTTACAGGCTGAGCCACCG 40091
Qy 3753 TGCCTGGCGGATTAAGTGTCTTCTTTA-----TTGCTATATCCCCAGATCTAG 3803
Db 40092 AGCCTGGCCAGAAATAAGATAATCTTAAACAATCATGGAGTCTTAGCTAGTGCCAGAC 40151
Qy 3804 AGCAGTGTCTGACATATAGTAGGTGTCTCAATAAATAATTGATGATGACAGCTTAGATA 3863
Db 40152 GGCAGTGCAGGCTCTACCTACATCGCTCCATGAAGTCTTCAATAAAACCCATCAGGA 40211
Qy 3864 TAACTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTGACAAATTAATAACAATCT 3923

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Db 40212 GTGTGATTATTAATCATCTCTGTTTATATAGTAGAGAACACCCAGTCTTCAAGGGGTAAAA 40271
Qy 3924 TGCATTCGTGTTT-TTCACTATATACCTGTTGTTATGACTTTTTTCATATATGCTTCAAACTTT 3982
Db 40272 ATCACTACCCAAAGGTACACAAGCACAGGAGCCAGGACTTGAACCAAGATCAGTTTAT 40331
Qy 3983 TATTGTTACTGTTTTTTCATTTGTTTACTATTTTATTTAGTCACTGAATAATATGCTTAATTTGC 4042
Db 40332 GCAGGTTTCAAACTTTAAGTTCAGTGATTTGATTCATGACTAGAGCAGCATAAATGTTG 40391
Qy 4043 TTATACATCTCTCTGCTCCACTTTAGAGGCCAAATTTTACAAATCTGATGAAGAGCTATGA 4102
Db 40392 TGGGAAGTACAAAAACACTATCAGCTGTGACATCCAGTTTATGTTCTGAACAGACTG 40451
Qy 4103 ACCCTCTCCAGAGAAATACACACACACACACTCA-----CACA 4146
Db 40452 CACATTAATTTGTTTAAATAGCCATGATAAAATGATGATAGCACTCATTTGTTTGAGCATA 40511
Qy 4147 CAGTTTTTTTAAATGTTTGCAACTAAGACAAGAAACCTGSCATTAGAGGATGTTTCTTC- 4205
Db 40512 CGCTTTTCTGCAAGTATCAATACTGATAACAGACCTCAGAGGAAAGTATTAATTTTCC 40571
Qy 4206 -----ATATTAATTAATAAATAACTCAGTTGGGCACAGTGAAGCTTGAACCA 4256
Db 40572 TGACTTTATAGATGAAAAACAATCTCAGGCGCCGAGGGGCTGCTCATGCTGTAATCC 40631
Qy 4257 CAGTACTTTGGAAGTCCAAAGTGGGTGGATCACTTGAGGTGAGAAAGTTTGAGACAGCCT 4316
Db 40632 CAGCACTTTGGGAGGCCAAGCGAGGAGATCGCCTGAGGTGAGAGTTGAGACAGCCT 40691
Qy 4317 GGTCAATATCGTGAACCCCTATCTCTACTAAAAATACAAAAATAGCTGGGTAGTGAT 4376
Db 40692 GGCCAACTGGCAAAACCCCATCTCTACTAAAAACAAAAATAGTTGGGTAGTGGC 40751
Qy 4377 GCATTCCTGATGCCAGCTACTCGGAGGCTCAGGCAAGAGAAATGCTTGAACCTGGGA 4436
Db 40752 AGTGCTCTGAGTCCCACTTCTTGGAGGCTAAGGAGGAGAAATCGCTTGAACCCAGGA 40811
Qy 4437 GGCAGAGTTGAGTAGGCGAGATCCCACTCACTGCACTCCAGCTCGGCGGACACAGCA 4496
Db 40812 GCGGAGATTTGCAGTGAACATGAGATCGTGCCATTGCACTCCAGCTCGGAGACAGAGCAA 40871
Qy 4497 GACTCTATCTCAAAAAATAAATAAATAAATAAAGATCGGAGAGAAACAAACTAATA 4556
Db 40872 GACTTCGTCTCAAAACAAACAACTCTTAGAGAGATTTGTTGAACTCACACACAGTGAA 40931
Qy 4557 AGATTCTCGAAGGTAA--GCAGAGATACGTAAATTTATATGTAATAAAGTTTAAATGCATT 4614
Db 40932 ATGTGGCTGATCCAAATGAGATGCTCTGCTGAAATATATACACAGATTTCAAAGACTTA 40991
Qy 4615 TTAACGTAACTATTGTTTATTTTGGTTAT 4646
Db 40992 GTATCAGAAAAGAGAAATTTAATATTTCTTTTTT 41023
```

RESULT 16

```
US-10-322-281-314/c
; Sequence 314, Application US/10322281
; Publication No. US20040126762A1
```

GENERAL INFORMATION:

```
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: Fast-Seq for Windows Version 4.0
```

```
; SEQ ID NO 314
```

```
; LENGTH: 227246
```

```
; TYPE: DNA
```

```
; ORGANISM: Homo sapiens
```

```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(227246)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-314
```

```
Query Match 8.1%; Score 405.8; DB 7; Length 227246;
```

```
Best Local Similarity 59.7%; Pred No. 1.3e-81;
```

```
Matches 898; Conservative 1; Mismatches 558; Indels 48; Gaps 11;
```

```
Qy 3082 TTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTTGTAGACAGAGGCTTC-TC 3140
Db 140336 TGGTAATTTGTAATTTTTTTTCTCTTTTTTTTATTTCTGAGACGGAGTTTGTCTTC 140277
```

```
Qy 3141 TGTCAACCAGGATGAGCAGTGTGCAACCATAGTCTACTGCGACCTCAACCTCCTGA 3200
Db 140276 TGTCAACCAGGCTGGAGTGCATATCTTGCGTCACTGCAACCTCTCATCCCGG 140217
```

```
Qy 3201 GCTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACC 3260
Db 140216 GTTCAAGCAATTTCTCTGCTCAGCCACTGAGTATCTGGGATTTACAGCAGCTGCCACC 140157
```

```
Qy 3261 ACGCTGCTAATTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTAGTTGGCAGGC 3320
Db 140156 ACACCTGGCTAATTTTGTGA--TTTTAAGTAGGGACAGGGTTTCGCAATGTTGGCCAGGC 140099
```

```
Qy 3321 TTGTCCTTAACTCTCGGCTTCAAGCAATCCTCTACTTGGCATCCCAAGAGTCTGGGAT 3380
Db 140098 TGGTTTCAAACTCTGACCTCAGGTGATCCGCCGCCCTCGGCCCTCCCAAGTCTGGGAT 140039
```

```
Qy 3381 TACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTTACATTCCTCTTTTCCAATA 3440
Db 140038 TACAGCGGTGAGCCACCACTTGGCCCTACTTTTTTGTGTTTCTTTTTT----- 139988
```

```
Qy 3441 ATGTAAGATCCACAGAACAGGATTAATCTGCTTATTTTCTCTCTTTTGTGACACAGA 3500
Db 139987 -----GAGATAAGGTCTCACTTTGTGCCCAGGCTGGAGTGCAGTG 139947
```

```
Qy 3501 GTCTCACTTCATCACTCAACCTCGGTTCAAGTCTCACTGCAACCTCTGCTCCCGGTTCA 3560
Db 139946 GTGTAATCTTGCTCAGTAGCATGATCTTGGCTCACTGCAACCTCTGCACTCCAGGTTCA 139887
```

```
Qy 3561 AGYGATTTCTCTGCTCAAGCCCTCCTGAGTAGCTGGAATTAACAAGCTGCACCACTATGT 3620
Db 139886 AGCAATTTCTCTGCTCAGCCACCTGAGTATCTGGGATTAACAGGACGCTGCCACACACC 139827
```

```
Qy 3621 TGGCTAAATTTTTTGTATTTTGTAGACAGATGGGTTTTTACATGTTGCCAGGCTGGTCT 3680
Db 139826 TGGCTAA--TTTTTGTATTTTAAAGTAGGACAGGGTTTCGCAATGTTGGCCAGGCTGGTTT 139768
```

```
Qy 3681 CAAACTCCTGACCTCAAGTGATCTGCCCTGCTCAGTCTCCCAAGTGTGGAATTTATAGG 3740
Db 139767 CAAACTCCTGACCTCAGGTGATCTGCCCGCTCGGCCCTCCCAAGTGTGGAATTTACAGG 139708
```

```
Qy 3741 CQTGAGTCACTGTGCTGCCCGCA--TTACTGTCTATTTTCTTTTATTTGCTATATCCCCA 3798
Db 139707 CGTGAGCCACCACTTGGCCCTACTTTTTTGTGTTTCTTTTGTAGATAAGTCTCAC 139648
```

```
Qy 3799 TCTAGAGCAGTGTCTGACATATAGTAG--GTGCTCAATAAATAAATTTGATGATGACAGCC 3857
Db 139647 TTTGTTGCCAGGCTGGAGTGCAGTGTAGTCTTGGCTCAGTAGCATGATCTTGGGCTC 139588
```

```
Qy 3858 TAGATATAAATTTTCTTTTTTTTAAACAATCTTGACAACCTTTGCAAGATAAATA 3917
Db 139587 ACTGCAACCTCTGCTCTCTGGGTTCAAGTAATTTCTTGCCTCAGCCTCCAGAGTAGCTG 139528
```

```
Qy 3918 CAATCT--TGCATTTCTGCTTTTTTCTTATCATCTTGTATGACTTTTTTCATATTCCTCA 3976
Db 139527 GAAATTACAGGCGCCGCCACCATACCTAGATAAATTTTATATTTTTTTAGTAGAGATTTCAC 139468
```

```
Qy 3977 AACCTTTATTTGTTACTGTTTTTTTCAATGTTTACTATTTTAGTCACGTAATAATATGGCTTA 4036
Db 139467 CATGTTGGCCAGGCTAGTCTCGACATCCGACCTCAGGTGATGCTGCTCAGCCTCCCA 139408
```

Qy	4037	ATTTGGTTATACATCCTCTCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGAAAG	4096
Db	139407	AAATCTGAGATTACAGCATGTGCCACCGCACCACCCGCTATGTTGATATTTTGTGAGAAC	139348
Qy	4097	CTATGAAACCTCTCCCCAGAGAA---TACACACACACACACACTCACACACACTTTT	4153
Db	139347	CACCATGCTGTGTTTCCACAGTGACTCACCATTTTACGTTCTTACAGTGGTGATGAA	139288
Qy	4154	TTTTTAATGTTTGCAACTAAGACAAAGAACCTGCATTAGAGGATGTTTGTTCATATTAAT	4213
Db	139287	GGCTCCAAATTTCCACATCTCTCCACACACTTATATCTGCTGTGTTGGTTATAGTCCT	139228
Qy	4214	TAAAAATAACTCAGTTG-----GGCACAGTACTCAAGCTGTAAACACAGACTTTTG	4266
Db	139227	AAGAAAGTGGTATCTCAGGGGCCAGTGCAGTGGCTCATGCTGTTAATTCAGGAGTTTG	139168
Qy	4267	GAAGTCCAAAGTGGGTGATCACTTTGAGTGCAGAAAGTTCGAGACCAAGCCTGGTCAATATG	4326
Db	139167	GGAGGCCAAAGTGGACAGATCACTTTAGTCAGAGTTCGAGACCAAGCCTGGCCAAACATG	139108
Qy	4327	GTGAAACCCCTATCTCTACTTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCTGT	4386
Db	139107	GTGAAACAGCATCTCTACT-AAAAATACAAAAATTAGCTGGGTGTGGGGCAGGCACCTGT	139049
Qy	4387	AGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTCGTTGAACCTGGAG-CAAGAGGT	4445
Db	139048	AATCCCAGCTACTCGGGAGGCTGAGGCAAGAGAAATTCGTTGAACCTGGAGTTCGGAGGT	138989
Qy	4446	TGCAGTGAGCCAGATCCACACCTGCATCCAGCCTGGGGCAGACAGCGAGACTCTATC	4505
Db	138988	TGCAGTGAGCCAAAGATCGGCCACTTGCATCCAGCCTGGGAGACAGAGCAAGACTCCGTC	138929
Qy	4506	TCAAAAAATAAATAAATAAATAAAGGATCGGAGAGAAAACAAACTAAATAAGATTTCTTC	4565
Db	138928	TTGGAAGAAAAAAGAAAAAAGAGAAAAAAGAAAGAAAGTGGTATCTCATTTAGTC	138869
Qy	4566	AAGGT	4570
Db	138868	ATCAT	138864

```

RESULT 17
US-09-740-043-3/c
; Sequence 3, Application US/09740043
; Publication No. US20020086810A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL000972
; CURRENT APPLICATION NUMBER: US/09/740,043
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 23639
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(23639)
; OTHER INFORMATION: n = A,T,C or G
US-09-740-043--3

Query Match      8.1%;   Score 403.6;   DB 3;   Length 23639;
Best Local Similarity 59.6%;   Pred. No. 1.1e-81;
Matches 882;   Conservative 1;   Mismatches 545;   Indels 52;   Gaps 10;

Qy    3099  TTGGGTTTTTTTGTGTGTTAGACAGGGTCTTGCTGTCACCCGCATGAGC 3158
Db    10204  TTTCTTTTTTTTTTTTTTTTTTTTGAACAACAGACTTGTGTGTGCCGAGCTGGAGT 10144

```


QY 3723 AAGTGCTGGAATATATAGGCGTAGTCACTGTGCTGGCGGATTAATCTATTTCTTTTA 3782
Db - 131911 AAGTGCTGGGATATATAGGCTGAGCCACACCCCTGGCC-----TCCTCTTACTTTTCTT 131856
QY 3783 TTGCTATATCCCGAGATCTAGAGCAGTGTCTGACATATATAGTAGGTGCTCAATAAATAATT 3842
Db 131855 ATGAGATAAATTGTAGATTACCTTGCAGTCATATAGAAAATAATAGACAGATCATATATACC 131796
QY 3843 GATGAATGCACAGCTAGATATAAACTTTCTTTCTTTTAAACAATCTTGACAAC 3902
Db 131795 TTCTACAGTTATCCCATGTATACATCTTCCAAAC-TATGTGTATATACAGCCGAGA 131737
QY 3903 TTTCGAGAATAAATAAATCTTGCAATCTGCTTTTTCACCTATCACTTTGTTATGACTTT 3962
Db 131736 ATGTTAAATATGATACAGTCCACCAATCTGATTTAGACTTTCCCACTTTTACTTCAATTG 131677
QY 3963 TTCATATTCGCTCAAACTTTATTTGTTACTGTTTTTCAATGTTACTATTTTAGTCACGTG 4022
Db 131676 TGTGTATTTAGTTCTGTGCAGTTTTGTCAAGGTTGTGTACGGGTGAGGTT-TTCCTATCTGTCAACATA 131618
QY 4023 AATAATATGGCTTAATTTGCTTATATACATCTCTGCTCCACCTTTAGAGGCCAAATTTAC 4082
Db 131617 GTCAACATACGAAGATTCATCACCATAGCTCCCTGTCATATCCCTTTAATAACAT 131558
QY 4083 AAATCTGATGAAGCTATGAACCTCTCCCGAGAGAAATACACACACACACACTCA 4142
Db 131557 ATACCTCTTCCACACCTCCCATTCCTAACCCCTGCGCCACTAATCTATCTCCAT 131498
QY 4143 CACACAGTTTTTTTTTAATTTGTTGCACTTAAGCAAGAAACCTGCAATAGAGGATTTTG 4202
Db 131497 TTCTATAATTTTGTCTCTTCCAGTTGTTATATCAATAAAC----- 131457
QY 4203 TTCATATTAATAAATAACTCAGTTGGGCACAGTCACTCAAGCCTGTAACACAGTAC 4262
Db 131456 -----ATTATATAAACAATGATAGGCTGGCATGTTGGCTCAACCTGTAATCCCGAC 131403
QY 4263 TTGGAAGTCCAGGTGGGTGATCACTTTGAGTGAGAAATTCGAGACAGCCTGGTCAA 4322
Db 131402 TTGGCAGGCTAAGGCAGGCAGATCA--TGAGGTACAGGATTCGAGACAGCCTGGSCAA 131345
QY 4323 TATGTTGAACCTATCTCTCTATAAATAACA-----AAATTAGCTGGGTGTAGTGAT 4376
Db 131344 TATGTTGAACCCCGCTCTCTCTATAAATAACAATAATGAATAATAGCTGGCATGGTGGC 131285
QY 4377 GCATGCTGTAGTCCAGCTACTCGGGAGCTGAGGCAAGAGAAATGCTT-----GAAC 4430
Db 131284 ATGTTCTGTATCCCGCTACTTGAAGCTGAGCAGAGAAATGCTTTTAACCTGGGAC 131225
QY 4431 CTGGGAGGAGAGTTGCACTGAGCGAGATCCCACTGCACTCCAGCCTGGGCGACA 4490
Db 131224 CAGGGAGGAGAGGTTTTCAGTGAGCCAAGTTGCACCACTCCAGCCTGGGCTACA 131165
QY 4491 CAGCGAGACTCTATCTCAAAAAAATAAATAAAA 4526
Db 131164 GAGCAAGACTCTCTCTCAAAAAAATAAATAAAA 131129

RESULT 19

US-10-756-149-2307/c
; Sequence 2307, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2307
; LENGTH: 103574

; TYPE: DNA
; ORGANISM: Homo Sapiens
; US-10-756-149-2307
Query Match 8.0%; Score 401.8; DB 9; Length 103574;
Best Local Similarity 59.7%; Pred. No. 6.9e-81;
Matches 862; Conservative 1; Mismatches 478; Indels 104; Gaps 7;
QY 3105 TTTTCTTTTGTGTTCTTTAGAGACAGGGTCTGTGCTGTGCACCCAGGATGAGCACAGTG 3164
Db 17285 TTTATGTATGTATTTATTTAGACAGGGCTCAGTCTGTGACCCAGGCTGGAGTGCAGTG 17206
QY 3165 GTGCAACCATAGTGCATGCGAGCCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAG 3224
Db 17205 ATGTGATGATGCTCAGTGCAGCTCGATCTCTGGGCTCAGGTTATCTCTGCTCAG 17146
QY 3225 CTTCCAAAGTAGCTGGGACTAGAGCGTGCACCCAGCCTGGCTTAATAAAAAATTT 3284
Db 17145 TCTCCAAAGTAGCTGGGACTATAGCGGTGTGCCACACACCCAGCTAACTCTCTTTGTATTT 17086
QY 3285 TTTTCTGAGAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAAACTCTCTGGCTTCAAG 3344
Db 17085 TTTAGTAGAGCGAGTTTCCACATGTTTCCAGGCTGATCTCAAACTCTCTGGGCTCAG 17026
QY 3345 CAATCTCTCTCTCTGGGATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGGC 3404
Db 17025 TGATCCACCCACTCGGCTTCCGGAAGTGTGATATTACAGGCATGAGCCTTTGAACCTG 16966
QY 3405 GCTACTTATTTCTTTTCAATTCCTTTTCCAAATAGATGTTAAGATCCACAGAACAGGGAT 3464
Db 16965 GCTATTTTTTTTTTTGAGTAGGAGTCTCCCTCTGTCGCGAGGCTGGAGTGCAGTGGTGC 16906
QY 3465 TACTGCTTATTTCTCTCTCTTTTGGAGACAGAGTCTCATCTTCACTCAACCTCAACCTC 3524
Db 16905 GA----- 16904
QY 3525 CGTTCAGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTTCTCTGCTTAAGCCTCC 3584
Db 16903 -TCTGGGCTCACTGCAACCTCTGACTCTCCCTGGTTCAAGGATTTCTCTGCTCAGCCTCC 16845
QY 3585 TGAGTAGCTGGAATTTAAGCGGTGCACCAATGCTTGGCTTAATTTTTTGTATTTTGTAGC 3644
Db 16844 CTAGTAGCTGGGATTTGAGGCAATCCGCCACCAAGCTGAGCTAA-TTTTGTATTTTGTAGT 16786
QY 3645 AGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCT 3704
Db 16785 AGAGACAGGTTTTTACCCTGTTGGCCACAGTGGT-----CTCCTGACCTC--GTGATCT 16734
QY 3705 GCTGCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGTGATCTAGTGTGCTGGCCGAT 3764
Db 16733 GCTGCTGCTGCGCTCCCAAGTGTGCGGATTTACAGGTGTGAGCCAACGCGCCGCGC--T 16677
QY 3765 TACTGTCTATTTCTTTTATGCTATATCCCGAGATCTAGAGCAGTGTCTGACATATAGTA 3824
Db 16676 CTGGCTATTTTTTTTTTAAAGTGCATTTATGAATAATTTTTTAACTTGTGTGTTAGATCA 16617
QY 3825 GGTGCTCAATAAATAATTTGATGAATGCACAGCTAGATATAAACTTTCTTTTCTTTTTT 3884
Db 16616 TGTGCTTTAAATATGATTTATGTTATGTTGTTGCTTTAGTCTACTATTTATTTGTTTTTT- 16558
QY 3885 TAAAAAATCTTGACAACCTTTGAGAATAAATAAATACTTGTGATTTCTGCTTTTTCACATTA 3944
Db 16557 -----ATTTCACCTTTTCTGTGTTTTGTTGTTCTCTGTTTTTTC 16524
QY 3945 TCACCTGTTATGACTTTTTTCATATTTGCTCAACCTTTATTTGTTACTGTTTTTTCATTTG 4004
Db 16523 CTTTTCTCTCTCTTTTGGATTTATCAAACTATTTTATAGTACTCTCAATTTTAAATTTAT 16464
QY 4005 TTACTATTTTAGTCACTGAATAATATGCTTTAAATTTGCTTTATACATCTCTCTGCTCCACT 4064
Db 16463 TTATTTGATTTTCTACTATATATCTTTGCAAGTTTAAAGTGTGCTCTACGGATTATGG 16404
QY 4065 TTAGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACCCCTCTCCCCAGAGAAATACA 4124

32348	CAACCCCTTCCAAAGTTGGTCATAAATTATATGATTTTAACTGTGGGATTAATTGTCCTCATTTAG	32288
2801	MMCGGTACACCCACACCTATTTCATACTCGTGTCTGTGGCTCGGCAATCACCTGTAGCAGTA	2860
32288	ACCGAATGGATGTGAGATGACAGAGCCCTAATTGTTTGTATAT - TGCTGCGCTGACGC	32230
2861	GGTTTATCCCTTCCTTGACCTATGAATTCCTAGTTGGTCTCAGTAGGCCGGGGGAAATA	2920
32229	GCAGTAGGATTTCATAGAAAGGCAGCACAGATTAGTGGCTCAAAATGGAATGCTGTGAGTCTA	32170
2921	ATAGTAACACGCCATGATTAGTGTAAATTCTCTTGTTCTGGCAGTGTCTCTTTA	2980
32169	GTATGTCACTCACTTGGCCCTTAGACACAGGCTACTTTAACTTGGGGTTTAGTTGCCTCAT	32110
2981	ATCCTCAGAACACACTATGGGATAGGTACAATTATCCTCACTTAACAGATAAGAAAAC	3040
32109	CT-----ATAATAGGAATAACAGTCTCTACTACTCAAGTTGTCTATGAAGATT	32062
3041	GAGGCTCAGAAGGCTGAGCTATTGTCGCCAAGATCAACACAGCTTGTAAAGTGTGACAGTTT	3100
32061	CAGTCAGTGAATATTATTAAACATGGTTAAAGACATATATATATATATATATATATTT	32002
3101	GGGTTTTTTTTTGTGTTTGTAGACAGAGGTCCTGTCTGTCAACCAGCATGAGCAC	3160
32001	TTTTTTTTTTTTTTTTTTTTTTTGAGACA - GTCTCACTCTGTGCCCAGGCTGGAGTGC	31944
3161	AGTGGTCAACCATAGTCACTGACGCCCTCAACCTCCTGAGCTCAAGGATCTGCTGACC	3220
31943	AGTGGCGTGAATCTTGGCTCACTGCAAGCTCCACTCCCGGTTCAATGCCATTCCTCTGCC	31884
3221	TCAGCCTCCCAAGTAGCTGGGACTAGAGCGTGCACCCACCCAGCCTGGCTAAATTAATAAA	3280
31883	TCAGCCTCCGAGTAGCTGGGACTACAGGCGCGCCACCCAGCCCACTAATTTTTTGT	31824
3281	ATTTTTTTGTAGAGACTGGGCTTACTAGCTTGGCCAGGCTTGCTTTAACTCCTGGCTT	3340
31823	ATTTTTTAT - TAGAGACGGGGTTTCACCAATTTTAGCCAGATGGTCTCTATCTCTGACCT	31765
3341	CAAGCAATCCTCTACTCTGGCAATCCAAAGTCTGGGATTACAGGGGTGAGCCACCATG	3400
31764	C--GTGATCCGCGCGCTCGGCCCTCCAAAGTCTGGGATTACAGCGGTGAGCCACCGCG	31707
3401	TGCGGCTACTTATTTCTTTTACATTCCTATTTTCCAATAGAAATGTAAGATCCACAGAACAG	3460
31706	CCTGGCCTTTTTTTTTT-----	31690
3461	GGATTACTGCCTATTTTCTCTCTCTTTTGTGACAGAGTCTCACTTCATCACTCAA	3520
31689	-GTTTGTGTGAGACAGAGTCCCGCTCTGTATGCAAGCCTGGAGTGCAGTGGTGCCATC-	31633
3521	CCTCCGTTCAAGTCACTGCAAACTCTGCTCCCGGTTTCAAGYGATTCTCTGCTGCTAAGC	3580
31632	-----TTGGCTCACTGCAACTCTGGCTCCCAAGTTCGAAGTTCGAAGTCTTGTGCGCTCAGC	31580
3581	CTCCTGAGTAGCTGGAATTACAGCGTGCACCACCATGCTTGGCTAAATTTTTTGTATTTT	3640
31579	CTCCCAAGTAGCTGGGATTATATGATGTGCCACCCAGCCAGCTAA--TTTTTGTGTTTC	31521
3641	TAGCAGAGATGGGGTTTTTACATGTTGCCAGGCTGTCTCAAACTCTGACCTCAAGTG	3700
31520	TTGTAGAGACAGGGTTTCGCCATGTTGGCCAGACTAGTCTCAAACTCTGCTCAAGTG	31461
3701	ATCTGCTGCTCAGTCTCCCAAAGTGCTTGGAAATTATAGCGGTGAGTCACTGTGCTGGC	3760
31460	AGTCGCTGCTTGGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACTGCGCTGGA	31401
3761	CGAATTACTGTCTAT-----TTTTCTTTATTGCTATATCCCCAGATCTAGACAGTGTCTGA	3815
31400	CAAGAAATTTCTATATTATTTTCTCTCAACAAATTATCAACCATCTGTACATCTTGA	31341
3816	CATATAGTAGGTGCTCAATAAATAATTATGATGAATGACAGCCTAGAT-----	3862
31340	CAGGCAACAGATAGCATGAATAAGGACATGGGTCAACAACTCTCACTGGGGACAGATGA	31281

RESULT 23

RESULT 23
US-10-087-192-1978

US-10-087-192-1978
: Sequence 1978. Application US/10087192

; sequence 1978, Application US/1
: Publication No. US20020182586A1; PUBLICATION NO: 0320
: GENERAL INFORMATION:

APPLICANT: Morris, David W.

APPLICANT: Engelhard, Eric K.

; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: CANCER

FILE REFERENCE: 529452000122

; CURRENT APPLICATION NUMBER: US/10/087,192

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: US 09/747,377

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: US 09/798,586

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 2059

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1078

```

; SEQ ID NO 1978

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; LENGTH: 87687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(87687)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1978

Query Match      8.0%; Score 399; DB 5; Length 87687;
Best Local Similarity 60.1%; Pred. No. 2.1e-80;
Matches 900; Conservative 1; Mismatches 511; Indels 85; Gaps 11;

QY 3111 TTGTTGTTGTTTATAGACAGGGCTTGTCTGTCAACCCAGGCGATGAGCAGTGGTGCAA 3170
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5754 TTTTGTGTTTGTGAGACAGTCTGTCTGTCAACCCAGGCGTGGAGTGAGTGGCGCA 5813
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3171 CCATAGTGTCACTGAGCCTCAACCTCTGTAGCTCAAGGGA-TCTGTGCTACCTCAGCCTCC 3229
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5814 TCTTGGCTCACTCAAGCTCTGCTCTCTGGGTTTCAAGCCATTCTCTGTGCTCAGCCTCC 5873
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3230 CAAGTAGCTGGGACTAGGAGCTGACCCAGCCTGGCTTAATTAATAAATTTTTTTG 3289
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5874 CGAGTAGCTGGGACTAGGAGCTGACCCAGCCTGGCTTAATTAATAAATTTTTTTG 5933
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3290 TAGAGACTGGGCTTACTACTGTTGGCCAGGCTTGTCTTAACTCTCTGGCTTCAAGCAATC 3349
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5934 TAGAGACTGGGTTTCACT--GTTAGCAGGATAGTCTCGATCCCTTGAC--CTTGTGATC 5989
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3350 CTCTACTTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGCTAC 3409
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 5990 TGCCCGCTCAGCCTCCCAAGTGTGGGATTACAGCGGTGAGCCACTGCGTCTGTCCTT 6049
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3410 TTATTTCTTTACATTCATCTTTCCAAATAGAAATGTAAGATCCACAGAAAGGGATTA--C 3467
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6050 ACCTTTATACAATGTATAGAAATGTATAGGAGGCTTTAGGTAAGAGACTGGCAATTAGTT 6109
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3468 TGCCTATTTTCTCTCTTTCTTTTTCAGACAGAGTCTCACTTCATCACCTCAACCTCCGT 3527
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6110 TTTTAAATTTGTTACTTTTTTTTTTTTGAGACAGACTCTCACTCTGTGTCCGGACTGGAGT 6169
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3528 TCA-----GCTCACTGCAACCTCTGCTCTCCGGGTTCAAGYGATTTCTCTG 3573
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6170 GCAGTGGCATGATCTTGGCTCACTGCAACCTCTGCTCTCCCGGTTCAAGTGATTTCTCTG 6229
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3574 CCTAAGCCTCTGATGATGGAATTTACAAGCGGTGACACCACTGCTTGGCTAAATTTTTT 3633
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6230 CCTCAGCCTCCCTAGTAGCTGGGATTACAGGCGATGTGCCACCATGCCAGCTAAATTTTTT 6289
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3634 GTATTTTTCAGAGATGGGGTTTACCATGTTTCCAGGCTGGTCTCAAACTCCTGACC 3693
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6290 GTATTTTTCAGAGACAGGGTTTGTGTCATGTTAGCAGGCTGGTCTCGNACTCCCAAG 6349
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3694 TCAAGTGATCTGCTGCTCAGTCTCCCAAGTGTGGAAATATAGGCGTGGAGTCACTGT 3753
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6350 CCAGGTGATCTGCCACCTCAGCACCCCAAGTGTGGGATTACAGGCGTGAGCCACCAC 6409
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3754 GCCTGGCCGATTAAGTCTATTTTCTTT-----ATTGCTATATCCCGAGATCTAGA 3804
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6410 ACATGGCCTAAAAATTTCTTCTTATTTGAAAAATGAGTTTATGAGGGACATTTTGTCAA 6469
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3805 GCAGTGTCTCAGATATAGTAGGTGCTCAATTAATTAATGATGAATGCACAGCCTAGATAT 3864
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6470 TCTGGCTTCAAAAAGATGAATGAATCAATGTTAAATTTGTTTAAACGTGCTCGTTTC 6529
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3865 AAACTTTTCTTTTCTTTTAAAAACAATCTTGACAA-----CTTTGCAAGAT 3912
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6530 AGCAGCACATACACTAAATTTAGACTGATACAGAGAAGATTAGCATGGCCCTCGCCAAA 6589
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 3913 AAATACAACTTGTGATCTCTCTTTTTCACCTTATCAGCTGTTGATGACTTTTTCATATGC 3972
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6590 GATGACACGCAAAATTTCAITTTTAAAAAAGCAATAAATATTGTTTAAAAAATCATTTTAA 6649
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 3973 CTCAAACCTTTATTGTTACTGTTTTCATTGTTACTATTTTAGTCACTGAATAATATGG 4032
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4033 CTTAAATTTGCTTATACATCTCTCTGCTGCATTTTGAAGGCCAAATTTTACAATCTGATG 4092
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4093 AAAGCTATGAACCTCTCTCCCGAGAGAAATACACACA----- 4128
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4129 -----CACACACACACTCACACAGTTTTTTTTTAAATGTTTGCACCT- 4173
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4174 GACAAGAAACCTGCAATAGAGGATGTTTGTTCATATTAATTAATAAATACTCAGTTG---- 4230
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4231 GGCACAGTGACTCAAGCCTGTAAACACACAGTACTTTTGGAGTCCAAAGTGGTGGTCACT 4290
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 6950 GGCACAGTGGCTCATGCTCTAATACCCAGCACTTTGGGAGGCCAAGCGGGCAGATCAC 7009
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4291 TGAGGTGAGAAATTCGAGACCAAGCCTGTGCTCAATATGTTGAAACCCCTATCTCTAC--TAAAA 4349
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7010 TGAGCCAGGAGTTTGAGATCAGCTGGGCAACATGGCAAAACCCCGTCTCTACGAAAAA 7069
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4350 ATACAAAAATTAGCTGGGTAGTATGATGATGCCCTGTAGTCCAGCTACTCCGGAGGCTG 4409
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7070 ATACAAAAATTAGCTGGGTGTTGGTGGCGCCCACTGTAGTCCCACTACTCAGGGGGCTA 7129
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4410 AGGCAAGAGATTGCTTGAACCTGGGAGGAGAGTTCAGTGAGCCGAGATCCCAACAC 4469
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7130 AGTGGGAGGACTGCCAGGCTTAGGAGTGGAGGTTCAGTGAGCTGAGCTGCACCA 7189
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4470 TGCATCTCCAGCCTGGCGCACACAGCGAGACTCTATCTCAAAAAAATAAATAATAA 4526
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 7190 TGCATCTCCAGCCTGGTGACACAGCAGCGCTGTCTCAAAAAACAACAACAAAAA 7246
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 24
US-10-087-192-148
; Sequence 148, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 174448
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(174448)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-148

Query Match      8.0%; Score 398.6; DB 5; Length 174448;
Best Local Similarity 59.8%; Pred. No. 5.1e-80;
Matches 879; Conservative 0; Mismatches 524; Indels 66; Gaps 10;
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Db 147414 CCTCAGGTGATATGCCCACTTGGCCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACT 147355
Qy 3398 ATGTGGG-CTACTTATTTCTTACATTCCATCTTCCCAATAAGATGAAGATCCACAGA 3456
Db 147354 GTGCCGGCCATAATTTATTTATGTGTTGTTTTGTTTTTTTTTTTTTTTTTTTGA 147295
Qy 3457 ACAGGGATTACTGCCTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCATCACG 3516
Db 147294 GACCGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 147235
Qy 3517 TCAACC----TCGGTTACAGTCACTGCAACTCTGCTCCCGGGTTCAAGYGATTCCT 3572
Db 147234 TCCTCCGCAACCTCTCAAGATTTTCGCAACCTCTGCTCTCTGAGTTCAAGCGATTCCTGT 147175
Qy 3573 GCCTAAGCCCTCCTGAGTGTGGAATTTACAAGCGTGCACACCATCTTGGCTAAATTTT 3632
Db 147174 GCTTCAACCTCTGGAGTGTGAGATTACAGGTGTGTCACCATGCTTGGCTAA-TTTT 147116
Qy 3633 TGTATTTTTAGCAGATGGGTTTTACCATGTTGGCCAGGCTGGTCTCAAACTCCTGAC 3692
Db 147115 TGTGTTTTAGTAGATGGGTTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC 147056
Qy 3693 CTCAAGTGATCTGCTGCTCAGTCTCCCAAAGTGTGGAATTTATAGGCGTGAAGTCACTG 3752
Db 147055 CTCAAGTGTGTC-ACCTGCTTTCGCTCTCCCAAAGTGTGGGATTACAGGCATGAGCCTCCA 146997
Qy 3753 TGCTGGCCGA-----TTACTGTCTATTTCTTTATTTGCTATATCCCCAGATC 3800
Db 146996 TGCCACCCCATAGCTCCTATTTTAAATGTACCTGTAAATGTTGGCTGCCCTTTAAATC 146937
Qy 3801 TAGACAGTGTCTGACATATAGTAGTGTCTCAATAAATAATTTGATGAATGCACAGCCTAG 3860
Db 146936 AACTCAACCCCATGTTAATGCATCAGTCACTAACTAGGATAAAGTAGGAGTTACTGAA 146877
Qy 3861 ATATAAACTTTCTTTTCTTTTTTTTAAACAATCTTGACAACTTTGCAGAAATAATA- 3917
Db 146876 ATGCTGCTTTCCACTGCGCACCACTTTGTGAGAAAAGGAAACCTAGAAAAATAACATTG 146817
Qy 3918 ----CAATCTTGATCTGCTTTTTTACATTTACACCTGTGTATGACTTTTTTCATATTGCC 3973
Db 146816 TGGGCATGATTTCTTTATCTGACGGTGAATTCAGCCCTTGCAGTGATTTTTTCAGAGATGA 146757
Qy 3974 TCAAACTTTATTTGTTACTGTTTTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGGC 4033
Db 146756 ACAGAAATTAAGTGTAGAACTCATTTGGAGGCTAAGCAGGTAAAGTCTTGAGCCC 146697
Qy 4034 TTAATTTGCTTTATACATCTCTGCTCCACTTTTGAAGGCCAAATTTTCAAAATCTGATGA 4093
Db 146696 AGGAGTTTGAGACA-AGGCTGGGTAAACATAATGAGAAACCTGTCTCTACAAAACAAACAA 146638
Qy 4094 AAGCTATGAACCTCTCCCGAGAGAATACACACACACACACACTTCACACACAGTTTT 4153
Db 146637 AAACCTATGTTCTCCGCTTTCCCAACATTTAATCTTTTACATACAGATTGATTTTCA 146578
Qy 4154 TTTTAAATGTTGCACTAAGACAAGAAACCTGCATTTAGAGGATGTTTGTTCATA----- 4208
Db 146577 TCCCTTAAG-TAGCAAAAGAGAGATGGAGGTGCTGAAGTGTGTAATTTGTGATAACTGTT 146519
Qy 4209 -----TTAATTAATAATACTACGTTGGGCACAGTGACTCAAGCCTGTAAACACAG 4259
Db 146518 TGCTTCTTTAGAATATGTTTCTTGGCCAGGAGCGTTTGGTGACGCGCTGTAAATCCAG 146459
Qy 4260 TACTTTGGAAGTCAAGTGGGTGGATCACTTCAGGTGTAGAAGTTCGAGACAGCCTGGT 4319
Db 146458 CAGTTTGGGAGGCCAAGTGGGTGGATCAGTGAAGTTCAGAGATCGAGACCATCTCTGGC 146399
Qy 4320 CAATATGGTGAACCCCTATCTCTACTAAAAAATAC--AAAAATTTAGCTGGGTGTAGTGATG 4377
Db 146398 TAACATGGTGAACCCCTGTCTCTACTAAAAAATAACAAAAAATTTAGCCGGGCATGGTGGTG 146339
Qy 4378 CATGCTGTAGTCCAGCTACTCGGAGGCTGAGGCNAGAGAAATGCTTGAACCTGGAG 4437
Db 146338 GGACCTTATAGTCCCAGCTACTCGGAGGCTGAGGCAGGAGAAATGGCATGAACACAGGAG 146279

RESULT 26

US-09-964-824A-273/c
; Sequence 273, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 273
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-273

Query Match 8.0%; Score 398.4; DB 3; Length 167343;
Best Local Similarity 60.1%; Pred. No. 5.5e-80;
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;

Qy 3098 TTGCGGTTTTTTTTTTGTTGTTGTTTGTAGACAGGGCTTGTCTCTGCACCCAGGCATGAG 3157
Db 147653 TTTTTTTTTTAATTAATTTATTTTGTAGACGGAGTCTGTCTCCTACCTAGGCTGGAG 147594
Qy 3158 CACAGTGTGCAACCATAGGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTG 3217
Db 147593 TGCAGTGGCACAACTCTTGCTCAGTGCAGCCTCCGCTCCGGGTTGAAGCATTTCTCT 147534
Qy 3218 ACCTCAGCCTCCCAAGTGTAGTGGGACTAGAGCGTGCACCAACCGCTGGCTAATTAAA 3277
Db 147533 GCCTCTGCCTCGCCAGTAGTTGGGATTACAGGTGTGTGTACACGCCCAGCTAATTTT 147474
Qy 3278 ABAATTTTTTTGTAGAGACTGGGTCTTACTAGTTTGGCCAGGCTTGTCTTAACTCCTCG 3337
Db 147473 TGTA-TTTTTAGTAGAGCGGAGTTTCCACTGTTGGCTAGGCTAGTCTTGAATCTCTGA 147415
Qy 3338 CTTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCAC 3397
Db 147414 CTTAGGTGCATATGCCACCTTGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCT 147355
Qy 3398 ATGTGGGG-CTACTTATTTCTTTTACATTCCTTTCOAATAGAATGTAAGATCCACAGA 3456
Db 147354 GTGCCTGGCCTAAATTTATTTATTTATGTTGTTTTTTTTTTTTTTTTTTTTTTGA 147295
Qy 3457 ACAGGGATTACTGCTCTATTTCTCTCTCTTTTGTAGACAGAGTCTCACATTCATCAC 3516
Db 147294 GACCGACTCTCTCTCTGTTGCCCTAGGCTGGAGTGCAGATCTCTGCTCACTCTC 147235
Qy 3517 TCAACC----TCGGTTACAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYGATTTCTCT 3572
Db 147234 TCCTCCGCAACCTCTCAAGATTTTCGCAACCTCTGCTCCCTCCTGAGTTCAAGCATTTCT 147175
Qy 3573 GCCTAAGCCTCTCTGATGAGTGTGAATTTACAAGCGTGCACCATGCTTGGCTAATTTT 3632

Db 147174 GCTTCAACCTGTGAGTAGTGAGATTACAGGTGTGTGCCACCATGCTCGGCTAA-TTTT 147116
Qy 3633 TGTATTTTATGACAGATGGGTTTTACCATGTTGCCAGGTGGTCTCAAACTCTGTAC 3692
Db 147115 TGTGTTTTATGATAGATGGGTTTACCATTGTGGCCAGGTGGTCTTGAACCTCTGTAC 147056
Qy 3693 CTCAGTGATGCTGCGCTCAGTCTCCCAAGTGTCTGGAATATATAGGCGTGAATCACTG 3752
Db 147055 CTCAGGTGGTC-ACCTGCTTTCGCTCCCAAGTGTCTGGAATATACAGGCATGAGCTCCA 146997
Qy 3753 TGCCTGGCCGA-----TACTGTCTATTTTCTTTATTTGCTATATCCCGATC 3800
Db 146996 TGCCAGCCCATAGCTCTTATTTAATTTGCTGTAATTTGCTGCTCCCTTTAATP 146937
Qy 3801 TAGAGCAGTGTGTGACATATAGTAGTGTCTCAATAAATTAATGATGAATGCACAGCTAG 3860
Db 146936 AAACCTCACCCCATGTTAATGATCAGTCACTAACTAGGATAAGGTAGGATTACTGAA 146877
Qy 3861 ATATAAACTTTCTTTTCTTTTAAAAAATCTTTGACAACCTTTGCAAGATAAATA--- 3917
Db 146876 ATGCTGCTTTCCACTGSCACCACTTTGTGAGGAAGGAAACCTAGAAAAATAACATTG 146817
Qy 3918 ----CAACTGTGATCTGCTTTTTCACCTTATCACCCTGTTATGACTTTTTCATATGCC 3973
Db 146816 TGGGCATGATTTCTTTATCGTACGCTGAATTCAGCCCTTGCAGTGATTTTTCAGAGATGA 146757
Qy 3974 TCAAACTTTATTTGTTACTGTTTTTCAATTTGTTACTATTTTAGTCACTCAATAATATGCC 4033
Db 146756 ACAGAATTTAAAGTGTAGAACTCATTTGGGAGGCTAAGGAGGTAAAGTGTGAGCCC 146697
Qy 4034 TTAATTTGCTTATPACATCTCTCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGA 4093
Db 146696 AGGAGTTTGAGACA-AGGCTGGGTAACTAATAATGAGAAACCTGTCTCAACAAACAA 146638
Qy 4094 AGCTATGAACCTCTCTCCAGAGAAATACACACACACACACTCACACAGTTTTT 4153
Db 146637 AAACCTATGTTCTCGCTTTCCCAACATTTAACTTTTACATACACAGTTGATGTTTCA 146578
Qy 4154 TTTTAAATGTTTCAACTAGAACAAACCTGCAATTAGAGGATGTTTGTTCATA----- 4208
Db 146577 TCCTTTAAG-TAGCAAGGAGATGGAGTTGCTGAAGTGTGAATTTGTGATACTGTT 146519
Qy 4209 -----TTAATTAATAATRACTCAGTTGGGCACAGTGACTCAAGCCTGTAACACAG 4259
Db 146518 TGCTTTCTTTAGAAATATGTTTTCTGCGCAGGAGCGTTTTGGTGACGCTGTAATCCCAG 146459
Qy 4260 TACTTTGGAGTCCAAAGTGGGTGGATCACTTGAGGTGAGAAAGTTGAGACACAGCTGTT 4319
Db 146458 CAGTTTGGAGGCGCAAGGTGGGTGGATCAGTGAGGTGAGGATCGAGACCATCTCTGTC 146399
Qy 4320 CAATATGGTGAACCCCTATCTCTACTAAAAATAC--AAAAATTTAGCTGGGTGTAGTGATG 4377
Db 146398 TAACATGGTGAACCCCTGCTCTACTTAAAAATACAAAAAATTTAGCCGGGCATGGTGGTG 146339
Qy 4378 CATGCTGTAGTCCCACTACTCGGAGGCTGAGGCAAGAGAAATTCGTTGAACCTGGGAG 4437
Db 146338 GGCACCTATATGCCAGTACTCGGAGGCTGAGGCAGGAGATGCAATGAACACAGGAG 146279
Qy 4438 GCAGAGTTGACGTAGCGGAGATCCCACTGCACTCCAGCTGGGCGACACAGCGAG 4497
Db 146278 GCGAGCTTGCAGTGAGCGGAGATCGTGCACCTGCACTCCAGTCTGGGCAACCGAGCGAG 146219
Qy 4498 ACTCTATCTC 4507
Db 146218 ACTCCTTCTC 146209

RESULT 27

US-10-843-641A-2740/c
; Sequence 2740, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; FILE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2740
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-2740

Query Match 8.0%; Score 398.4; DB 9; Length 167343;
Best Local Similarity 60.1%; Pred. No. 5.5e-80;
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;

Qy 3098 TTTGGGTTTTTTTTTTGTTGTTTGTAGAGACAGGGTCTTGCTCTCAACCCAGGCATGAG 3157
Db 147653 TTTTATTTTAAATTAATTTATTTTGTAGACGGAGTCTTGCTCTCACTAGGCTGGAG 147594
Qy 3158 CACAGTGTGCAACCATAGGTCATGCGACCTCAACCTCTGAGTCAAGGATCTGCTG 3217
Db 147593 TGCAGTGGCAAACTCTTGCTCACTGCGACCTCCCGGTTGAAGCGATTTCTCT 147534
Qy 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACCAACCCAGCTGGCTAATAA 3277
Db 147533 GCCTCTGCTCGCCAGTAGTTGGGATTACAGGTGTGTGTACCGCCAGCTAATTTT 147474
Qy 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTAGCTTGGCCAGGCTTGTCTTAAACCTCGG 3337
Db 147473 TGTA-TTTTGTAGAGAGCGGATTTTCACTGTTGGCTAGGCTAGTCTTGAACCTGTA 147415
Qy 3338 CTTCAAGCAATCTCTCACTTGGCATCCAAAGTGTGGGATTACAGGGTGAAGCCAC 3397
Db 147414 CCTCAGGTGATATGCCACCTTGGCTCCCAAGTGTGGGATTACAGGCATGAGCCACT 147355
Qy 3398 ATGTCGGG-CTACTTATTTCTTTTACATTTCCATCTTTTCAATAGATGTAAGATCCACA 3456
Db 147354 GTGCTGCGCCCTAAATTTATTTATTTGTTGTTTGTGTTTTTTTTTTTTTTTGA 147295
Qy 3457 ACAGGAGTTACTGCTCTTCTTTCTTTTGTAGACAGAGTCTCACTTCAATCACC 3516
Db 147294 GACCGACTCTCTCTGTTGCTAGGCTGGAGTGCAGTGTACGATCTCTGCTCACTCTC 147235
Qy 3517 TCAACC---TCCGTTCAAGTCACTGCAACCTCTGCTCCCGGGTTCAAGGATTTCTCT 3572
Db 147234 TCCCTCCGCAACCTCTCAAGATTTCCGCAACCTCTGCTCCCTGAGTTCAAGCGATTTCTGT 147175
Qy 3573 GCCTAAGCCTCTGAGTAGTGGAAATTAACAGCGTGACCAACCATGCTTGGCTAATTTT 3632
Db 147174 GCTTCAACCTCTGGAGTAGGTAGATTACAGGTGTGTGCCACCATGCTGGCTAA-TTTT 147116

QY 3633 TGATATTTTACGAGATGGGTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTGAC 3692
Db 147115 TGTGTTTTATAGATAGAGTGGGTTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC 147056
QY 3693 CTCAAGTGATCTGCCTGCCCTCAGTCTCCCAAGTGTGGAATATATAGGCGTAGTCACTG 3752
Db 147055 CTGAGTGGTC-ACCTGCTTTCGCTCCCAAGTGTGGAATATACAGCATGAGCCTCCA 146997
QY 3753 TGCTGGCCGA-----TTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATC 3800
Db 146996 TGCCAGCCCATAGCTCTCTATTTAAATTTGACGTGAATTTGGCTGCCCTTTAAATC 146937
QY 3801 TAGAGCAGTCTGCATATAGTAGTGTCTCAATAAATATTTGATGAATGCACAGCCTAG 3860
Db 146936 AAACCTACCCCATGTTAATGCATCAGTCACCTAACTAGGATAAAGGTAGGAGTTACTGAA 146877
QY 3861 ATATAAACTTTCTTTTCTTTTAAACAATCTTGACAACCTTTGCAGAAATAATA--- 3917
Db 146876 ATGCTGCTTTCCACTGGCACCACTTTGTGAGGAAGGGAACCTAGAAAAATAACATTG 146817
QY 3918 ----CAATCTTGCATCTGCTTTTTCACCTTTATCAGCTTTGTTATGACTTTTTCATATGCC 3973
Db 146816 TGGCATGATTTCTTTATCGTACGGTGAATTCAGCCTTTCAGTGATTTTTCAGAGATGA 146757
QY 3974 TCAAACTTTATGTTACTGTTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGC 4033
Db 146756 ACAGAAATTTAAAGTGTAGAACTCATTTGGGAGGCTAAAGCAGTAAAGTGTGAGCCC 146697
QY 4034 TTAATTTGCTTATACATCTCTGCTCCACTTTAGAAAGGCCAAATTTACAAATCTGATGA 4093
Db 146696 AGAGTTTGAGACA-AGGCTGGGTAACTAATAGAAACCTCTGCTCTACAAACAAACAA 146638
QY 4094 AAGCTATGAACCTCTCTCCAGAGAAATACACACACACACACACTCACACAGTTTT 4153
Db 146637 AAACCTATGTTCTCGCTTCCCAACATTTAACTTTTACATACACAGTTGATGTTTTCA 146578
QY 4154 TTTTAAATGTTTGCNACTAAGCAAGAAACCTGCATTAGAGGATGTTTGTTCATA----- 4208
Db 146577 TCCCTTAAG-TAGCAAGAGGAGATGGAGGTGCTGAAGTGTGTAATTTGGATACTGTT 146519
QY 4209 -----TTAATTAANAATAACTCAGTTGGGCACAGTGCACCTCAAGCCTGTAAACCACAG 4259
Db 146518 TGCTTTTCTTAGAATATGTTTCTGGCCAGGAGCGTTTGGTGACGCGCTGTAATCCGAG 146459
QY 4260 TACTTTGGAAGTCAAGGTGGGTGGATCACTTGAGGTGAGAAATTCGAGACAGCCTGTT 4319
Db 146458 CAGTTTGGAGGCCAAGGTGGGTGGATCAGTGAAGTTCAGGAGATCGAGACCATCTCTGGC 146399
QY 4320 CAATATGTTGAACCTCTCTCTACTAAAATAC--AAAAATTAGCTGGGTGATGATG 4377
Db 146398 TAACATGTTGAACCTCTCTCTACTAAAATAAATAAATAAATAAATAAATAAATAAATAA 146339
QY 4378 CATGCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAGAAATGCTGAACTCGGAG 4437
Db 146338 GGCACCTATAGTCCAGCTACTCGGAGGCTGAGGAGGAGATGGATGAACACGAGAG 146279
QY 4438 GCAGAGTTGCAGTGAGCCGAGATGCCACACTGCCTCAGCCTGGGCGACACAGCGAG 4497
Db 146278 GCGAGCTTGCAGTGAGCCGAGATCGTGCCACTGCATCTCAGTCTGGGCAACCGAGCGAG 146219
QY 4498 ACTCTATCTC 4507
Db 146218 ACTCCTTCTC 146209

RESULT 28
US-10-843-641A-5576/C
; Sequence 5576, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5576
; LENGTH: 167343
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5576

Query Match 8.0%; Score 398.4; DB 9; Length 167343;
Best Local Similarity 60.1%; Pred. No. 5.5e-80;
Matches 872; Conservative 1; Mismatches 532; Indels 45; Gaps 11;
QY 3098 TTTTGGGTTTTTTTTTGTGTTGTTTATGAGACAGGCTCTGTCTGCACCCAGGATGAG 3157
Db 147653 TTTTGTATTAATTAATTTATTTTGTGACGGAGTCTGTCTGTCACTAGGCTGGAG 147594
QY 3158 CACAGTGTGCAACCATAGGTCACTGCAGCCTCAACCTCTGAGCTCAAGGATCTGCTG 3217
Db 147593 TGCAGTGGCACAACTTGTGCTCACTGCAGCTCCGCTCCCGGTTGAAGCATTTCTCT 147534
QY 3218 ACCTCAGCCTCCCAAGTAGCTGGGACTAGAGCGGTGCACACCGCTGGCTAATAATAA 3277
Db 147533 GCCTCTGCCTCGCCAGTAGTTGGGATTACAGGTGTGTCTACACGCCAGCTAATTTT 147474
QY 3278 AAAATTTTTTGTAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCTCTGG 3337
Db 147473 TGTA-TTTTTAGTAGAGAGGAGTTTCCATGTTGGCTAGGCTAGTCTTGAACCTCTGA 147415
QY 3338 CTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACC 3397
Db 147414 CCTCAGGTGATATGCCACCTTGGCTCCCAAGTGTGGGATTACAGGATGAGCACT 147355
QY 3398 ATGTGGGG-CTACTTATTTCTTTTACATTCATTCATTTTCCAAATAGATGTAAGATCCACAGA 3456
Db 147354 GTGCCTGGCCCTAAATTTATTTATGTTTGTGTTTGTGTTTTTTTTTTTTTTTGA 147295
QY 3457 ACAGGATTACTGCTCTATTTCTCTTTTGTGAGACAGAGTCTCACATTCATCACCC 3516
Db 147294 GACCGACTCTCTCTGTTGCTAGGCTGGAGTGCAGTGTACAGATCTCTGCTCACTCTC 147235
QY 3517 TCAACC---TCCGTTTCAGCTCACTGCACACCTCTGCCTCCCGGGTTCAAGYATTTCTCT 3572
Db 147234 TCCTCGCAACCTCTCAAGATTTTCGCAACCTCTGCCTCCTGAGTTCAAGCATTTCTGT 147175
QY 3573 GCCTAAGCCTCTCTGAGTAGCTGGAATTTCAACGCTGCACACCATGCTTGGCTAATTTTT 3632
Db 147174 GCTTCAACCTCTGGAGTAGGTAGAGATTACAGGTGTGTGCCACCATGCTCGGTGTA-TTTT 147116

Qy	2979	TAATCCTCAGAACAACTATGGGATAGGTACAAATTATCCTCCTCATTAAACAGATAAGAAAA	3038
Db	131534	GAAGACGGCGCTGTTCCGAACACAGGTAGCACCAAAGTCCTAGTTTACACCCCTAAATAGGA	131593
Qy	3039	CTGAGGC-----TCAGAAGGCTGAGCTATTTTGGCCAAAGATCATCACAGC	3081
Db	131594	GCTAAGCAGCTGGGAATGCAGAAAAACGCAATAAGTGAATGTCGCCGCGTGGGCTCTC	131653
Qy	3082	TTGTAAAG-----TGGTGACAGCTTGGGTTTTTTTTTTTGTGTTGTTTAGAGACAGGGCTTT	3136
Db	131654	CTGTGTGACATTTCTCGCCACATTTCTATTTTTTTTTTTTTTTTTTTTGTGAGATGGAGCTCT	131713
Qy	3137	GCTGTGTCAACCAGGCGATGAGCACAGTGGTGCACCATAGTGTCACTGACGCTCAACCTC	3196
Db	131714	GCTCTGTCAACCAGGCTGGAATGCAATGGTGTGTGATTTTCAGCTCAGGGCAACCTCTGCTTT	131773
Qy	3197	CTGAGCTCAAGGGATCTGTGTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCAC	3256
Db	131774	CGAGTTTCAGCGGATTTCTCTCGCTCAGTCTCCGAGTAGCTGGGATTACAGGCACCTGC	131833
Qy	3257	CACCAAGCTGGCTAAATTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTGGCC	3316
Db	131834	CACCATGCCAGCCAAATCTTTTGTATTTTGTAGTAAACAGGATTTTGCCATGTGGCC	131893
Qy	3317	AGGCTTGTCTTAAACTCTGGCTTCAAGCAATCCTCTACCTTGGCATCCCAAGTGGCTG	3376
Db	131894	AGGCTGGTTTGGAACTCTGACCTCAAGTGATCCACACAGCCTTGGCCTCCCAAGTGGCTA	131953
Qy	3377	GGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTTACATTCCATCTTTCCAA	3436
Db	131954	GGATTACATGCTGGAGACACCATGCTCCGCGCTCTCCCCACATTTATTTATTTAT----	132009
Qy	3437	TAGAAATGAAGATCCACAGAACAGGATTAATGCGCTATTTCTCTCTTTTTTTTGAGA	3496
Db	132010	-----TTATTTTATTTATTTTGTAGACGGAGTCTTGCTCT	132042
Qy	3497	CAGAGTCTCACTTCATCACCTCAACCTCGTTTCAGCTCACTGCAACTCTGCTCTCCGGG	3556
Db	132043	ATGCCCAAGGTGGAGTGGAGTGGACACATCTCAGCTCACTGCAAGCTCCGCTCCGGG	132102
Qy	3557	TTCAAGYGATTCTCTGCTTAAGCCTCTGAGTACTGGAAATTACAAGCGTGCACACCA	3616
Db	132103	TTCAAGCGCATTTCTCTGCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGCCACACCA	132162
Qy	3617	TGCTTGGCTAAATTTTTTGTA-----TTTTTACAGAGATGGGGTTTTT	3658
Db	132163	TGCCAGCTAAATTTTTTCTTTTTTCTTTTTTTTTTTTTTTTGTAGTAGAGCGGGGTTTC	132222
Qy	3659	ACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATGCTGCTGCTCAGTCT	3718
Db	132223	ATGGTGTTAGCCAAGATGGTCTCGATCTCTGACCTCA--TGATCCGCGCGCTTGGCCT	132280
Qy	3719	CCCAAGTGCTGGAAATTATAGCGGTGAGTCACTGTGCTGGCGGATTAATGCTATTTC	3778
Db	132281	CCCAAGTGCTGGGAATACAGGCATGAGCCACTGTGCGCGGCTCCCCACATTTTTTAAG	132340
Qy	3779	TTTATTTGTATATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAAT	3838
Db	132341	TCCATGG-----CCAGATCTTCTCCTCGCTACTCTCTGTGATC-----	132379
Qy	3839	AATTGATGAATGCAAGGCTAGATATAAACTTTCTTTTTTCTTTTTTAAAAAATACTTGA	3898
Db	132380	-----AGATCGTGAGGGGGTTGCTTCTCTCCCAAAAGGCGCTGT	132419
Qy	3899	CAACTTTCAGAAATAATACAACTTTGCAATCTGCTTTTTTCACTATACCTTTGATATCA	3958
Db	132420	TTAGGCCCGAG-----CACCCTCACTTTGACTTTGTTTCCCAAAATCTTTTATGG	132471
Qy	3959	CTTTTTTCATTTGCGCTCAAAACCTTTTATTTGTTACTGTTTTTTCATTTGTTACTATTTAGTC	4018
Db	132472	AGCTGTGCGTCCGGCAGTCTCCGGGAATCAGCAGCTTGGGAAGGGGGGTTGTTGTGTC	132531

Qy	4019	ACTGAATAATATGGCTTAATTGGTATTACATCTCTCTGCTCCACTTTTAGAAGGCCAAAT	4078
Db	132532	CAGCGCTGTGTCTGGCCAGATGACTCGCGGGTGTGTGGGCGCGCCCGCCACTGCGCCTGA	132591
Qy	4079	TTACAAATCTCATGAAAGCTATGAA-----CCCTCTCCCCAGAGAAATACACACACACA	4132
Db	132592	TTCTTCACGAGAGCGCAGGCGAGGNACAAAGCTGACCCAGAGAGCCAGGCCCATAGCAGG	132651
Qy	4133	CACACACTCACACAGTGTTTTTTTTAAATGTTTGGCAACTAAGACAAGAAACCTGCAATTAG	4192
Db	132652	GGCTGAGGATGCCTGGTGAATGGATGCCTGGGAGAAAAGATGGCAGAAATTACACATGAG	132711
Qy	4193	AGGATGTTTGTTCATATTAAATTAATAAATA-----ACTCAGTTGGGCACAGT	4238
Db	132712	TCTATGAGACAGGNAAGNATCAATAAATAAAGAGGCGCGGCACGGCGCGGT	132771
Qy	4239	GACTCAAGCCTGTAAACCAAGTACTTTGGAAAGTCCAAAGTGGGTGGATCACTTTGAGGTGA	4298
Db	132772	GGCTCATGCCTGTAAATCCAGACACTTTGGGAGGCTTGAGGACGCGGATCA--TGAGGTGTG	132839
Qy	4299	GAAGTTCGAGACGACGCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAATACAAAAA	4358
Db	132830	GGAGTTTGAGACCAAGCCTGGCTTAATGATGAACCCAGTCTTCTACTAAAAATACAAAGA	132889
Qy	4359	TTAGCTGGGTGTAGTGATGCATGCTGTAGTCCCAGTACTCTGGGAGGCTGAGGCCAAGAG	4418
Db	132890	TTAGCCAGGTGTGGGGGTGCATGCCTGTAGTCCCAGTACTCAGGAGGCTGAGGCAGGAG	132949
Qy	4419	AATTGCTTGAACCTGGGAGGCGAGGTTGCACTGAGCCGAGATCCACCACCTGCCTCCA	4478
Db	132950	AATTGCTTGAACCTGGGAGGCGAGGTTGCACTGAGCCGAGATTTGTGCCACTGCCTCCA	133009
Qy	4479	GCCTGGGCGCACACGCGAGCTCTATCTCAAAAAATAAATAAATAAATAAATAA	4530
Db	133010	GCCTTGGCGACAGACGACAGATCTTCATCTTTGAAAAAATAAATAAATAAATAAATAA	133061

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RESULT 30
US-09-880-107-3949
; Sequence 3949, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3949
; LENGTH: 76798
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z84718
US-09-880-107-3949

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Query Match 7.9%; Score 396; DB 3; Length 76798;
Best Local Similarity 53.6%; Pred. No. 1.3e-79;
Matches 1300; Conservative 2; Mismatches 942; Indels 180; Gaps 16;

QY	2278	AAAAATCGCTTTTCAGGCGAGCGCGGTGCTCATGCTGTAATCCACGACACTTTGGGAGG	2337
Db	12199	AAAAAAAAAAAAAGCGAGGTGCGTGTATACGTGTAATCACGACACTTTGGGAGG	12256
QY	2338	CCGAGGCGGCGCGATCACTTTGAGGTGAGAGTTTCGAGACCGCTTGGCCAAATGGTGAA	2397

Db	12259	CCGAGCAGCGAGATCAC--AAGGTcaggagTTCgagACCACTCTGGGTAAATATGGTGAA	12316
Qy	2398	ACCCTGCTCTACTAAAAATACAAAAATTAGCCGGAATGTTGGCGAGCGCTGTAAACC	2457
Db	12317	ACCCCATCTCTACTAAACTACA AAAAATTAGCCAGGCATGTTGGCAGCGACCTGTAGTT	12376
Qy	2458	CCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTCAG	2491
Db	12377	CCAGCTACTTGGGAGGCTGAGCGAGGAGAATCACTTGAACCGGAGGTGGAGGTTGCAG	12436
Qy	2492	TGAGCCAAGGTCGTGTCACTGCTGTCAGCCTGGGTAAcagAGCAAACTCTGTCTCAAAAA	2551
Db	12437	TGAGCCAAGATCGCACCACTCGCACTCCAGCCTTGAGCGAGCAGAGCGAGACTCCGTATCAA	12496
Qy	2552	AAAAAATGCTTTCAAATAATATGATAAAAAGGACTTATATTTTTTCAAGCCATAGGAT	2611
Db	12497	AAAAAAAAGGGACTATGTATGAATAccAGCACAGTGCCTTCCCTTACCCATCAT	12556
Qy	2612	CATTTCTCTGAAGCATTTGGC-----GAAAGTCATCCCC	2646
Db	12557	GACCCCACACACAGTGTGCCATCTGCTCTACTGAGCGCAAAATAAAGGTCCCT	12616
Qy	2647	ACTGTTCTTGAGATGGGAGGTGAGGCTGACCTATTGCTCTGCACCTTACTCTATCT	2706
Db	12617	GACTACTGTTACCCTCAGGACCTTGCAGGCCGCTGCCGTGTGGATGAGTAGCTGGCATGG	12676
Qy	2707	CAGCTGTCCCTCCACTTTCcAGGTGCTGCCAGACATGACAACTGCTATVGACCAGGCC	2766
Db	12677	CAGCACAGACTCTGCGGAGAGCTGCCCTCCGGC-CTTGTGGCAATAGGTGAGGCTGGG	12735
Qy	2767	AAGAAGCTGACAGCTGTAAATTTCTGTGGGACAMMCOGTACACCCACACCTATTTCATAC	2826
Db	12736	AATGTGGGGGGCAGCAGAGACATTCCCAAAGGTGTTcAGGCACcAGTCTCTCTTT	12795
Qy	2827	TCGTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTGACCTATGAA	2886
Db	12796	TCAGTTTGTGGATATTATTCTACTGACCTGTCTTTTGCCCTTCAcAGATTCTTTCCCTGTGTTG	12855
Qy	2887	TTCTAGTTCGGTCTCAGTAGGCGGGGGAAATAATAGTAACAAcAGCCATGATTTTAGTG	2946
Db	12856	GCCAAATGCTATTAGCCCATCAAATACATTCTTTGTTTGAGATATGATTTTTTCAGCT	12915
Qy	2947	TTAATTTCTTGGTCTGGGCAGTGTCTCTTTAATCTCTCAGAACAAcACTATGGGATAG	3006
Db	12916	CTGGAAATTCcATTGGTTGTTTTTAgAATTTCCACTTCTCTGATGAATTCACCACT	12975
Qy	3007	GTAcaATATcCTCACTTAACAGATAAGAAAACTGAGGCTCAGAGGCTGA-	3057
Db	12976	GTTTCATCCATTTTATCTGTCTTTCTTGTAATTTCTTTAAcATATTTATCACTGTACCT	13035
Qy	3058	-----GCTATTGCCCAGATAcACAGCTTGAAGTGGTCACAGTTGGGTTTTTTTT	3111
Db	13036	AAAAATCTTTGTCAAATAATTCAACAGTAGGTGTTCTGTGGGCTCGGTTTTTTGTTT	13095
Qy	3112	TGTTGTTGTTTAGAGCAGGGTCTTGCTCTGTcACCCAGGCATGAGCACAGTGGTCAAC	3171
Db	13096	TGTTTTGTTTTGAGATGGGTTCTCACTCTGTcACCCAGGC-TGAGTGAATGGTGCAT	13154
Qy	3172	CATAGTCTACTGAGGCTCAACCTCTCTGAGCTCAAGGGATCTGTGAcCTCAGCcCTCCA	3231
Db	13155	CTCAGCTCACTGCAAcCTCCAcCTCCcAGGCTCAAGCGATTCTCTGCTCAGCcCTCGT	13214
Qy	3232	AGTAGCTGGACTACGNGCGTGCACCACcAGCCTGGCTAAATAAAAAATTTTTTCTGA	3291
Db	13215	CGTAGCTGGGATTTACAGGCACCCcACAGCACcCTGGCTTACTTTGTGA-TTTGTAGTG	13273
Qy	3292	GAGACTGGGTCTTACTAGCTTGGCCAGGCTGTCTTTAAACTCCTGGCTTCAAGCAATCCT	3351
Db	13274	GAGACcAGGTTTCAcCATGTTGGCCAGGCTGGTTTCGAActCTCCAcCTGAAGTATCG	13333
Qy	3352	CCTACCTTGGCATCCCAAAGTGTGGGAATTACAGGGGTGAGCCAATATGTGCGG-----	3405

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QY 4386 TAGTCCAGCTACTCGGAGGCTGAGCAAGAGAATGCTTGAACCTGGAGGCAGAGT 4445
Db 14471 TAAATCCAGCTACTCAGGATGCTGAGGCAGGAGAATGCTTGAACCCAGGGGGCAAGTT 14530
QY 4446 TGCAGTGGCCGAGATGCCACCACTGCACCTCCAGCTGGGCGACACAGCGAGACTCTATC 4505
Db 14531 GGCAGTGTGCCGAGATGGTCCCACTTCACTCCAGCCTGGGTGACAGAGCTGAACACTGTG 14590
QY 4506 TCAAAAAAATAAATAAATAAATA 4529
Db 14591 TCAAAAGAAAAAATAAATAAATA 14614

RESULT 31
US-10-317-271A-4
; Sequence 4, Application US/10317271A
; Publication No. US20040110156A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF NRF EXPRESSION
; FILE REFERENCE: RTS-0456
; CURRENT APPLICATION NUMBER: US/10/317,271A
; CURRENT FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 160
; SEQ ID NO 4
; LENGTH: 19300
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
US-10-317-271A-4

Query Match 7.9%; Score 394.6; DB 7; Length 19300;
Best Local Similarity 60.1%; Pred. No. 1.2e-79;
Matches 908; Conservative 1; Mismatches 520; Indels 82; Gaps 12;

QY 3099 TTGGGTTTTTTTTTTGTTGTTTATAGACAGAGGTCTTGTC-TGTCACCCAGGCATGAG 3157
Db 8747 TTTTGTGTTTTTTTTTTTTTTTGTGATGGAGTTTCACTCTGTTGTTGCCAGGCTGGAA 8806
QY 3158 CACAGTGGTCAACCACTAGTCACTGCAGCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217
Db 8807 GGCATAGTGTGCGATCTCGGCTCACTAAACCTCTGCTCCAGGTTCAAGCGATTCTCCT 8866
QY 3218 ACCTCAGCTCCCAAGTAGCTGGGACTACGAGGTGTCACACCAACCGCTGGCTAAATAA 3277
Db 8867 GTCTCAGCTCCCAAGTAGCTGGGATTACAGGATGCGCCATCACACCCGGCTAAATTTT 8926
QY 3278 AAAATTTTTTTGTAGACTGGGTCTTACTACGTGTGGCCAGGCTTGTCTTAAACTCCTGG 3337
Db 8927 GTATTTTGTAGAGACA---GGTTTCTATGTTGTCAGGCTGGTCTCGAATCCCGA 8983
QY 3338 CTTCAAGCAATCTCTTACCTTGGCATCCCAAGTGTGGATTAAGGGGTGAGCCACC 3397
Db 8984 CCTCAGTGATCTGCTGCTGCTGCCCTCCCAAGTGTGGGATTACAGGCGTGAGCCACA 9043
QY 3398 ATGTGCGGCTACTTATTTCT-----TTACATTCCTCTTTTCAATA 3438
Db 9044 CGCGCCCGGCTTTGTTTTTATCTCACTTTTGAANAATGTACTCCCAAAATTTGAATGG 9103
QY 3439 GAATGTAAGATCCACAGAACAGGATTAATCTGCTATTTTCTCTTCTTTTGTAGACA 3498
Db 9104 AAGTGATATGTAGAAATGATGTTGTTTATTTTATTTTATTTATTTTATTTTGTAGACA 9163
QY 3499 GAGTCTCACTTATCACTCAACTCAACT-----CCGTTTCACTCACTGCAACC 3543
Db 9164 GAGTCTCGCTCTTGTCTGCTCCAGGCTGGAGTGGCAATCTCAGCTCACTGCAACC 9223
QY 3544 TCTGCTCCCGGGTTCAAGYATCTCTGCTGCTCAAGCTCTCAGTAGCTGGAATTACAA 3603
Db 9224 TCCGCTCCCGGGTTCAAGCAATCTCTGCTGCTCAGCTCTCAGTAGCTGGGATTACAG 9283
QY 3604 CGGTGCACCAACCATGCTTGGCTAAATTTTTTTGTATTTTTTTAGCAGAGATGGGGTTTTTACCAT 3663
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RESULT 32

US-10-719-993-6815
; Sequence 6815, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:

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Db 9284 GGCCTGCTACCAACCCAGCTAA-TTTTGTATTTTATAGTAGACGGGTTTTTACCAT 9342
QY 3664 GTTGCCCAAGGTGCTCAAACTCTGACCTCAAGTATCTGCTGCTGCTCAGTCTCCCAA 3723
Db 9343 GTTGGGTAAAGTGGTCTTGAACCTCTGACCTCAGGTATCTGCCACCTCAGCTCCCAA 9402
QY 3724 AGTGTCTGGAATATATAGGCGTGAATCACTGCTGCTGCGGATTAATCTGCTATTTTCTTAT 3783
Db 9403 AATGTTGGGATTTACAGGTGTGAGCCACCCGCCAGCCATATGTGT-TTTAGACTGTGC 9461
QY 3784 TGCTATATATATATATAGTGTGCTGACATATAGTAGTGTCTCAATAAATAATG 3843
Db 9462 TTTCTGATCTTCAGATAAGAGTCAATGAAATAAATAATTAATCTCTGTTTAAATACTCG 9521
QY 3844 ATGAATGCACAGCTAGATAT-----AACTTTCTTTTCTTTTAAACAAT 3893
Db 9522 TGCTAGCTTTTACGACGACAGTGTGTCAGTGGGAAGTACAGGTATACAACAGAGCTAGCTTC 9581
QY 3894 CTTGACAACTTTGACAGATAAATAAATACTTCTGCTTCTGCTTTTTCACATTACA-CCTTTG 3952
Db 9582 CAGCAGTCTGTCGGGAGGCGACCGTGCCTTGAATCTGCTTTGGTGGAAATGATACGTG 9641
QY 3953 TTATGACTTTTTTATATATGCTTCAACCTTTATGTTACTGTTTCTTCTTCTTCTTCTATTT 4012
Db 9642 ATGGGTGTGCAACCTGTTCTACTGAAATGGAATAATGTTACCTCTCTCTGTTTCAAGAAC 9701
QY 4013 TTAGTCACTGAATAATATGCTTAAATTTGCTTATACATCTCTCTGCTC----- 4060
Db 9702 TGATTCATGTAAGGTATGATAGTTACTCAATTTTTCAGAACTTTCTTCCCAATGCTACCAG 9761
QY 4061 ----CACTTTAGAGGCGCAAAATTTTACAAATCTGATGAAAGCTATGAACCTCTCTCCCA 4116
Db 9762 GAATCTCTTTTGTGCTGCTAGGCTGGGAGAGCTCTGAAGGTAGGAGGAGAGAGGTA 9821
QY 4117 GAAATACACACACACACACACTCACACACAGTTTTTTTTT-----AATGTTT 4165
Db 9822 ACCGTATAAACCAACACTTCACTTGAGCTCTGTTTCTGTTCTCTGTAGTAAATGTTA 9881
QY 4166 GCACTAAGACAAAGAAACCTGCAATTAGAGGATGTTGTTTCATATTAATTTAAATAA--A 4222
Db 9882 TTCTATCAAGCAGCAATCTTCATAAGGAGCCTTTTTTTTTTTTTTTTAAAGAGACCGT 9941
QY 4223 CTCAGTTGGGACAGTGAAGCTCAAGCTGTAACACACAGTACTTTTGAAGTCCAAGGTGGGT 4282
Db 9942 CTCAGCGGCTCAGTTGCTGCTACACTGTAATCTTAGCACTTTGGAGGCTGAGGAGGT 10001
QY 4283 GGATCACTTGAGTGAGAGTTTCGAGACACAGCTGCTGCTCAATATGTTGAAACCTCTCTCT 4342
Db 10002 GGATTAACCTGAGTCAAGGATTTCAAGGTCAGGCTGGCCAACTGGCAAAACCTCTCTCT 10061
QY 4343 ACT-AAAAATACAAAAATTTAGCTGGGTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTG 4401
Db 10062 ACTAAAAATACAAAAATTTAGCCAGCGGTGGGCGCATGCTGTAATCCCAGCTACTGTTG 10121
QY 4402 GGAGGCTGAGGCAAGAGAAATGCTTTGAACCTGGGAGGAGAGGTTCGAGTGAGCCGAGAT 4461
Db 10122 GGAGGCTGAGGCAAGAGAGAGTCTTTGAACCCGGAGGTGGAGGTTCGAGTGAGTAT 10181
QY 4462 CCCACCTCTGCACTCCAGCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAA 4521
Db 10182 TGTGCACTGCACTCCAGCTGGGAGACAGACGAAAGACTCCCTCTCAAAAAAATAAATAA 10241
QY 4522 ATAAAAATAAG 4532
Db 10242 AAAAAAATAAG 10252
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Qy	2408	TACTAAAAATACAAAAATTAGCCGACATAGTGGCGAGCGCTGTAAACCCAGCTACTTT	2467
Db	9747	TACTAAAAATACA-AAAAAATTAGCCAGGTGTGGCGCGTGTGCTGT-AGTCCAGCTACTTT	9804
Qy	2468	GGGAGACTGAGTTGGAGGTTTCAGTGAGCCAAAGGTCGTGCTACTGCTCTGCAGCCTGGGT	2527
Db	9805	GGAGGC-----AGAGGTTGAGTTAGCTGAGATCATGCGACTGCATCTCCAGCCTGGCA	9858
Qy	2528	A-ACAGGACCACTCTCTCTCAAAAAAATAAAATGCTTTCAATAAATATATATATAAAAGGA	2586
Db	9859	ACAGAGTGAGACTCTATCTCAAAAAAATAAATATATATATACACATATATATATACG	9918
Qy	2587	CTTATATTTTTCAAGCCATAGATCATTTCTCTGGAAGCATCTTGGGGAAGTCAATCCCC	2646
Db	9919	TATATATATATACA---CATATATATACGTATATATATATATATATGTATATATATATAT	9975
Qy	2647	ACCTGTTCTGAGAGTGGCAGGTGAGGGCTGACCTATTTGCTCTGCACTTACTCTCTATCT	2706
Db	9976	ACGTATATATATATGTTATATATATATACGTATATATATATGTTATATATATATATGTTTT	10035
Qy	2707	CAGCTG-----TCCTCTCCCACTTTCCAGGTGCTGCCAGACACATGACACTGCTAYGA	2759
Db	10036	TTTTTGAGATAGATATATCTATATATATATATACGTATATATATATATGTGTATATATAT	10095
Qy	2760	CCAGGCCAAAGAG-CTGGACAGCTGTAAATTTCTGCTGGACMMCCGTACACCCACCT	2818
Db	10096	ACGTATATATATATATATATGTGTATATATATATATATATATATGTGTATATATATATAT	10155
Qy	2819	ATTTCATCTGTCCTGCTCGGCATCACCTGTAGCAGTAGGTTTATCCTTCCCTTCTT--	2876
Db	10156	ATACGTATATATATATATGTATATATATATATATATAAAAAAATTTTTTACTGCATCTTTTC	10215
Qy	2877	GACCTATGAATTTCTAGTTGGTTCTCAGTAGGCGGGGGAATAATAGTAAACAACAGCCA	2936
Db	10216	TATGTTTAGATACAAAAATGTCCTACCATTTGTGTCAAGTTGCTCATAGTATTTAGTACAG	10275
Qy	2937	TGATTTAGTGTAAATTTTCTTGGTTCTGGGCAAGTGTCTCTTTAATCTCAGAAACAAC	2996
Db	10276	TAACATGCTACACAGGTTTGTAGACCAGGACAAATAAGCTACATATATAGCCTAGGTGT	10335
Qy	2997	TATGGATAGGTACATTTATCTCATTAAACAGATAAGAAACTCAGGCTCAGAAGGCTG	3056
Db	10336	GTAGTGGTAGGTTATCCCAATTTGGGTTGTGTAAAGATGCCCTGTGGTGTACGGATAGCA	10395
Qy	3057	AGCTATTTGCCAAGATCACAGCTGTGAAGTGGTGACAG-----TTTGGGTTT	3105
Db	10396	GTGAATTTGCCTAACACACACTTTCAGAAATGCATCCCTGTCTATAGGTGATGTATGAC	10455
Qy	3106	TTTTTTTTTGTGTTTGTAGACAGGGTCTTCTCTGTGCACCCAGGCATGACACAGTGG	3165
Db	10456	TATTGCTTTTTTTCTTTTGAACAGGGTCTAGCTCTGTCAACCAGGCTGGGAATGCACGTG	10515
Qy	3166	TGCAACCATAGGTCACTCAGGCTCAACCTCTCTGAGCTCAAGGGATCTGTGACCTCAGC	3225
Db	10516	CTTGATCTCAACTCACTCGGGCTCAACCTCCAGGCTCAAGCAATCTCTCCACCTTAGT	10575
Qy	3226	CTCCCAAGTAGCTGGGACTACGAGCGTGACCAACACAGCCTCGGCTTAA-TTAAAAAATTT	3284
Db	10576	CACCTGAGTAGCAGGACCAAGGCTGCGCCACACACCTGGCTAAATTTTTTGTATTTTTT	10635
Qy	3285	TTTTTGTAGACTGGGCTCTTACTAGCTTGGCCAGGCTTG-TCTTAACTCTCGGCTTCAA	3343
Db	10636	TTTTTGTGGACAGGGTTTTCCACCGTTGCCAGGCTGCTCTTGAACCTCTGGACTTAA	10695
Qy	3344	GCAATCTCTCTACTTTGGCATCCCAAAGTGTCTGGATTTACAGGGGTGAGCCACCATGTGC	3403
Db	10696	ACGATCCTCTGCTCGGGCTCCCAAAGTGTCTGGGATTTACAGGGCGTAGCTACCAACCT	10755
Qy	3404	GGCTACTTATTTCTTTTACATTTCCATCTTTTCCAATGATGTAAGATCCACAGAACAGGA	3463
Db	10756	GGCCACTGACATTCCTCTTTTTTTTTT-----	10783
Qy	3464	TTACTGCTATTTTCTTCTCTTTCTTTTTTGTAGACAGGTCTCACTTCTATCACTCAACCT	3523

10784 TTTTTTTTTTTTTTCTGAGACAGTTTCATCTCTGTTGGCCAGGCTGGAGTGCATAGGGCT 10843

3524 CCGTTCAGCTCAGTGCAGCAACCTCTGCGCTCCCGGTTCAAGYGATTTCTCTCGCCTAAGCCCTC 3583

10844 GATCTCAGTTTCACTGAGCCTCCCGCTCTCTGGGTTCAAGTGATTTCTCTCGCCTCAGCCTC 10903

3584 CTGAGTAGCTGGGAATTACAAGCTGTCACCAACCATGCTTGGCTAAATTTTTTGTATTTTAG 3643

10904 CTGAGTAGCTGGGAATTACAGGCATGTACCACCATCCAGCTAA--TTTTGTATTTTAG 10961

3644 CAGAGATGGGGTTTTACCATGTTGGCCAGGCTGCTCAAACTCCCTGACCTCAAGTGATC 3703

10962 TAGAGACGGAGTTTCTTCATGTTGGTCAGGCTGGTCTTGAACCTCTTGACCTCAGGTGATC 11021

3704 TGCCTGCTCAGTCTCCCAAAGTCTGGAAATTATAGGCTGAGTCACTGTGCTGGCCGA 3763

11022 CACCTACTCAGCCTCCCAAAGTCTGGGATTACAGGTGTAGCCACCAACGCCGCCAA 11081

3764 TTA-----CTGTCTATTTTCTTTTATTGCTAT 3789

11082 CTAATCCATTTTGTGGCGAGATTTTTTTGTTTTGTTTTGTTTTTAATCTTCCTTC 11141

3790 ATCCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTCTCAATAAATAATGTATGAAT 3849

11142 TTAGGAGCTGTAAGACATTTTACAGAGAGTTTCAGAAAGGCCAATAATGGAAAGTAATGGCT 11201

3850 GCACAGCTAGATATAAATTTCT-----TTTTCTTTTTTTTAAAACAATC 3894

11202 TCCACTCTTCTCTTAAAGAACTACTAAATACAGTGTCTTGGGTATTTTCTAAAGTTT 11261

3895 TTGACAACTTTGCAGAAATAAATAAATCTTTGCAATCTGCTTTTTCACTTATCACCTTGT 3954

11262 TTAATAAATGAAATTATTTTGCATTTTGTTCACCTTGGTAAATTTTGGAGGTCACTCATC 11321

3955 ATGACTTTTTTCATATTGCTCAAAACCTTATTTGTTACTGTTTTTCAATTGTTACTATTTT 4014

11322 AGTATATTATCTTTCCGATGTTTTTCTAGGAGTTATGTTTTTACATGTGAAGAACTT 11381

4015 AGTCACCTGAATAATATGGCTTAATTTGCTTATACATCTCTGCTCCACTTTTGAAGGCC 4074

11382 TAGAAAAATACATTTAGCCAGTGTCTGTAACACTGTAATGTATACTAGTTTGTAGCTGACA 11441

4075 AAATTTTCAAACTGTAGTAAAGCTATGAACCC---TCTCCCCAGAGAAATACACACAC 4131

11442 TAAGCAGTGTGTCAGTCCCTTTATATGTAACCTATTGTTGTAGGTACAACTGGTCCCTGCG 11501

4132 ACACACTCACACACAGTTTTTTTTTAAATGTTTGCACTAAGACAAGAAACCTGCA--- 4188

11502 TTATGAGTTTGAACCTGATTTTTTTCGACTTTTACAATGGTGTATAACCATCTTTTGAGCA 11561

4189 -TTAGAGATGTTTGTTCATATTAATTTAAAA-----TAACCTAGTTTGGGCACAGTCA 4240

11562 CTCACAGTTGTTTTTTTTTCTTTTAAAGACAGGGTCTCTTGGCTGGGAGCAGTGG 11621

4241 CTCAGGCTGTAAACCAACAGTACTTTTGAAGTCCAAGTGGGTGGATCACTTGAAGTGAGA 4300

11622 CTCAGCCTGTAAATCCCAACACTTTGAGAGGCCAGGGTGGC--GGATCACTTGAAGTCTCAGG 11681

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11681 GGTTTGAGAACAGCTGGGCAACATAGTGAGACCTTGTCTCTAAAAAACAACA-AAAAAATT 11739

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11740 AGCCTGGTGTAGTGGCAGCGACCTTGGTCCCAGGTACTTCAGGAGGCTGAGGTGGAGAG 11799

4421 TTGCTTGAACCTGGGAGCAGAGTTGCACTGAGCCGAGATCCCACTCACTGCCTCCAGC 4480

11800 TAACTTGAGCCTAGGAGTGGAGCTACAGTGGGCCACAGTCAATGCCTACACTCTAGC 11859

4481 CTGGCGACACAGCGAGACTTATCTCAAAAAAATAAATAAATAAATAAAG 4532

Db	119611	GGACAGTGGCCTGATACACAGCTCACTGACGGCTCTACCTCTGTGACTCAAGTGCCTCTCC	119559
Qy	3217	GACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGACACACACGCTCGGCTAAATTA	3276
Db	119551	TTACCTCAGTTTCCGAGTAGCTAGGACTACGTGGTGACACGACACACTTGGCTAATTTT	119492
Qy	3277	AAAAATTTTTTTGTAG---AGACTGGGCTTTACTAGTTTGGCCAGGCTTGTCTTAACT	3332
Db	119491	TTATTTTATTTTGTAGACACACAGGGCTTTGCTAAGTTGGCCAGGCTGTCTCAAACT	119432
Qy	3333	CTGGGCTTCCAGCAATCTCTCTACCTTGGCATCCCAAGTGCTGGGATTAACGGGTGAG	3392
Db	119431	CCTGAGCTCAAGCAATCCGCCACTTTGACCTCCCAAGGGCTGGGATTAACGGGTGAAG	119372
Qy	3393	CCACCATGTCGGGCTACTATTTCTTTACATTTCCATCTTTCCATAGAAATGAAGATCCA	3452
Db	119371	CCACCATGACGGCCAAATATTTTTTGTTTTTT-----	119340
Qy	3453	CAGAACAGGGAATACATGCGCTATTTTCTTCTTTTGTGGAGACAGAGTCTCACTTCAT	3512
Db	119339	-AATGCTAGTTAAATTTTTTTTTTTTGTGGACAGCTCTTATCTCTGTGGCCAGACTGGAG	119281
Qy	3513	CACCTCAACCTCCGTTCACTCACTGCAACCTCTGCGCTCCGGGTTCAAGYGATCTCTCT	3572
Db	119280	TGCAATGGCGTGATCTTGCTCCCTCAAGCTCAACCTCTGGGTTCAAGTAATTTCTTT	119221
Qy	3573	GCCTAAGCCTCTGAGTAGCTGGATTAACAGCGTGACACCACTGCTTGGCTAAATTTT	3632
Db	119220	GGCTCAGCTCCCGATAGCTGGGATTAACAGCATGGCCACCAACGCCGCGGCTAAAT--T	119163
Qy	3633	TGTATTTTTAGCAGAGATGGGGTTTATCATGTTTGGCCAGGCTGGTCTCAAACTCTGAC	3692
Db	119162	TGTATTTTTAGTAGAGTGGGTTTCTCCATGTTGGTCAAGCTGCTTGAATCTCCAC	119103
Qy	3693	CTCAAGTGATCTGCTGCTCAGTCTCCCAAGTCTGGAAATTAAGCGTGAGTCACTG	3752
Db	119102	CTCAGGTAATCCACCGCCAGCGCTCCCAAGTCTGGGATTAACAGCATGAGCGGTGG	119043
Qy	3753	TGCGTGGCCGA--TTACTGCTATTTTCTTATTTGCTATATCCAGATCTTAGAGCAGTGT	3811
Db	119042	TGCCACGCTATTTTTTATTTATTTTATTTTGTAGATGGAGTCTGTCTGTGGCCT	118983
Qy	3812	CTGACATAGTAGGTGCTCAATAAATTAATGATGAATGCACAGCCT--AGATATAAAT	3869
Db	118982	AGGCTGGATGCAATGGCGGATCTATCTCACTGCAACCTCTGCCCTCTGGGTTCAAGC	118923
Qy	3870	TTCTTTTTCTTTTTTAAACAATCTTGACAACCTTGCAGAAATAAATCAATCTTGCAAT	3929
Db	118922	TATTTCTGTCTCAGCCTCCCAAGTAGCTGAGATTAACAGCGTGACACCACCATGCCAG	118863
Qy	3930	CTGCTTTTTCACTTATCACTTGTATGACTTTTTTATATGCTTCAATGCTTCAACCTTATGTT	3989
Db	118862	CTAATTTTTTGTATTTTATAGTAGCAGCAGATTTTACCATTGTGGCCAGGCTGTCTCGAA	118803
Qy	3990	ACTGTTTTTTTCA---TTGTTACTATTTTGTACTGAATAATATGCTTAAATTTGCTTA	4045
Db	118802	CTCTGACCTCAGGGGTTCTGCCACCTTGGCTCCCAAGTGTGGGATTTATGCTGTG	118743
Qy	4046	TACATCCTCTGCTCCACTTTTAGAAGGCCAAATTTACAATTC-----TGATCAAAGCT	4098
Db	118742	AACCTAGCGCTAAATTTTTTAAAGTGTAAAGTTATATACCTCTTGTAAAAAATAA	118683
Qy	4099	ATGAACCTCTCCCNAGAAATACACACACACACACTCACACAGAT-----4151	
Db	118682	ATGCAGACCATATAGAAATGTATAAATCTCAATTTTACAGAGCTAACCACTGTTTAAAGTA	118623
Qy	4152	-----TTTTTTTAAATGTTTCAACTAAGACAAGAAACCTGCAATAGAGATGTTT	4201
Db	118622	TGGTTGTATATCCTTTCCAAATTTACAAATATATACATATATATAATTTTCACTTTATTT	118563
Qy	4202	GTTTCATATTAATTAATAAATAAATCACTAGTTGGGCAGT-----GA4240	

RESULT 41

US-10-981-277-55/c

: Sequence 55, Application US/10981277

Publication No. US20050181389A1

; PUBLICATION NO. 0320
: GENERAL INFORMATION:
: GENERAL INFORMATION:

APPLICANT: Harris, Cole

APPLICANT: HALLIS, COREY
APPLICANT: DAVIS, LISA

APPLICANT: DAVIS, LISA
TITLE OF INVENTION: Compositions and Methods for Glioma Classification

; TITLE OF INVENTION: COMPO
; FILE REFERENCE: 03-968-IJS

FILE REFERENCE: 03-968-US
CURRENT APPLICATION NUMBER: IIS/10/981 277

; CURRENT APPLICATION NUMBER: US/11-033400
 ; CURRENT FILING DATE: 2004-11-03

; CURRENT FILING DATE: 2004-11-03
 ; PRIOR PUBLICATION NUMBER: US 60/516 817

;; PRIOR APPLICATION NUMBER: US 2002/11 03

;
PRIOR FILING DATE: 2003-
NUMBER OF SEQ. IN NO. 57

; NUMBER OF SEQ ID NOS: 57

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; SOFTWARE: Patent
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; SEQ ID NO 55

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; LENGTH: 1

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; TYPE: DNA

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; ORGANISM: HO

Query Match	7.8%	Score	388	8:	DB	9:	Length	150275:
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Query Match	7.8%;	Score 388.8; DB
Best Local Similarity	54.6%;	Pred No 8 6e-78

BEST LOCAL SIMILARITY 34.6%; FREQ. NO. 8.0E-78;
Matches 1266. Conservative 2. Mismatches 914. Gaps 19.

2276 TTTAAAAATCGCTTTCAGGCCAGGCCGGTGGCTCATGCCGTGTAATCCCAGCACTTTGGGA 2335

QY
Z276 1TAAHAA1CGCTTTCAGGCCAGGGCGGGTGGCTCATGGCCGTGTAATCCAGACCTTGGGA 2355

[illegible]

On 2336 GGGCGAGGGCGCGGATCACTTGAGGTCAGGAGTTCGAGACGAGCTGGCCACATGGTG 2395

Dh 7444 GGCCGAGGTGGTGGATCA--TGAGGTCAAGAGATAGAGGCTATCCTGGCCAACATGGTG 74387

B

Dh 74386 GAACCCCTCTCTACT-AAAAATACAAAAATTAGCTGGGCATGGTGGTGCCTGTAG 74328

2456 CCCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTC 2489

.....

QY 2490 AGTGAGCCCAAGGTCGTGTCACTGTGTCTCAGCCTGGGTA-ACAGAGCAACTCTGTCTCAA 2548

Db 74267 AGTGAGCTGAGATCGTGCCACTGTACTCCAGCCTGGCAACAGAAATGAGACTCTTTCTCAA 74208

Db	74147	CTGGGCTCAAGTGATCTTTGGGCGCTCAACTCCCAAAGTGTGTGATTATAGGTGTAAGC	74088
Qy	2657	GAGAGTGGGAGGTGAGGCGTGACCTATTGC--TCTGCACTTACTCCTCATCTCAGCTGTC	2714
Db	74087	CACAGTCCCTGGACTAAGGGCAAAATCTTGAAATTTGGAAATCAGAGTAGATTTTAAGACTTT	74028
Qy	2715	CCTCCCACTTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGA-CCAGGCCAAGAAC	2773
Db	74027	GGGGATAATTTCAATTTTGTAABAAATCTCTATATTTTCTAAGATTCATTTCTTTAATA	73968
Qy	2774	TGGACAGCTGTAAATTTCTGCTGGACAMMCGGTAACCCACACACTTATTCATACTCGTGCT	2833
Db	73967	TGTTTAAATAGAAATGCTCTTTAAGGTTAGGTGGCATTTGGGGGTATTTTGGGACTTAAT	73908
Qy	2834	CTGGCTCGGCAATCACTGTAGCAGTAGGTTTATCCCTTCTTGACCTATG--AAATCT	2890
Db	73907	TATTTGATAAAATATTTAAATCTTTAGAAAGTAAATGCTCGAAGAACTGTGTCTAAATTT	73848
Qy	2891	AGTTGGTTCTCAGTAGGCGGGGGGAAATAATAGTAAACAACAGCCATGATTTAGTGTAA	2950
Db	73847	TATCATAAATAATTTTCTGAATGGGACTGGGAATCATAAATTTTAAGTCTTATTCGT	73788
Qy	2951	TTTTCTTGGTTCTGGGAGTGTCCTTTAACTCTCAGAAACAACACTATGGGAT-AGGTA	3009
Db	73787	TCCTCTGTTTCAATAGACTCACCATCTGTTCATATCAGTAAATTTGGTACCCCATCCGTTG	73728
Qy	3010	CAATTATCCTCACTTAACAGATAAGAAACTGAGGCTCAGAGGCTGAGCTATTTGCCCCA	3069
Db	73727	GAATTAACCTTTATAATATGCTTTAAAGGTTCAATCTAGAGTTTGTCACTGCACGTA	73668
Qy	3070	AGATCACACAGC--TTGTAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTAGAGA	3127
Db	73667	TGATCACAGTGCCATTTTCATTTAGTGTATAATAAGCCACTTTTTTTTCTTTGAGA	73608
Qy	3128	CAGGTCCTGCTGTGTAACCCAGGCATGACACAGTGGTGCACCAACATAGGTCACTGCA	3187
Db	73607	TGGAGTCTCGCCCTGTGTCCACGGCTGGAGTGCATATGGTGTGATCTCAGCTCACTGC	73548
Qy	3188	CTCAACTCTGAGCTCAAGGATCTGCTCAGCTCAGCCTCCCAAGTAGCTGGGACTACG	3247
Db	73547	CTCTGCTCTCTGGGTTCAAGCCATCTCCTCTCAGCTCCCTAGTAGCTGGGACTACA	73488
Qy	3248	AGGCTGACCACACAGCGCTGGCTAAATTAATAAAATTTTTCTGAGAGCTGGGTCTACT	3307
Db	73487	GGCGCTGCCACCATGCCTGGCTAAATTTTGTGTTTTTGTAGAGACGGATTCCTACT	73428
Qy	3308	ACGTTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAGCAATCCTCCTACCTTGGCATCCC	3367
Db	73427	GTGTTAGCCAGGCTGGTCTCGATCT----GACCTCGTATCTGCCCGCTCGGCTCCC	73373
Qy	3368	AAAGTCTGGGATTAACAGGGTGAGCCACCACTGCGGCTACTTATTTCTTTACATTC	3427
Db	73372	AAAGTCTGGGATTAACAGGGGTGAGCCACCATTCACGCCCACTTTTTTTTTTTTTTT	73313
Qy	3428	TCCTTCCAATAGAAATGTAAAGATCCACAGAACAGGATTACTGCTATTTTCTTCCTTTCT	3487
Db	73312	TTTTTTTGAAGCAGGTTTCGCTCTTGTAC-----	73282
Qy	3488	TTTTTTGACAGAGTCTCACTTCATCACTCAACCTCCGTTCAGCTCACTGCAACCTCTG	3547
Db	73281	-----TCAGGCTGGAGTACAATGSCAAATCTTGGGCTCATTTGCAGCCTTCA	73236
Qy	3548	CCTCCGGGTTCAAGYGATTCCTCGCTAAGCCTCTCAGTAGCTGGAAATTTACAAGGT	3607
Db	73235	CTACCCAGGTTCAAGGATTCCTCGCTCAGCCTCCTCAGTAGCTGGGC-TACAGGCAC	73177
Qy	3608	GCACCACTGCTTGGCTAAATTTTTGTATTTTGTACAGAGATGGGTTTTTACCATGTTG	3667
Db	73176	CTGCCACCAACCGGCTAA-TTTTTTGTATTTTGTGTAGACAGGTTTACCAATGTTG	73118
Qy	3668	CCCAGGCTGCTCAAACTCCTCACTCAAGTGAATCTGCCTGCCTCAGTCTCCCAAGTG	3727

D	b		73117	TCCAGACTAGCTTTGAACCTCCTGACCTCAAAATGATCCACC--GTCTTGGCCTCCCAAAGTG	73059
Q	y		3728	CTGGAATTATAGCGTGAGTCACCTGTGCCTGGCCGGAATTA	3787
D	b		73058	CTGGAATTATAGCGTGAGCCACCACCCAGCCTAGTTATT	72999
Q	y		3788	ATATCCCCAGATCTAGAGCAGTGTCTGACAATATAGTAGGTCTCAATAAATTAATTGATGA	3847
D	b		72998	TTTTTAAACA-ACWTGGGTATGTGAGTCTACTTTATATAAATAGTAAATTTTATGAAATCTAA	72940
Q	y		3848	ATGCACAGCCTAGATATAAACCTTTCTTTTTTTTTTTTTAAAAACAATCTTGACAACCTTTGC	3907
D	b		72939	ATACAGTTACGCTATTTCTTTTTTTTTTTTTTTTTTTAGTTTAGCTATTCTCGATGAAAATGTA	72880
Q	y		3908	AGAATAAATAACAATCTTGCAATCTGCTTTTTCACCTATCACCTTGTATGACTTTTTCAT	3967
D	b		72879	CAAATTTGAGA-----TGTGCTGAAGTCGTAAAGTACATACTGTATATAGAAAGCTTTTAGT	72826
Q	y		3968	ATTGCCCTCAAAACCTTTATTGTGTACTGTFTTTTTCATTTGTTTACTATTATTTAGTCACTCAATAA	4027
D	b		72825	GCAAAAGCAAGTGTAAATACCTAAATTAAATTTTTTGTGTTGATCATACGTT-GAAATGA	72767
Q	y		4028	TATGGCTTAAATTTGCTTTATACATCTCTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATC	4087
D	b		72766	TATTTTAGATATATTGATTAAAGAAATATTATTAAAACTAATTTTCCACTTTTTTAAACCTTT	72707
Q	y		4088	TGATGAAGCTATGAACCCCTCTCCCGAGAAATACACACACACACACACTCAACAC	4147
D	b		72706	TTACTACAGTATCTAGTATGTGTGCTGATAGAAATAAACACAAGCTCATAGAAATTTAA	72647
Q	y		4148	AGTTTTTTTTTAATGTTTGGCACTAAGACAAGAAACCTGCATTTAGAGGATGTTTGTTCAT	4207
D	b		72846	AAATTTCTAGTACTATATTTTAAAAAGTCTTAAGTTTTCATATAAACTT-----	72597
Q	y		4208	ATTAATPAAAAATPACTCAGTTGGGCACAGTCAAGCTTGTAACCAAGTACTTTGG	4267
D	b		72596	-----AAGGGGTAGGATGGAACGGTGACTTTACGCTTGTAATCTCGCACCTTTGG	72547
Q	y		4268	AAGTCCAAGTGGTGGATCACTTTGAGTGTGAGAAAGTTTCGAGACCAAGCTGGTCAATATGG	4327
D	b		72546	GAGGCCAAGGTAGGGGGATCACTTGAAGTCAGAGTTTGAGACCATCTCTGGCCAAATGG	72487
Q	y		4328	TGAAACCTTACTCTACTAAAAATACAAAAATTTAGCTGGGTGTAGTATGCAATGCTGTA	4387
D	b		72486	TGAAACTCTGCTCTACTAAAAATACAAAAATTTAGCCAGGCGTGATGGTGGCTGCTGTA	72427
Q	y		4388	GTCCAGCTACTCGGAGGCTGAGGCAAGAGAAATTCGTTGAACCTTGGGAGGCAGAGTTG	4447
D	b		72426	ATCCAGCTACTTTGGGAGGCTGAGGCAGGAGAAATCACTTTGAACCTTGGAAAGTGGAGGTTG	72367
Q	y		4448	CAGTGAAGCCAGAGATCCCAACCACTTGCACTCCAGCCTGGGCGACACAGCCAGACTCTATCTC	4507
D	b		72366	CAGTGAAGCCAGAGATCATACCATTTGCACTCCAGCCTGGGCGCAAAAGCGAGACTCTGTCTC	72307
Q	y		4508	AAAAAAAAATAATAATAAATA	4529
D	b		72306	AAACAACAACAACAAAAATA	72285

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RESULT 42
US-10-087-192-904
; Sequence 904, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Eggehard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22

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;; PRIOR APPLICATION NUMBER: US 09/798,586
;; PRIOR FILING DATE: 2001-03-02
;; NUMBER OF SEQ ID NOS: 2059
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 904
;; LENGTH: 75252
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-087-192-904

Query Match 7.8%; Score 388; DB 5; Length 75252;
Best Local Similarity 60.5%; Pred. No. 8.9e-78;
Matches 868; Conservative 1; Mismatches 511; Indels 54; Gaps 12;

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DB 3084 GCAATCTCGGCTCACTGCAAGTCCACTTCCCGGTTACGCCATTCTCTGCTCAGCC 3143
QY 3227 TCCCAAGTAGTGGGACTAGAGCGTGCACACACCGCTGGCTAATTAATAAATTTTT 3286
DB 3144 TCCCGAGTAGTGGGACTGAGGATCGCGCCACACCGCCAGCTAATTTTGTGA--TTTT 3201
QY 3287 TTGTAGAGTGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCCTGGCTTCAAGCA 3346
DB 3202 TAGTAAGAACGGGGTTTCAACATGTTGTCCAGGATGGTCTTAACCTCTTGACCTC--GTG 3259
QY 3347 ATCCTCTTACTTGGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCATGTGCGGC 3406
DB 3260 ATCTGCCACCTCAGCCTCCCAAAATGCTGGGATTACAGGCATGAGCCACTGTGCTGCG 3319
QY 3407 TACTTATTTCTTACATTCCTTCCAAATAGATGTAAGATCCACAGAACAGGATTA 3466
DB 3320 CGAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 3373
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DB 3374 -----TCTCACTCTGTCAACCAGGCTGAGTGCAGTGCATGATC----- 3413
QY 3527 TTCAGTCTCACTGCAACCTCTGCTCTCCGGGTTCAAGYGATTTCTCTGCTCAAGCCTCTG 3586
DB 3414 -TCGGCTCACTGCAAGCTCTGCTCTCTGGTTTCAATGCCATTTCTCTGCTCAGCCTCTG 3472
QY 3587 AGTAGCTGGAATTACAGCGTGCACACCATGCTGGCTAAATTTTTT-----TATT 3638
DB 3473 AGTAGCTGGGACTTACAGAGCGCGCCACACACCTGGCTAAATTTTTTTTTTTTATATAT 3532
QY 3639 TTTAGCAGAGATGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAG 3698
DB 3533 TTTAGTAGAGATGGGGTTTACCATGTTAGCCAGGATGGTCTCGATCTCTGACCTC--G 3590
QY 3699 TGATCTGCTCTCTCACTCTCCCAAGTGTGGAATTTATAGGCGTGAATCACTGTGCTGCTG 3758
DB 3591 TGATCACCAGCTCTCAGCTCTCCCAAGTGTGGAATTTATAGGCGTGAATCACTGTGCTGCTG 3650
QY 3759 GCGGATTAAGTCTATTTCTTTATTTGCTATATATCCCAAGTGTGGAATTTATAGGCGTGA 3818
DB 3651 GCCAGAAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 3706
QY 3819 ATAGTAGGTGCTCAATAAATAATTTATGATGATGATGATGATGATGATGATGATGATGAT 3878
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DB 3764 TGGAGTGAATGTTGCGATCTCAGCTCACTGCAACCTCCACCTCTCTGGGTTTGAAGTAT 3823
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QY 4059 TCC--ACTTTAGAGGCCAAATTTTACAAATCTGATGAAAGCTATGAAACCTCTCTCCCA 4116
DB 3944 TCCTGACCTCAGGTGATTTCATCTGCTTTGGCTCCCAAAAGTCTGATTGTCAGGTGTGAGC 4003
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DB 4064 GGAACAGTTTCTGAGGAAATGATT-TTTAGGTTAAACCCCAAAATAGGCCAGCGTA 4122
QY 4237 GTGACTCAAGCTGTAAACACAGTACTTTTGAAGTCCAAAGTGGGTGGATCACTCTGAGGT 4296
DB 4123 GTGGCTCATTCGGTAAATCCAGCACTTTTGGAGCGCGAGGTGGCGGATCAC--GAGGT 4180
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DB 4181 CAGGCAATTGGAGACACACCTGSCCAACATGGTGAACCCCGTCTCTACTTAAATAACAA 4240
QY 4357 AATTAGCTGGGTGTAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4416
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QY 4417 AGAATTGCTTGAACCTGGAGCAGAGGTTCAGTGTGAGCCAGATGCCACCACTGCACTC 4476
DB 4301 AGAATTGCTTGAACCTGGAGCAGAGGTTCAGTGTGAGCCAGATTTGTGCCATTTGCACTA 4360
QY 4477 CAGCCTGGCGGACACACAGCAGTCTTATCTCAAAATAAATAAATAAATAAATAAATAA 4530
DB 4361 CAGCCTGGGTGACAGGCGAGACTCCATCTCAAAATAAATAAATAAATAAATAAATAA 4414
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RESULT 43

US-10-304-107-4
; Sequence 4, Application US/10304107
; Publication No. US20040101855A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Kenneth W. Doble
; FILE REFERENCE: RTS-0433
; TITLE OF INVENTION: MODULATION OF PPAR BINDING PROTEIN EXPRESSION
; CURRENT APPLICATION NUMBER: US/10/304,107
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 148
; SEQ ID NO 4
; LENGTH: 48001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1662, 1665, 1668, 1671, 12844, 13431-13530, 13749, 15475, 15509, 15576,
; LOCATION: 20466, 22014, 23092, 23094, 26394, 30518, 30524, 30673, 36595, 43474,
; LOCATION: 46942, 47193, 47198
; OTHER INFORMATION: n = A,T,C or G
US-10-304-107-4

Query Match 7.8%; Score 387.8; DB 7; Length 48001;
Best Local Similarity 58.2%; Pred. No. 7.7e-78;
Matches 891; Conservative 1; Mismatches 559; Indels 79; Gaps 9;

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QY 3089 TGGTGACAGTTTGGGTTTTTTTTTTTGTGTTTGTAGACAGAGGCTTGTCTGTGCAACC 3148
DB 19249 TGGCCAGTTTTTTTTTTTGGTTTTTGTGTTTTTTTGGAGACAGAGTCTCGCTCTGCCA-CC 19307
QY 3149 AGGCAATGACAGTGTGTGCAACCACTAGTCTACTGACGCTCAACCTCTCTGAGCTCAAGG 3208
DB 19308 AGGCTGGAATGCAATGGCATGATCTCGGTTCACTGCAACCTCCACCTCCCGGGTTCAAGC 19367
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QY 3367 CAAAGTGTGGGATTACAGGGTGAGCCACCATTGTGCGGTACTTATTTCTTTTACATTC 3426
Db 146541 CAAAGTGTGAGATTACAGGCATGAGCCACCACACCCAG-----AGGTTTTTGATCGT 146594
QY 3427 ATCTTTCCAAATAGAAATGTAAAGTCCACAGAACAGGGATTACTGCCTATTTTCTTCTTTTC 3486
Db 146595 TTTTTTGAGATAGTGT-----TC 146613
QY 3487 TTTTTTGACACAGAGTCTCACTTCATCACTCAACCTCCGTTTCAGCTCACTGCAACCTCT 3546
Db 146614 TCTCTGTTGCCAAGCTGAGTGCACTGGCGCAATC-----TCAGCTCACTGCAACCTCT 146668
QY 3547 GCTCCCGGGTTCAAGYGATTCCTCGCTCAAGCCTCCCTGAGTAGTGGAATTAACAAGCG 3606
Db 146669 GTCTCCAGGTTCAAGTGATTCCTGCGCTCAGCCTCCCAAGTAGCTGGGATTACAGGGG 146728
QY 3607 TGCACCAACATGCTTGGCTAAATTTTTTGTATTTTATAGCAGAGATGGGGTTTTACATGTT 3666
Db 146729 CCTGCCACCAAGACCAGTAA-TTTTTGTATTTTATAGTACAGACAGGGTTTCCACATGTT 146787
QY 3667 GCCAGGCTGTCTCAAACTCTGACCTCAAGTGATCTGCTGCCCTCAGTCTCCCAAGT 3726
Db 146788 AGCAAGGCTGGTCTTGAATTTCTTGACCTTAAGTGATCTGTCCGCTCAGCCTCCCAAGT 146847
QY 3727 GCTGGAATTTATAGCGCTGAGTCACTGTGCTGGCCGATTACTGTCTATTTTCTTTATTGC 3786
Db 146848 GCTGGGATTACAGTGTGAGCCACTGTGCCGACCCCGGGAATCATATTTCAACATGAGA 146907
QY 3787 TAT-ATCCCCAGATCTAGACGAGTGTGTGACATATAGTAGGTGCTCAATAAATAATATGAT 3845
Db 146908 CATAAAGGAATAAATCAATCAAAACCATATACATTTGATTGCAAGTAAAGTAACTACT 146967
QY 3846 GAATGACAGCCTAGATATAAATCTTTCTTTTCTTTTAAACAAATCTTGACAACTTT 3905
Db 146968 ATGAAAGAAATAGTGTGCAAAATGACTGAGAAACAGGAGGACCTATTTGTGTGGGG 147027
QY 3906 GCAGATAAATAACAATCTTGATCTGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3965
Db 147028 AATCAGATGCTCTACGAGGAAGCTGATACTGGAGATAGGTAGGAGTTTGCCCAAGTG 147087
QY 3966 ATATTGCCCTCAAACTTTATGTTACTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4025
Db 147088 AAGCAGTGGCGAAGGCAATCTGCGAGGGGAAACAGCAAGTGCAAAGCCCTAGAGGTAG 147147
QY 4026 AATATGGCTTAATTTGCTTATACATCCTCTGTC-TCACCTTTTGAAGGCCAAATTTACAA 4084
Db 147148 GAAATATGGTACAAATTTGTTAAAGAACTGCAAGCAGTCAGGGTGGCTTGCTGAGATGAAGA 147207
QY 4085 ATCTGATGAAAGCTATGAACCTCTCTCCAGAGAAATACACACACACACACACTCACA 4144
Db 147208 TGGGCAATGTATGCTTAAGATCTCAGAACGACAGACAAACAAACAGACAAACAGGACTT 147267
QY 4145 CACAGTTTTTTTTTAATGTTTGAACCTAAGACAAGAAACCTGCATTTAGAGGATGTTGTT 4204
Db 147268 ARAACAAAAGCTTCTGTACAGCAAAAGAAATAATCAAGATAATGAACCAACACACACA 147327
QY 4205 CATATTTAATAAATACTCAGTTGGGCACAGTGACTCAAGCCTGTAAACACAGTACTT 4264
Db 147328 CAATGAAGAAGAAATATCTGTGGGCCAGGCACAGTAGCTCACACTTGTAAATCCCAAGATTT 147387
QY 4265 TGGAACTCCAAGGTGGTGATCACTTGAGGTGAGAAAGTTTCAGACACAGCCTGGTCAATA 4324
Db 147388 TGGAGGCCAAGGTGGGCGAGATCACCTGAGTCCAGGAGCTTGAGACACAGCCTGGCCCAACA 147447
QY 4325 TGGTGAACCCCTATCTCTACTAAAAATACAAAAATTAGCTGGGTGTAGTGATGCATGCCT 4384
Db 147448 TGGTAAAAACCCCTCTCTACTAAAAATGTAAAAATTAGCTGGGTGTGGGTGATGTAACCT 147507
QY 4385 GTAGTCCACGCTACTCGGAGGCTGAGGCAGAGAAATTTGTTGAACTCTGGGAGCAGAGG 4444
Db 147508 GTAAATCCAGCTACTTTGGGAGGCTGAGGCACGAGATTGTTTGAACCCCGGAGATGGATG 147567

QY 4445 TTGCACTGAGCGAGATCCCACTGCACTCCAGCCTGGGCGACACACGAGAGACTCTAT 4504
Db 147568 TTTCACTGAGCGCAAGATTGCACTGCACTCCAGCCTGGGAGACACAGAGTGAGACTGCT 147627
QY 4505 CTCAAAAAATAAATAAATAAATA 4529
Db 147628 CAAAAAATAAATAAATAAATAAATA 147652
RESULT 45
US-10-703-210-33
; Sequence 33, Application US/10703210
; Publication No. US20040121384A1
; GENERAL INFORMATION:
; APPLICANT: Gelb, Bruce D.
; APPLICANT: Niemeyer, Charlotte
; APPLICANT: Tartaglia, Marco
; TITLE OF INVENTION: PIPN11 (SHP-2) Mutations And Cancer
; FILE REFERENCE: 02420/100M124-US1
; CURRENT APPLICATION NUMBER: US/10/703,210
; CURRENT FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/424,170
; PRIOR FILING DATE: 2002-11-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 300000
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(300000)
; OTHER INFORMATION: where n may be a or g or c or t/u, unknown or other
US-10-703-210-33

Query Match 7.8%; Score 387.8; DB 7; Length 300000;
Best Local Similarity 58.0%; . Pred. No. 2.2e-77;
Matches 849; Conservative 1; Mismatches 558; Indels 57; Gaps 7;
QY 3067 CCAAGATCACAGCTTCTGAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTAGAG 3126
Db 146243 CCAACACTGGAAATCATATTTTTCATATCTCTTTTGTGTTGTTTGTGTTGAG 146302
QY 3127 ACAGGCTCTGCTGTGTCACCCAGGCATGAGCACAGTGGTGCACCATAGGTCACCTGACG 3186
Db 146303 AGGAGTCTGCTCTGTCACCCAGGCTGAATTTGCAAGTGGCGGATCTTGGCTCACTGCAA 146362
QY 3187 CTTCAACTCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTAC 3246
Db 146363 CTTCCACCTTCTGGGTTCAAGCAATTTCTCTGCTCAGCCTCTCGAGTAGCTGGAATAC 146422
QY 3247 GAGCGTGCAACCAACGCTGGCTAATTAATAAATAATTTTTTGTAGAGACTGGGTCTTAC 3306
Db 146423 AGACACATGCCACCAACGCTGAGCTAATTTTGTGTA--TTTTTAGTAGAGACAGGGTTTAC 146480
QY 3307 TACGTTGGCAGGCTGTCTTAAACTCTGCTGGCTTCAAGCAATCCTCCTACCTTGGCATCC 3366
Db 146481 CATATTGCTCAGGCTGTTCTTGAATTTCTGACCTCAGGTGATCCACCCGCTCAGCCTCC 146540
QY 3367 CAAAGTCTGGGATTACAGGGGTGAGCCACCATGTGCGGCTACTTATTTCTTTTCAATTC 3426
Db 146541 CAAAGTCTGAGATTACAGGCATGAGCCACACACCCAG-----AGGTTTTTGTATCGT 146594
QY 3427 ATCTTTTCAATAGATGTAAAGTCCACAGACAGGATTACTGCCTATTTTCTTCTTCTTC 3486
Db 146595 TTTTTTGATAGATG-----TC 146613
QY 3487 TTTTTTGACACAGACTCTCACTTCATCACCTCAACCTCCGTTTCAGCTCACTGCAACCTCT 3546
Db 146614 TCTCTGTTGCCCAAGCTGAGTGCAAGTGGCGAATC-----TCAGCTCACTGCAACCTCT 146668
QY 3547 GCCTCCCGGGTTCAAGYGATTTCTCTGCTAAGCCTCTGCTGCTAAGCCTCTGAGTAGCTGGAATTAACAAGCG 3606


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Db 13748 CAGAGAAAGCAGAGTTGAGAGATGGCAAGAGAAAAAT--TGCTAATGTCAATGAGTCAAG 13805
Qy 3036 AAACCTCAGGCTCAGAGGCTGAGCTATTATGCCCCAAGATCACAGAGCTTCTGAAGTGGTGAC 3095
Db 13806 TTCTCGATCCAAACCATACCTGAAGCTGTAATATTCACATTTGTCAATGAGCCTGGGTAGT 13865
Qy 3096 AGTTTGGGTTTTTTTTTTGTTGTTTGTAGAGACAGGCTCTGCTCTGTGTCACCCAGGCATG 3155
Db 13866 AATTTTCCTTTTTTTTTTTTTTTTTTTGGATGGAGTCTCGCTCTGTGTCGCCAGGCTAG 13925
Qy 3156 AGCAGAGTGTGAAACCATAGTCACTGAGCCCTCAACCTCTCTGAGCTCAAGGGATCTGC 3215
Db 13926 AETGCAGTGGCGCAATCTCAGCTCACTGCAAGCTCGCTCTCTGGGTTTCATGCCATTCTC 13985
Qy 3216 TGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCTGACCAACACAGCCTGCTGCTAAATTA 3275
Db 13986 CTGCTCAGCCTCTCTGAGTAGCTGGGACTACAGGTCGCCACCAACAGCCTGCTGCTAATTT 14045
Qy 3276 AAAAAATTTTTTTGTAGAGCTGGGTCTTACTAGCTTGGCCAGGCTTGTCTTAAACTCCT 3335
Db 14046 TTGTGA-GTTTGTAGTAGACAGAGGTTTCACCGTGTAGCCAGGATGGTCTCGATCTCT 14104
Qy 3336 GGCTTCAAGCAATCTCTACCTTGGCATCCCAAAGTGTGGGATTTACAGGGGTGAGCCA 3395
Db 14105 GACCTC--GTGATCCACCCACCTTGGCTCCCAAAGTGTGGGATTTACAGGGGTGAGCCA 14162
Qy 3396 CCATGTGCGGCTACTATTCTTTTACATTCCTTCCATCTTTCCAAATAGATGTAAGATCCACAG 3455
Db 14163 CCGCGCCCGC--CTTATTTTTTTTTTTTTTAAATTTTTTTTTTTTGACAAAG----- 14212
Qy 3456 AACAGGGATTAAGTCTATTTCTTCTTCTTTTGTAGAGAGAGTCTCACTTCAATCAC 3515
Db 14213 -----TCTCATTTCTGTCACCGAGGCTGGAGTGCAAGTG 14245
Qy 3516 CTCAACTCCGTTCACTCACTGCAACCTCTGCTCCCGGGTTCAAGYGAATCTCTCTGCC 3575
Db 14246 CACAATC-----TCTGCTCACTGCAACCTCTGCTCTCGGGTTCAAGCGAATCTCTCTACC 14300
Qy 3576 TAAGCTCTGAGTAGCTGGAATTACAAGGTGCACCAACATGCTTGGCTCAATTTTTTGT 3635
Db 14301 TCAGCTCTGAGTAGCTGGGATTAACAAGCATGTGCCAATGTCCAGCTAA-TTTTTGT 14359
Qy 3636 ATTTTGTAGCAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTC 3695
Db 14360 ATCTTTGTGAGACGGGTTTCATCAGTTGSCCAGGCTGTTCTTGAATCTCTGCGCTC 14419
Qy 3696 AAGTATCTGCTGCTCAGTCTCCAAAGTGTGGAATATATAGGCGTGAGTCACTGTGC 3755
Db 14420 AAGTATCCGCCACCTCGGCTCCCAAAGTGTGGGATTAACAGGCGTGAGCCACCGGAC 14479
Qy 3756 CTGGCGGATTAAGTCTATTTCTTTATTG----- 3785
Db 14480 CCGGCCACTTTTCTTTTGTGTTTATCGTGGGAGTGGTGTGTTTAAATGACTGGCAAAA 14539
Qy 3786 -----CTATATCCCGAGACTAGACAGTGTCTGACATATAGTAGGTGCTCAATAAATA 3839
Db 14540 GAATGTTGATAGCGCTTTCTGCGTAATGTTAAGATCTTGGAAATTTCTGGAATAGCT 14599
Qy 3840 ATTGATG---AATGCACGCTAGATATAAACTTTCTTTTCTTTTAAACCAATCTT 3896
Db 14600 ATGGGGGGAAGCGCTAGGACCTGAGAGTCACTCCCAAATTTATTTATTTATATATTT 14659
Qy 3897 GACAACTTTCAGAAATAAATACAACTTTCGATCTCTTTTCA----- 3940
Db 14660 GTCATAGACGGGAGTCTTGTGCTGCTGCCAGGATGGTCTCAAACTCTCGCCTCAAG 14719
Qy 3941 -----CTTATCACCTTGTATGACTTTTTCATATGCTTTTTCATATGCTCAAACTTTT 3983
Db 14720 AGAACCTCTCGCTCCCGCTCCCAAAGTACTGCGAATACAGGATGAGCGCGAGTGCCTG 14779
Qy 3984 ATTGTTACTGTTTTTTTCAATTTGTTTACTTTTATTTAGTCACTGAATAATATGCTTAAATTTGCT 4043
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Db 14780 GCAGTTCACATTCCTCAATTTGTTAAGAGTCTGAAGCCAGAGACAGTTGGTCTTTTCATGCT 14839
Qy 4044 TATACATCTCTCTGCTCCACTTTTAAAGGCCAAAAATTTTACAAATCTGATGAAAGCTATGAA 4103
Db 14840 CAACTGGGTAGCATGTTGTCAGTGCAGCGAGGGTGCCTAGCACATGAGTGCAGTGAG 14899
Qy 4104 CCCTCTCCCCAGAGAAATACACACACACACACTCACACAGTGTTTTTTTTAAATGT 4163
Db 14900 GTGGCCCTGTGGCAAAACCCAGGAGCTGGAGGGTCCAAAAGGCCACAATAGACTGGGG 14959
Qy 4164 TTGCAACTAAGACAGAAGAACTGCTAGATTAGAGATGTTTGTTCATATTAATTAATAAATAAC 4223
Db 14960 GAGATTTGAAGAGAAAGCCTGAAAACTCAAGGTTTCAAGTATCAGCAAAACCATGGGAG 15019
Qy 4224 TCAGTTGGGCACAGTGAAGTCAAGCCCTGTAACACACAGTACTTTGGAAAGTCCAAAGSTGGGTG 4283
Db 15020 AGGCCAGGTGNAATGGCTGACATCTGTAATCCCGCAGCTTTGGGAGCGGAGGAGGTG 15079
Qy 4284 GATCACTTGAAGTGAAGTTCGAGACCAAGCCTGTGTAATATGTTGGTGAACCTTATCTCTA 4343
Db 15080 GCTCACTGAGTCAAGGATTCGAGACCAAGCCGGTCAACATGGTGAACCCCGTCTCTA 15139
Qy 4344 CTAAAAATACAAAAATTTAGCTGGGTGTAGTATGATGCCTGCTAGTCCAGCTACTCCGG 4403
Db 15140 CTAAAAATACAAAAATTTCCAGGCATGGTGGCAGTGCCTGTAATCCAGCTATTTGGG 15199
Qy 4404 AGGCTGAGGCAAGAAATTTGCTTGAACCTGGGAGGAGAGGTTGCAGTGAGCGGAGATCC 4463
Db 15200 AGGCTGAAGTAGGAGAAATCACTGAACTGAGAGCGGAGGTTGCAGGAGGCAAGATTG 15259
Qy 4464 CACCACTGACTCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAA 4521
Db 15260 CACCATTGCACACAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAATAAATAA 15317
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RESULT 47

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US-10-087-192-58
; Sequence 58, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 61103
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(61103)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-58
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Query Match 7.7%; Score 385.2; DB 5; Length 61103;

Best Local Similarity 59.4%; Pred. No. 3.5e-77;

Matches 869; Conservative 1; Mismatches 499; Indels 95; Gaps 9;

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Qy 3099 TTGGGTTTTTTTTTTCTGTTGTTTGTAGACAGAGGTTCTGTCTGTCAACCCAGGCATGAGC 3158
Db 34982 TTTTATTTTATTAATGTTATTTATTTGAGACAGAGTCTCGCTCTGTCAACCCAGCTGGAGT 35041
Qy 3159 ACAGTGGTGCAACCATAGGTCACTCAGCCTCAACCTCTCTGAGCTCAAGGGGATCTGCTGA 3218
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Db 35042 GCAATGGCACAGTCTCTGCTCACTGCAAACTCCGCGCTCTCTGAGTTCAAGCGATTTCTCCTG 35101
Qy 3219 CTTACGCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACGCGCTGGCTAAATTAATA 3278
Db 35102 TCTACGCTCCCAAGTAGCTGGGATTAACAGGCCATGCGCGTACGCCCGAGCTGATTT--TT 35159
Qy 3279 AAAATTTTTTTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTAAACTCTCTGGC 3338
Db 35160 TTGTATTTAGTAGAAGCGGGTTTCACTGTGTGGCCAGGCTGTCTGACTCTCTGAG 35219
Qy 3339 TTCAAGCAATCTCTCACTCTGCGATCCCAAGTGTGGGATTAACAGGGGTGAGCCACCA 3398
Db 35220 CTGAGGCGAGTCCACCGCGCTTGGCTCTCAAGTGTGTGATTAACAGGCGTGAAGCCACTG 35279
Qy 3399 TGTGGCGCTACTTATTTCTTATCAATCCATCTTTCCAAATAGATGTAAGATCCACAGAAC 3458
Db 35280 CGTCCGCGCCCTTTTTTTT----- 35299
Qy 3459 AGGATTAAGTCTATTTTCTCTCTTTTGTGAGACAGAGTCTCACTTTATCACTCTC 3518
Db 35300 -----TTTAGATGGAGTTTCGCTCTGTAGCCAGGCTGGAGTGCAGTGGCG 35346
Qy 3519 AACCTCGTTTACGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYGAATTTCTCTGCTAA 3578
Db 35347 AAACCTGGT-----TCACTGCAAGCTCTGCTCCCGGTTTCAGGCCATTTCTCTGGCTCA 35401
Qy 3579 GCCTCTGAGTAGCTGGAATTACAAGCGTGCACACCATGCTTGGCTAATTTTTTGTATT 3638
Db 35402 ACCTCCGAGTAGCTGGGACCAAGCGCGCCGACCAAGCGCGGCAATTTTTTGTATT 35461
Qy 3639 TTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTCAAG 3698
Db 35462 TTTAGTAGACCGGGTTTCAACGTTAGCAGAGATGGTCTCGATCTCTGACCT--TG 35519
Qy 3699 TGATCTGCTCTCACTGCTCTCCCAAGTGTGGAATTAAGGCGTGAGTCACTGTGCGCTG 3758
Db 35520 TGATCTGCGCGCTCAGCTCCCAAGTGTGGGATTAACAGGCGTGAGCCACCGCACCG 35579
Qy 3759 GCCGATTACTGTCTATTTTCTTTATTTGCTATAT-----CCCCAGATCTAGAGC 3806
Db 35580 GCTCCCTTTTATTTTATTTGATTTTTTTTTTTTGTGAGGCGAGTCTGCTCTGCTCG 35639
Qy 3807 AGTGTCTGACATATAGTAGGTGCTCAATAATAATGATGAATGCACAGCTAGATATAA 3866
Db 35640 CGAGGCTCGAGTGGGACAGATCTCGGCTCGCTGCAACCTCCACCTCCTGGGTTCAA 35699
Qy 3867 A--CTTTCTTTTCTTTTAAACAACTCTGACAACTTTGAGAAATAAATAAATCTTT 3924
Db 35700 ATGATTTCTCTGCTCAGCTTCTGAGTAGCTGGGATTAACAGGCACACACTACACGCCA 35759
Qy 3925 GCATTTGCTTTTTCACCTATACCTTGTATGACTTTTTCATATTGCGCTCAAACTTTTA 3984
Db 35760 GGCTCTTTTCTTTTCTTTTGGTCAAGAGGGGTTTTTACCATGTCAAGCCAGGTTGGT 35819
Qy 3985 TTGTTACTGTTTTTTCATCTGTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTT 4044
Db 35820 CTCAAACTCTGACAAAGTCTGAGATTACAGCATGAGGCACCTGACCTGGCCTTTTTT 35879
Qy 4045 -----ATACATCTCTCTGCTCCACTTTTAGAAGGCCA--AATTTACAAATCTGA 4090
Db 35880 GCCTTTTTTAAAAAATGTTTTTCTTGTAATTTAGTATGTAATTTCTTTGAAACACCTGA 35939
Qy 4091 TGAAGCTATGAACCTCTCCCGACAGAAATACACACACACACACACTCACACAGT 4150
Db 35940 CTTTCAAGCCAGGCAATGACTCACTGCTGTAATCTCAGCACTTTGGGAAGTCAAGGGGG 35999
Qy 4151 TTTTCTTTTAAATGTTTGAACATAAGACAAAGAACTG-----CATTAGAGGATGTTTGTTC 4205
Db 36000 AGAATCTTTGAGCCAGGAGTTGAAGAACAGCGCTGGGCAACATATAGACACTACTCTC 36059
Qy 4206 ATATTAAATTAATAAATCACTGAGTTGGGCACAGTGAAGTCAAGGCTGTAAACACAGTACTTT 4265
Db 36060 TACAAAAAATAAAAAAATTTGGCCAGGTATGGTGGCTCAGGCTGTAATCCAGCACTTT 36119

Qy 4266 GGAACTCCAAGTGGGTGGATCACCTTGAGGTGAGAAGTTTCGAGACGAGCTTGGTCAATAT 4325
Db 36120 GGGAGGCTGAGGTGGCGGATCGCTTGAGGTCAAGAGTTTGAGACGAGCTTGGCCAAAT 36179
Qy 4326 GGTGAAACCCCTATCTCTACTAAAAATATAAAAAATAGCTGGGTGTAGTATGCATGCTG 4385
Db 36180 GGCAAAACCCCTGTCTCTACTAAAAATACAAAAATGAACTGGGCGTGGTGGCACAATGCTG 36239
Qy 4386 TAGTCCCAAGTACTCGGAGGCTGAGGCAAGAGAAATTCCTTGAACCTGGGAGGCAGAGT 4445
Db 36240 TAAATCCCAAGTACTTTGGAGGATGAGGCATGAAAAATCACTTTGAACCTGGGAGGCAGATG 36299
Qy 4446 TGCAGTGAGCCGAGATCCCAACCACTGCACCTCAGGCTGGGCGACACAGCGAGCTCTATC 4505
Db 36300 TGCAGTGAGCTGGGATTAACCACTGCACCTCAGGCTGGGTGACAGAGTGAGACTCTGTC 36359
Qy 4506 TCAAAAAAATAAATAAATAAATA 4529
Db 36360 TTAATAAAAAAATAAATAAATAAATA 36383

RESULT 48
US-10-482-065-22
; Sequence 22, Application US/10482065
; Publication No. US20040260058A1
; GENERAL INFORMATION:
; APPLICANT: AXARON Bioscience AG
; TITLE OF INVENTION: Novel endothelially expressed DNAs and proteins, and
; FILE REFERENCE: OZ0091/00010-AT
; CURRENT APPLICATION NUMBER: US/10/482,065
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 13104
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-482-065-22

Query Match 7.7%; Score 385; DB 8; Length 13104;
Best Local Similarity 59.0%; Pred. No. 1.6e-77;
Matches 847; Conservative 1; Mismatches 511; Indels 76; Gaps 8;

Qy 3106 TTTTCTTTTGTGTTTGTAGACAGGGTCTTGTCTGTCCACCCAGGCATGACAGCTGG 3165
Db 11400 TATTCTTTTCTCTTTTGTGAGTCTTGTCTGTCCACCCAGGCTGGAGTCCAGTGG 11459
Qy 3166 TGCACCATAGTCTACTGCAGGCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGC 3225
Db 11460 CATGATCTCAGTCTACTGCAACCTCGCTTCTGGGTTCAAGCATTTCTCTGCTTCAGC 11519
Qy 3226 CTCCAAGTAGCTGGGACTACAGCGTGCACCAACCGCTCGCTAAATTT-----AAA 3277
Db 11520 CTCCTGAGTAGCTGGGATTTACAGGCGCCACCAACATGCCAGCTAAATTTTGTGTGTG 11579
Qy 3278 AAAATTTTTTTGTAGAGCTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCTCTGG 3337
Db 11580 GTGTATTTTGTAGAGATGGGGTTTACCATGTTTGGCCAGGCTAGCTTTGAATCTCTGA 11639
Qy 3338 CTTCAAGCAATCCTCTACTCTTGGGATCCCAAGTGTGGGATTAACAGGGGTGAGCCACC 3397
Db 11640 CTTCAAGTATCCACACACTTGGCTCCCAAGTGTGGGATTAACAGGCATGAGCCGCT 11699
Qy 3398 ATGTGCGGCTACTTATTTCTTATTCATTCATCTTTTCCAAATAGAAATGAATCCACAGAA 3457
Db 11700 GTGCCCATCCAATGCTTGGCTTTTCTGATTTT----- 11734
Qy 3458 CAGGGATTAAGTCTTATTTTCTTCTCTTTTGTGAGACAGAGTCTCACTTTCATCACCT 3517
Db 11735 -----TTTTTTTAGAGGAGTTTGTCTTTTCCGCCAGGCTGGAGTACAG 11780

69585	Db	GATACAAATATCAGCTTGGTACATCTGGTCCCAAGTTATAGCAAGTTATAGGGGATTAAGTTTTTA	69523
3876	Qy	TTCTTTTTTAAACCAATCTTGACAACTTTGACAGATAAATAACAATCTTGCAATCTCGCTT	3935
69525	Db	AATGGCAAGTAGGGCATTTGTATCAGAAATGCAACTTGTGTGGGAACCTTAATGCTTATC	69466
3936	Qy	TTTCACTTATATCAGCTTGTATGACTTTTTCATATTTGCCCTCAAACTTTATTTGTTTACTGTT	3995
69465	Db	CTGGGAAGAAAAAGAGAGAGAAAAATAGAAATCTCTACTATTCTCTCTTAACCTTCTCAA	69406
3996	Qy	TTTTTCATTTGTTACTATTTTGTAGTCACTGAATAATATGGCTTAATTTGCTTATACATCTCTCC	4055
69405	Db	ATATGGCTCTAGCCCCAATTTATCTATATAGAACCTTACCAAGAGAGACCCAGGACCACCT	69346
4056	Qy	TGCTCCACTTTTAGAAGGCCAAATTTTACAAATCTGTATGAAGCTATGAACCTCTCTCCACG	4115
69345	Db	TAACTTAAATGCAATAGTCTTCTCTCCATCTTTTCCATTTGCTCTGAGGCATGGGAATCT	69286
4116	Qy	AGAAATACACACACACACACACTCACACACAGTTTTTTTTTAAATGTTGCACTAAAGA	4175
69285	Db	GCTCATCTGTGCATGCCATTCCTCAAGTTGAGAATGATGGGCATTCCTTTTCT-----	69236
4176	Qy	CAAGAAACCTGCATATAGAGATGTTTGTTCATATTAATTTAAAAATAAATCAGTTGGGCAC	4235
69235	Db	-----CTCTCTCATCTCTCATGATAATCATTAAGATTCCCCTACAGGCGGGGAC	69184
4236	Qy	AGTGACTCAAGCCTGTAAACACAGACTTTTGGAGTCCAAAGTGGGTGGATGCACTTGAGG	4295
69183	Db	AGTGGCTCAGCCTCTGTAATCCACAGCACTTTGAGGCTGAGGTGGGCCGATCACA--AGG	69126
4296	Qy	TGAGAAAGTTTCGACACAGCAGCTTGCTCAATATGTTGAAACCTTATCTCTACTAAAAATAC-A	4354
69125	Db	TCAGGAGATTGAGACCATCCCGCTAACATGGTGAACCCCGTCTCTACTAAAAATACAA	69066
4355	Qy	AAAAATTAGCTGGGTGTAGTATGCATGCCCTGTAGTCCCAAGCTACTTCGGGAGGCTGAGGCA	4414
69065	Db	AAAAATTAGTCAGCATGGTGGTACACGCTGTAGTCCCAGCTACGTCGGGAGGCTGAGGCA	69006
4415	Qy	AGAGAAATTCCTTGAACCTCGGAGGACAGGTTGCAGTGAGCCGAGATCCCACCTGCGAC	4474
69005	Db	GGAGAAATCGCTTGAACCTTGGGAGGACAGAGGTTGCAGTGAGCTGAGATCACACCATTTGCAT	68946
4475	Qy	TCCAGCCTGGGCGACACAGCGAGACTCTATCTCAAAAAAATAAATAAATAAATAAAGGA	4534
68945	Db	TCCAGCCTGGGCAACAGAAATGAGACTCCGCTCAAAAAAATAAATAAATAAATAAATAA	68886
4535	Qy	TCGGAGAGAAAAAAACTAATAAGATTCTCTGAAGGTAAAGCAGAGATACGTAA	4586
68885	Db	ATAATAATAATAAAAAAGATTCCCACTCCATTTCTTTAAAAAATAAAAAAATAAAAAA	68834

RESULT 50

US-10-741-601-5712/c

US 10 741 601 571270
; Sequence 5712, Application US/10741601

; Publication No. US20040166519A1

; GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER:

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ

; SOFTWARE: Fast

; SEQ ID NO 5712

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; LENGTH: 73237
; TYPE: DNA

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TYPE: DNA

Query Match

Query Machine 7.7%, Score 504.4, SD 1, Length 15257,
Best Local Similarity 58.8%; Pred. No. 6.6e-77;

Local similarity score, 1.00	Indels	Gaps
Matches 898; Conservative 3; Mismatches 526;	100;	10;

QY 4113 CAGAGAAATACACACACACACACACTCACACACAGTTTTTTTAAATGTTTGCACATA 4172
Db 16474 TGCCCACTATATATATTATTGCTACAAATTTAGCGAAATATACAAAATCCCTTCTATTTC 16415
QY 4173 AGACAAGAAACCTGCATTAGAGAGATGTTTGTTCATATTAATTAATAAATCACTCAGTTGGG 4232
Db 16414 ATGGTTTCATAAAAGTTATTATTAGATTATTAAATCTACACATTTAAATTAATGAGGCCAGG 16355
QY 4233 CACAGTGACTCAAGCCTGTAACACACAGTACTTTTGGGAAGTCCAAGGTGGGTGGATCACTTG 4292
Db 16354 CATGGTGGCTCACTCTCTATNATCCAGCATTTTGGAGGCTGAGATGGCGGATCACTTG 16295
QY 4293 AGGTGAGAAGTTCCGAGACCAAGCCTGGTCAATATGTTGAACCCCTCTCTACTTAAATAAATA 4352
Db 16294 AGGTGAGGAGTTTGGAGACCAAGCCTGGCCAAACGTTGATGAACCCCTCTCTACTTAAATAA 16235
QY 4353 CAAAAATTAGCTGGGTGTAGTATGATGCTGTAGTCCAGCTACTCGGAGGCTGAGG 4412
Db 16234 CAAAAATTAGCTGGGCTCATGGCACATGCTGTAAATTCAGCTACTCAGGAGGCTGAGG 16175
QY 4413 CAAGAGAAATTTGCTTTGAACCTGGGAGGCAGAGTTGCGAGTGGCCGAGATCCCAACCACTGC 4472
Db 16174 CAGGAGAAATCATTTGTGCTCCAGAGGAGAGGTTGCGAGTGGCCAAAGATCATGCCCACTGC 16115
QY 4473 ACTCCAGCCTGGCGACACACAGCAGACTCTATCTCAAAAAATAAATAAATAAATAAAG 4532
Db 16114 ACTTCAGCCTGGGCAACACACAGTGGAGTCTGTCTCAATAAAAAAATAAATAAATAAAT 16055
QY 4533 GATCGGAGAGAAACAAACTAATAAGA 4559
Db 16054 AAAAAATAAATCAATTAATAATGA 16028

RESULT 51

US-09-997-722-22/c
; Sequence 22, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 96594
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (659)..(1103)
; OTHER INFORMATION: "n" at positions 659 through 1103 can be any base.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (13097)..(13318)
; OTHER INFORMATION: "n" at positions 13097 through 13318 can be any base.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25404)..(26575)
; OTHER INFORMATION: "n" at positions 25404 through 26575 can be any base.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (66626)..(66645)
; OTHER INFORMATION: "n" at positions 66626 through 66645 can be any base.
US-09-997-722-22

Query Match

7.7%; Score 383.4; DB 3; Length 96594;

Best Local Similarity 59.6%; Pred. No. 1.2e-76;
Matches 859; Conservative 1; Mismatches 487; Indels 94; Gaps 9;
QY 3098 TTTGGGTTTTTTTTTTGTTGTTCTTTAGAGACAGGGTCTTGCTCTCTCACCAGGATGAG 3157
Db 12948 TTTTGTGTTTTTTTTTTTTTTTTTTTGTGACAGAGTCTGCTCTGTCAACCCAGGCTGGAG 12889
QY 3158 CACAGTGGTGCACCATAGGTCACTGCGACGCTTCAACCTCTCTGAGCTCAAGGATCTGCTG 3217
Db 12889 TGCAGTGGCACAATCTCAGCTCACTGCAACGCTCTGCTCCCGGTTTAAGGGATCTCTCT 12829
QY 3218 ACCTCAGCCTCCCAAGTGTGGGACTAGAGCGGTGACCAACACGCTCGCTGCTAATATAA 3277
Db 12828 GCCTCAGCCTCCCAATAGTGGGACTAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 12769
QY 3278 AAAATTTTTTTGTAGAGTGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCCTCG 3337
Db 12768 TTGTATATTTAGTAGAGTGGGTTTTCACCATGTTGGCCAGGCTGGTCTCAAAC----- 12715
QY 3338 CTTCAAGCAATCCTCTTACCTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACC 3397
Db 12714 --TCAGGCATTTGGCCACCTCAGCTCCCAAGTGTGGGATTTACAGGCATGAGCCACT 12657
QY 3398 ATGTGCGGCTACTTATTTTCTTACATTCATCTTTTCCAAATAGAAATGAATGCCACAGAA 3457
Db 12656 GTGCTGGCCAAAACCACTTTTCTTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 12621
QY 3458 CAGGATTTACTGCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3517
Db 12620 -----TTTATCTTTGGGACAGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 12587
QY 3518 CAACCTCGTTTCA-----GCTCACTGCAACCTCTGCTCTCCCGGTTCAAGYGATCTCTCC 3571
Db 12586 AGGCTGGAGTACAATCAAGGCTCACTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 12527
QY 3572 TGCTTAAGCCTCTCAGTAGTGTGAATTAACAGCGTGCAACCACTGCTGTGGCTTAATTTT 3631
Db 12526 CACCTCAGCCTCCCAAGTAGCTGGGACTACACATGTGCTTCAACCAAGCTGGCTAATTTCT 12467
QY 3632 TTGTATTTTAGCAGAGA-TGGGGTTTTACCATGTTGCCAGGCTGGTCTCAACTCTCTG 3690
Db 12466 TTGATTTTTTTGTAGAGACAGGGGTCTTACTATGTTGCCAGGCTAGTCTTGAATCTCTG 12407
QY 3691 ACCTCAAGTGATCTGCTGCTCTGCTCTCCCAAGTGTGGAAATTAATAGGCTGAGTCAAC 3750
Db 12406 GGCTCAAGTGATCTCTCCCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 12347
QY 3751 TGTGCTGCGGATTAAGTGTCTTATTTCTTATGCTATATCCCGAGATCTAGAGCAGTG 3810
Db 12346 CCGGCCAGCCAAAACCACTTTCTTATCAACATGATTAAT-----GTTTTATAACATG 12293
QY 3811 TCTGACATATAGTAGTGTCTCAATAAATTAATGATGAATGCACAGCTAGATATAAATTT 3870
Db 12292 TATTAATAAATTAATGATATCAATATATCTGCTACCCCAAGAGACAGAGATAAAC-- 12235
QY 3871 TCTTTTCTTTTTTAAACCAATCTTGACAACTTTTGACAAATAAATAACAATCTTGCAATTC 3930
Db 12234 -----CCCAAACTAGACATGAATATAAATACTTTTCTGCTCTCTACTT 12189
QY 3931 TGCTTTTTCACTTATCACTTGTGTTAGCTTTTTTCAATATGCTCTCAAACTTTATGTTTA 3990
Db 12188 TGTGTTTAGTTTGGGAAGTAATACTGTAGCTTTTGAACAAGAGACAAATCTTACTCAACC 12129
QY 3991 CTGTTTTTTCATGTTACTATTTTGTAGTCACTGAATAATATGCTTAAATTTGCTTATACAT 4050
Db 12128 AAAAACTTAAAGTGTAGCAGTAATGTA--GGAAATTTCTGCCATATATTTTATAAATAC 12071
QY 4051 CTTCTGCTCCACTTTTAGAAGGCCAAATTTTCAAAATCTGATGAAAGCTATGAACCTCTC 4110
Db 12070 TATAGAAATACATAAGGCCCAAGAAATCAGAGTATTTTAAAAAGATACTGTATGAGACA 12011
QY 4111 CCCAGAGAAATACACACACACACACTCACACAGTTTTTTTTTAAATGTTTGGCAAC 4170

Db 12010 AAATAAACATTCACCTACAACACAGAGAGGTGACAAATAAAAAATGACATTTTATTGAAA 11951
Qy 4171 TAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATAAAAAATACTCAGTTG 4230
Db 11950 TGAGGGATTTAGGTGACGTATTAAAAATAACTTCTTACATGCATAGATTATTA---TCAGCCA 11895
Qy 4231 GGCACAGTGAATCAAGCTGTACCAACAGTACCTTTGGAAAGTCCAAAGTGGGTGATCACT 4290
Db 11894 GGCATGTGTCTCAGCGCTGTAAATCCCAACACTTTGGGAGACCAAAAGCGGTGGATCAC 11835
Qy 4291 TGAGGTGAGAAGTTTCAGAGCCAGCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAA 4350
Db 11834 TGAAGTCAGGAGTTTCAGAGTACGCCGCCCAACATGTTGAAACCTGTCTCTACTAAAAA 11775
Qy 4351 TACAAAAATTAGTGGGTAGTGATGCATGCTGTAGTCCCAAGCTACTCGGGAGGCTGA 4410
Db 11774 TACAAAAATTAGTGGGCATGGTGGCATGTGCTGTAAATCCAGCTACTAGGTAGGCTGA 11715
Qy 4411 GGCAGAGAGATTGCTTGAACCTGGGAGGACAGGTTGCAGTGAGCCGAGATCCACCACT 4470
Db 11714 GGCAGAGAGATCACTTGAACCCGGGAGGACAGGTTGCAGTGAGCCGAGATTTGTCACCT 11655
Qy 4471 GCACTCAGGCTGGGCGAC-ACAGCGAGACTCTATCTCAAAAAATAAATAAAAAATA 4529
Db 11654 GCACTCAGGCTGGGCAACAGAGCAAAACTCCATCTCAAAAAAAAAGCATAGATTATC 11595
Qy 4530 A 4530
Db 11594 A 11594

RESULT 52

US-10-322-281-314
; Sequence 314, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 52945201000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 314
; LENGTH: 227246
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(227246)
; OTHER INFORMATION: n = A, T, C or G
US-10-322-281-314

Query Match 7.7%; Score 383.4; DB 7; Length 227246;
Best Local Similarity 59.6%; Pred No. 1.9e-76;
Matches 885; Conservative 1; Mismatches 542; Indels 57; Gaps 12;

Qy 3099 TTGGGTTTTTTTTTTGTTGTTTAGACAGAGGTTCTGCTGTGTCACCCAGGCGATGAGC 3158
Db 138536 TTTTCCTTCTTTTTTTTTTTTTTTTGTAGATGGAGTCTCACTGTGTCACCCAGGCTGGAGT 138595

Qy 3159 ACAGTGTGCAACATAGGTCACTGACGCTCAACCTCTCTGAGCTCAAGGGATCTGCTGA 3218
Db 138596 GCAGTGTGGGATCTCTGCTCACTGCAAGCTCCACCTCCCGGGTTTCAACGCAATTCCTCTG 138655

Qy 3219 CCTCAGCCTCCCAAGTAGCTGGACGTACGAGCGTGCACCAACCAACGCTGGCTAAATAAAA 3278
Db 138656 CCTTAGCCTCCCGAGTAGCTGGAGACTACAGCGCCGCCACACACTGGCTAAATTTTTT 138715

Qy 3279 AAAATTTTTTTGATAGACTGGGTCTTACTACTAGTTGGCCAGGCTGTGCTTAAACTCTCTGC 3338
Db 138716 GTA-TTTTTGTAGAGAC-GGGTTTTCATCGTGTAGCCAGGATGGTCTTGATCTCTCTGAC 138773

Qy 3339 TTCAGCAATCCTCCTACCTTGGCATCCCAAGTCTGGATTACAGGGTGCAGCCACCA 3398
Db 138774 CTCCTG--ATCGGCCCACTCGGCTCCCAAAGTCTGGATTACAGGGTGCAGCCACCG 138831

Qy 3399 TGTGCGGCTA-CTTATTTCTTTTACATTCGATCTTTTCCAAATAGAATGTAAGATCCACAGAA 3457
Db 138832 CACCGCGCAGAAATAAATTCGTTAAAGAAATCATCACTAAATAGATACCACTTTCT 138891

Qy 3458 CAGGGAATTAAGTCTATTTTCTCTCTTTTGGAGACAGAGTCTCACTTCATCACT 3517
Db 138892 TTTTCTTTTCTCTCTTTTTTTTTTTTTTTTCCAAAGCGAGTCTTGCTGTCTGCC 138951

Qy 3518 CAACTCCGTTCA-----GCTCACTGCAACCTCTGC-CTCCCGGGTTCAAG 3562
Db 138952 AGGCTGGAGTCAGTGGCGCGATCTTGGCTCACTGCAACCTCCGACCCCGAGATTTAAG 139011

Qy 3563 YGATTTCTCTGCTAAGCTCTCTGAGTAGCTGGAATTAACAAGCGTGCAACCATGCTTG 3622
Db 139012 CAATTTCTCTGCTCAGCTCCCGAGTAGCTGGGATTACAGGTGCTGCCCCACACCCA 139071

Qy 3623 GCTAATTTTGTATTTTGTAGCAGAGATGGGTTTTTCAATGTTGCCAGGCTGTCTCA 3682
Db 139072 GCTAATTTTT--GTATTTTAGTAGAGATGCTGTTTTCACCATGTTGGCCAGGCTGCTCG 139129

Qy 3683 AACTCCTGACCTCAAGTGATCTGCTGCTCAGTCTCCCAAGTCTGGAATTAATAGGCG 3742
Db 139130 AACTCCTGACCTAAAGTGATCTGCCCTTGGCCCTCCCAAACTCTGGAATTAACAGGA 139189

Qy 3743 TGAGTCACTGTGCTGGCGGATTAAGTCTGCTATTTTCTTTTATTTGCTATATATCCCACTTA 3802
Db 139190 TGAGCCACTGACCTGGCCCTGAGATACCACTTTC-TTAGGACTATAACCAACACAGACA 139248

Qy 3803 GAGCAGTGTCTGACATATAGTAGGTGCTCAATAAATAATTAATGATGAATGCACAGCCTAGAT 3862
Db 139249 GATAATAAGTGTGGTAGGATGTGGAGAAATTGGAGCCTTCATACCACTGGTAGGAA 139308

Qy 3863 ATAACTTTCTTTTCTTTTTTAAACAATCTTGACAACCTTTGCAGATAATAACAATC 3922
Db 139309 CGTAAATGGTGAAGTCACTGTGGAACCAAGCATGGTGGTCTCTCAAAAAATCAAAAT 139368

Qy 3923 TTGCAATTCGCTTTTTCACCTTATCACTTTGTTATGACTTTTTTTCATATTTGCCCTCAAACT 3982
Db 139369 AGGCTGGGTGGGTGGCAGATGCTGTAATCTCAGCATTTTGGGAGGCTGAGCAGGCGAT 139428

Qy 3983 TATTGTTACTGTTTTTTCATTTGTTACTATTTTAGTCACTG-----AATAATATGG 4032
Db 139429 CACCTGAGTGGATGTGAGACTAGCCTGGCCCAACATGGTGAAATCTCTACTAAAAATA 139488

Qy 4033 CTTAATTTGCTTATACATCTCTCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATG 4092
Db 139489 TAAAAATTAATCTAGGTATGGTGGCGGGCCCTGTAATTTCCAGCTACTCTGGAGGCTGAG 139548

Qy 4093 AAAGCTATGAACCTCTCCCCAG----AGAAATACACACACACACACATCAACACACA 4148
Db 139549 CAGGAGAAATTAATGAAACCCAGGAGGAGAGGTTCAGTGAGCCCAAGATCATGCTACTGA 139608

Qy 4149 GTTTTTTTTAAATGTTTGGCACTAAGACAGAAACCTGCATTTAGAGGATGTTGTTTCATA 4208
Db 139609 GCCAAGACTACACCACTGCACTCCAGCCTGGGCCAACAAAGTAGAGACCTTATCTCAAAAAG 139668

Qy 4209 TTAATAA-AAAATACTCAGTTGGGCACATGCTCAAGCCTGTAAACACAGTACTTTTGG 4267
Db 139669 AAAACAAACAAAAAGTAGGCCCAAGTGGTGGCTCAAGCCTGTAATCCAGCAGCTTGG 139728

Qy 4268 AAGTCCAAAGGTGGGTGGATCACTTTGAGGTGAGAAGTTCCAGACCAAGCCTGGTCAATATGG 4327
Db 139729 GAGGCGAGGCGGCGGATCACTGAGGTGAGGAGTTTGAACCAAGCCTGGGCCAATTTG 139788

Qy 4328 TGAACCCCTATCTCTACTTAAAAATACAAAAATTAGTGGGTGTAGTGATGCTGCTGTA 4387
Db 139789 CGAAACCCCTGCTCCCTACTTAAAAATACAAAAATTAGCAGGTGGTGGCCAGCTGCTGTA 139848

QY 4388 GTCCAGACTACTCGGAGGCTGAGGCAAGAGAAATTCCTTGAACCTGGGAGGCGAGGTTG 4447
|||||
Db 139849 ATCCAGATACCTAGGTGCTGAGGCGAGGAGAAATTCCTTGAACCTGGGATGCGAGGTTG 139908
QY 4448 CAGTGAAGCGAGATC-----CCACACTGCACTCCAGGCTCGGGCGA 4488
|||||
Db 139909 CAGTGAAGCGAGATCAGTCTGAGCCAGAAATTCACCACTGCACTCCAGGCTCGGGCAA 139968
QY 4489 CACAGGAGACTCTATCTCAAAAAATAAATAAATAAATAAAGG 4533
|||||
Db 139969 CAAAGTGAGACCTTATCTCAAAAGAAACAAACAAAGTAGG 140013

RESULT 53

US-09-764-877-3770/c
; Sequence 3770, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3770
; LENGTH: 6892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3770

Query Match 7.6%; Score 382.2; DB 3; Length 6892;

Best Local Similarity 60.1%; Pred. No. 5e-77;
Matches 893; Conservative 1; Mismatches 504; Indels 89; Gaps 12;

QY 3087 AGTGTGACAGTGTGGGTTTTTTTTTTGTTGTTTGTAGAGACAGGCTCTGTCTGTAC 3146
Db 6148 ACTTTTAAATTTTATTTTATTTTATTTTATTTGAGATGGAGTCTCCCTCTGTCTTAC 6089
QY 3147 CAGGATGAGCAGTGTGTGCAACATAGTCTGACGAGCTTCAACCTCTCTGAGCTCAA 3206
Db 6088 CCAGGCTGAAGTGCAGTGGCACAATCTGACTCACTGCAGCCTCCGCCCTCTCGGTTCAA 6029
QY 3207 GGGATCTGCTGACCTCAGCTCCCAAGTAGCTGGGACTACGCGTGCACACCGCT 3266
Db 6028 GCAATTTCTCTGTCTCAGCCTCCCGAGTAGCTGGGACTACGCGTGTGCCAACACCC 5969
QY 3267 GGCTAATTAATAAATTTTTTTGTAGAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCT 3326
Db 5968 GGCTAATTTTGTATTTTGTAGAGACAGGTTTCAACATGTTGGCCAGGCTGTCT 5910
QY 3327 TAACTCTCGGTTCAAGCAATCTCTACCTTGGCATCCCAAGTGTGGGATTCAGG 3386
Db 5909 CAAACTCTGACCTCAGTGCATCCACTGCTCGGCTCCCAAGTGTGGGATTCAGG 5850
QY 3387 GGTGAGCCACCATGTGGGCTACTTATTTTACATTCATCTTCCCAATAGATGTA 3446
Db 5849 CGTGAACCGCATGCTTGGCCCAAGGTAATTTCTATACCATGTAAGGAAACATAG 5790
QY 3447 GATCCACAGAACAGGATTAAGTCTGCTTATTTTCTTCTTTTGTAGACAGAGTCTCA 3506
Db 5789 GCAAGTGATTCAGCTAGCTTTTGTGAGATGGAGTTTGTCTT---GTTGCCAG 5734
QY 3507 CTTATCATCTCAACTCCGTTTCAAGTCTCACTGCAACTCTGCTCCCGGTTTCAAGYAT 3566
Db 5733 GCTGGAGTGAATGGACGCTCTCGTTTACTGCAACTCTCACTTTCCGGGTTTCAAGTAA 5674
QY 3567 TCTCTGCTTCAAGCTTCAAGTGTGGGATTTTACAAAGTGTGCACCACTGCTTGGCTA 3626
Db 5673 TCTCTGCTTCAAGCTTCAAGTGTGGGATTTTACAAAGTGTGCACCACTGCTTGGCTA 5614
QY 3627 A-TTTTTTGTATTTTGTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGTCTCAAC 3685

Db 5613 ATTTTTTGTATTTTGTAGATGGGTTTCCCATGTTGGCCAGGCTGTCTCAAC 5554
QY 3686 TCCTGACCTCAAGTATCTGCTCAGTCTCCCAAGTCTCTGGAATTAAGCGTGA 3745
Db 5553 TCCTGGCTCAACTGATCCACTGTCTCAGGCTCCCAAGTCTGGGATTAAGGATGA 5494
QY 3746 GTCAGTGTGCTGGCCGATTAAGTCTATTTTCTTTTATTTGCTATATCCCCAGATCTAGAG 3805
Db 5493 GCCACTGCGACCAAGCCCA--GCTAGCTTTTATCTAGTCTTAATGTTTCATANAATTCAC 5436
QY 3806 CAGTGTCTGACATATAGTAGGTGCTCAATAAATAAATAAATGATGAATGCACAGCCTAGATATA 3865
Db 5435 TATTC-----CAACAAAGATTTTATCATATAAGCC-----5404
QY 3866 AACTTTCTTTTCTTTTAAACAATCTTGACAACTTTTGACAGATATAAACAATCTTG 3925
Db 5403 -----TTATGCTGAGATCATATCTTACATGTCTCATGTAATAACATACTG 5359
QY 3926 CATCTGCTTTTCTACTTATCACCTTGTATGACTTTTTCATATTCCTTCAACCTTTAT 3985
Db 5358 CAAAC-----TCTCCTTTAGGNAATTAGAGCCAGAGAAATTAATTTACCTTCAACCTCAC 5304
QY 3986 TGTTACTGTTTTTTCATTTTACTTATTTTAGTCACTGAATAATATGCTTAATTTGCTTA 4045
Db 5303 AGTTTCAGATAGCTGGAGTTGATTTCCAAAGAGGGCTGGGAATGAGAAATGAACAA 5244
QY 4046 TACATCTCTCTGCTCCACTTTAGAGGGCCAAATTTTACAAATCTGATGAAGCTATGAC 4105
Db 5243 TATATAGGATGCTATGCTTACCAAAAAATCAATTTTATATTTGATAGTATGATAAC 5184
QY 4106 CTCTCCCCAGAGAAATACACACACACACACTCACACAGTTTTTTTTTTAATGTTT 4165
Db 5183 TTAT-----ATAGCACTATCAGGCTGAAGGCCAGCTCACTGCATTCATACAAAC 5133
QY 4166 GCAACTAAGACAAAGAACTGCAATTTAGAGATGTTTGTTCATATTAATTTAAATAAATCTC 4225
Db 5132 ACTACTTAGGAAA-----ACTAAAGGTATTTCTGATGTAAAAAGAACAAACAA 5085
QY 4226 AGTTGGCCAGAGTACTCAAGCTGTAAACCAGTACTTTTGAAGTCCCAAGGCTGGTGA 4285
Db 5084 GGCCAGCGTGGTGTGCTCATGCTTATATCCAGCACTTTTGGGAGACCGAGGCTGGTGA 5025
QY 4286 TCACCTGAGGTGAGAAAGTTTCAGACAGCAGCTGGTCAATATGTTGAACCTTCTCTACT 4345
Db 5024 TCACCTGAGGTGAGAAAGTTTCAGACAGCAGCTGGTCAATATGTTGAACCTTCTCTACT 4965
QY 4346 AAAAAATAC-AAAAATTAGCTGGTGTAGTATGCAATGCTGTAGTCCCAAGCTTCTGGGA 4404
Db 4964 AAAAAATACAAAAATTAGCCAGGATGTTGGTGGTGTGCTGTAATCCCAAGCTTCTGGGA 4905
QY 4405 GGCTGAGGCAAGAGAAATTTGCTTGA-----ACCTGGGAGGAGGTTTCAGCTGAGC 4455
Db 4904 GGCTGAGACAGAGAAATCAGTGGAGGTTTCAGTGGAGGTTTCAGCTGAGC 4845
QY 4456 CGAGATCCCACTGCACTCCAGCTGGGCGACACAGCAGACTCTATCTC--AAAAA 4513
Db 4844 TGAGATCGGCGCACTGCACTCCAGCTGGTGCACAAATGCAGATGCTATCTCCAAACAA 4785
QY 4514 ATAAATAAATAAAGGATTCGGAGAGAAACAAACTTAATAGAT 4560
Db 4784 ACAAACAAACAAACAAACAAACCAAGCTTACTATATACTAAGAGTT 4738

RESULT 54

US-10-242-515-3770/c
; Sequence 3770, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515

; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3770
; LENGTH: 6892
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-242-515-3770

Query Match 7.6%; Score 382.2; DB 6; Length 6892;
Best Local Similarity 60.1%; Pred. No. 5e-77;
Matches 893; Conservative 1; Mismatches 504; Indels 89; Gaps 12;

Qy 3087 AGTGGTGACAGTTGGGTTTTTTTTTTGTTGTTGTTAGAGACAGGCTTGTCTCTCAC 3146
Db ACTTTTAAAAATTTTATTTTATTTTATTTTATTTGAGATGGAGTCTCCCTCTGTCTTAC 6089

Qy 3147 CCAGGCATGACAGTGGTGCACCATAGGTCACTGCAGCCTCAACCTCTGAGTCAA 3206
Db CCAGGCTGAAGTGCAGTGGCACAACTCTGACTCACTGCAGCCTCCCGCTCTCGGTCAA 6029

Qy 3207 GGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGTGCACCAACGCT 3266
Db GCAATTTCTCTGCTCAGCCTCCGAGTAGCTGGGACTACGAGCGTGCACCAACACCC 5969

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Qy 3327 TAAACTCTGGCTTCAAGCAATCTCTACCTTGGCATCCCAAGTCTGGGATTACAGG 3386
Db CAAACTCTGACCTCAGGTGATCCACTGCTCGGCTCCCAAGTCTGGGATTACAGG 5850

Qy 3387 GGTGAGCCACCATGTGGGCTACTTATTTCTTACATTCCTCTTCCAATAGAAATGTA 3446
Db CGTGAACCGCATGCTTGGCCCAAGGTAAATATTTCTATAACAGTATAAGGAAACATAG 5790

Qy 3447 GATCCACAGAACAGGATTAAGTCTTATTTTCTTCTTCTTTTGTAGACAGAGTCTCA 3506
Db GCAAGTGATTCAGTAGCTTTTATTTTGTAGATGGAGTTTGTCTT---GTTGCCAG 5734

Qy 3507 CTTTCATCACCTCAACCTCCGTTCCAGTCACTGCACTGCTGCTCCCGGTTCAAGYAT 3566
Db GCTGGAGTGAATGGCAGGCTCTGTTTACTGCAACTCCACTTTCCGGGTTCAAGTAAT 5674

Qy 3567 TCTCTGCTTAAGCCTCTCAGTAGCTGGAATTAACAAGCGTGCCACCACCATGCTTGGCTA 3626
Db TCTCTGCTCAGCCTCCCAAGTAGCTGGGATTACAAGTGCCACCACCATGCTGGCTA 5614

Qy 3627 A-TTTTTTGTATTTTGTAGCAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAC 3685
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Qy 3686 TCCTGACCTCAAGTGATCTGCTGCTCAGTCTCCAAAGTCTCGAAATTATAGGCTGA 3745
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Qy 3746 GTCACTGTGCTGGCCGATTACTGTCTATTTTCTTTTATTTGCTATATCCCCAGATCTAGAG 3805
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Qy 3806 CAGTGTCTGACATATAGTAGGTGCTCAATAATAATTAATGAATGACACGACCTAGATATA 3865
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Qy 3866 AACTTTTCTTTTCTTTTAAAAACAATCTTGACAACTTTTGACAGATAAATAACAATCTTG 3925
Db -----TTATGCTGAGATCATATCTTACATGCTCATCAGTAAATTAACATACTG 5359

Qy 3926 CATCTGCTTTTTCATCTATACCTTTGTTATGACTTTTTCATATTTGCCCTCAAACTTTAT 3985
Db CAAAC-----TCTCCTTTAGGAATTAGAGCCAGAGAAATTAATTTACCTTCAACCTCTCAC 5304

Qy 3986 TGTACTGTTTTTTCATTTGTTACTATTTTAGTCACTGAATATATATATGGCTTAATTTGCTTA 4045
Db AGTTTTCAGAATAGCTGGAGTTGATTTCCAAAGAGGGCTGGGAATGAGAACATGAACAAA 5244

Qy 4046 TACATCCTCCTGCTCCACTTTTGAAGGCCAAATTTTACAAATCTGATGAAAGCTATGAACC 4105
Db TATATAGGATGCTATGCTACCAAAAAAATCAATTGATTTTATATTTAGATTAGTAAAC 5184

Qy 4106 CTCTCCCCAGAAATACACACACACACACACACACACACACACACACACACACACACAC 4165
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Qy 4166 GCAACTAAGACAGAAACCTGCAATTTAGAGGATGTTGTTGTTTATTAATTAATAAATAACTC 4225
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Qy 4226 AGTTGGGCACAGTACTCAAGCCTGTAACCAAGTCTTTGGAAGTCCAAAGTGGGTGA 4285
Db GGCAGAGGCTGGTCTGCTATGCTATATATCCAGCACTTTGGGAGACCGAGCGGGTGA 5025

Qy 4286 TCACCTTGAAGTGAAGTTTCGAGACAGCCTGGTCAATATATGGTGAACCCCTATCTCTACT 4345
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Qy 4346 AAAAAATAC-AAAAATAGCTGGGTGTAGTGTAGTGCATGCTGTAGTCCAGCTACTCGGA 4404
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Qy 4405 GGCTGAGGCAAGAGAAATGCTTGA-----ACCTGGAGGCAGAGGTTGCAGTGAGC 4455
Db GGCTGAGACACAGAAATCACGTGAGGTGGAGGTTGCAGTGAGGTGCAGTGAGC 4845

Qy 4456 CGAGATCCACACACTGCACTCCAGCCTGGCGACACAGGAGACTCTATCTC--AAAAA 4513
Db TGAGATCGCGCACCTGCACCTCCAGCCTGGGTGACAAATGCAAGATGCTATCTCCAAACAA 4785

Qy 4514 ATAAATAAATAAATAAAGGATCGGAGAGAAACAACTTAATAAGAT 4560
Db ACAAAACAAACAAACAAACAAACCAACCACTTACTATAACTAAGAAGTT 4738

RESULT 55
US-10-699-941-10
; Sequence 10, Application US/10699941
; Publication No. US20040146900A1
; GENERAL INFORMATION:
; APPLICANT: Burmeister, Margit
; TITLE OF INVENTION: Ataxia Associated Gene and Protein
; FILE REFERENCE: UM-08441
; CURRENT APPLICATION NUMBER: US/10/699,941
; CURRENT FILING DATE: 2003-11-03
; NUMBER OF SEQ ID NOS: 62

Query Match		7.6%;	Score 382;	DB 7;	Length 59884;
Best Local Similarity		60.1%;	Pred. No. 1.9e-76;		
Matches 901;		Conservative	1;	Mismatches 521;	Indels 77; Gaps 13;
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DB	32585	TAGTTTTGTTGTTGTTGTTGTTGAGATGGAGTCTCACTCTGTCAACCCAGGCTGGAG	32644		
QY	3160	CAGTGGTGCACCATAGTACATGCGAGCCTCAACCTCCTGAGCTCAAGGGATCTGCTGAC	3219		
DB	32645	CAGTGGCAGCATCTGGCTCACTGCAACCTCCGCTCCGGGTTCAAGCGATTCTCCTGC	32704		
QY	3220	CTCAGCCTCCCAAGTAGCTGGGACTAGAGCGTGACACCAACCGCTGCTGAATAAAAA	3279		
DB	32705	CTCAGCCTCTCTGA-TAGCTGGGATTACAGGTGCTCCACCATGCTCTCAATTTTGT	32763		
QY	3280	AATTTTTTTGTAGAGACTGGGCTTACTACTGTTGGCCAGGCTTGTCTTAAACTCTCTGGCT	3339		
DB	32764	A--TTTTTAGTAGAGATGGGTTTCACCATGTTGTCCAGGCTGGTCTCGAATTCCTGAGC	32821		
QY	3340	TCAAGCAATCCTCCTACTTGGCATCCCAAAAGTGTGGGATTCACAGGGGTGAGCCACCAT	3399		
DB	32822	TCAAGTGATCCTCTGCTCAGCCTCCCAAGTGTGGGATTCACAGCGTGAAGTCTGCTGC	32881		
QY	3400	GTGCGGCTACTTATTTCTTTACATTCATCTTTTCCAAATAGAAATGTAAGATCCACAGAA	3459		
DB	32882	GCCTGGCCCATCTGTATTT-TTGGAAATGACATCACTATACACGCCCTACACAGATTA	32940		
QY	3460	GGGATTAAGTCTTATTTCTCTCTTTCTTTTGTAGACAGAGTCTCACTTTCATCACTCA	3519		
DB	32941	TCCTTCATCTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTCTTGCTCTGTGGCC	33000		
QY	3520	ACCTCCGT-----TCAGTCACTGCAACCTCTGCTCCCGGGTTCAAGYGA	3565		
DB	33001	GCTGGAGTGCAGTGCAGCATCTCGGCTCACTGCAAGCTCCGCTCTCTGGTTTCATGSCA	33060		
QY	3566	TTCTCTGCTCAAGCTCTCTGAGTGTGGAATTAACAAGCTGCACACCATGCTTGGCT	3625		
DB	33061	TTCTCTGCTCAAGCTCTCTGAGTGTGGAATTAACAAGCTGCACACCATGCTTGGCT	33120		
QY	3626	A-ATTTTTTGTATTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAA	3684		
DB	33121	ATTTTTTTGTACTTTTAGTAGAGCGGGTTTACCATGTTAGCCAGGATGGTCTCGAT	33180		
QY	3685	CTCTGACCTCAAGTGAATCTGCTGCTCACTGCTCCCAAGTGTGGAATTAAGCGTG	3744		
DB	33181	CTCTGACCTC--GTGATCCGACGCTCTCGGCTCCCAAGTGTGGAATTAAGCGTG	33238		
QY	3745	AGTCACTGTGCGCGGATTACT-----GTCTATTTTCTTTATTG	3785		
DB	33239	AGCCACGACCCGGCTATCTCTTCTTGTAGGGGAGAACTGTACATAAACTATTT	33298		
QY	3786	CTATATCCCAGATCTAGAGCAGTGTCTGACATATAGTAGGTCCTCAATAAATATTTGAT	3845		
DB	33299	CCAAATCTCTGCACAAGAAATGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	33358		
QY	3846	-----GAATGCAGCCTAGATATAAATCTTTCTTTTCTTTTCTTTTCTTTTCTTTT	3897		
DB	33359	TTATATCCGTATGGACTCATAGACATTTATTTTACATCTTGGGTTATAATTTCAATATTC	33418		
QY	3898	ACAACCTTTGCAGAAATAAATAAATCTTGCAATCTGCTTTTCACTTATCACTTGTATG	3957		
DB	33419	ATTATTTATTTGGTGCACAACTGTTCCAGAAATGACATAGAGATCTCTCTGGTTGAC	33478		
QY	3958	ACTTTTTCATATTCCTCAAACTTTTATTTGTTACTGTTTTCATTTGTTACTATTTTAGT	4017		
DB	33479	TCAGGTTTTTGTGGGGTTTATCTATTTATTTATTTATTTTAAATCTTTTGTGTCATTTGA	33538		
QY	4018	CACAGTAATA-----TATGGCTTAATTTGGCTTTATACATCTCTCTCTCTCTCTCT	4057		
DB	33539	GAGTCAACAACTCATCAGACAGCAAAATCCACAGGGTTCGCCCTAGAGAGAAATTCAACTTA	33598		
QY	4058	CTCCACTTTAGAGGGCCAAATTTACAAATCTGATGAAAGCTATGAACCCCTC--TCCCCAG	4115		

Db	33599	CTAACTTATTTCAAAGTTTTTTGAAGTCATGTGATGCTGGGAAAAACCTTCA	33658	TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT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Db 13562 GCAGGCTGGTCTCGAACTCTGACCTCAGGTGATCCATACACCTTGGCTCCCAAGTG 13621
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QY 3908 AGAATAAATACAACTCTGCACTCTGCTTTTCACTTATCACTTATCACTTGTATGACTTTTCA 3967
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QY 4208 ATTAATTAATAAATACTAGTTGGGCACAGTGACTCAAGCTGTAAACACAGTACTTTGG 4267
Db 14098 GACATATTTTGGTGAATTAAGTGAATTTCAAGAAATGATTAATCAGAAATCCAGCACTTTGG 14157
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Db 14391 CCGCCCAAGGAAAAAGAAAAAAGAT 14418

RESULT 60

US-10-242-515-2623
; Sequence 2623, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31

; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2623
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-2623

Query Match 7.6%; Score 380.8; DB 6; Length 32193;
Best Local Similarity 58.2%; Pred. No. 2.5e-76;
Matches 855; Conservative 1; Mismatches 568; Indels 44; Gaps 9;
QY 3098 TTTGGGTTTTTTTTTTGTTGTTTGTAGACAGGGTCTTGTCTGTCAACCCAGGATGAG 3157
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Job time : 2581 secs

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OM nucleic - nucleic search, using sw model

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Listing first 150 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
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1	429.8	8.6	92600	10	US-10-857-780-1		Sequence 1, Appl
2	424	8.5	159440	13	US-10-960-414-12		Sequence 12, Appl
3	419	8.4	180531	18	US-11-114-798-57		Sequence 57, Appl
4	417.6	8.4	154548	17	US-11-121-086-33		Sequence 33, Appl
C 5	416.6	8.3	179892	17	US-11-112-908-39		Sequence 39, Appl
C 6	413.6	8.3	215974	11	US-10-330-773-500		Sequence 500, Appl
7	406.2	8.1	348101	11	US-10-330-773-122		Sequence 122, Appl
C 8	400.8	8.0	46878	10	US-10-995-561-13276		Sequence 13276, A
C 9	393.8	7.9	175416	17	US-11-121-086-43		Sequence 43, Appl
10	387.6	7.8	92199	18	US-11-114-798-50		Sequence 50, Appl
11	387.6	7.8	318488	18	US-11-114-798-58		Sequence 58, Appl
C 12	384.8	7.7	167891	17	US-11-121-086-14		Sequence 14, Appl
C 13	384.2	7.7	154548	17	US-11-121-086-33		Sequence 33, Appl
C 14	381.4	7.6	159440	13	US-10-960-414-12		Sequence 12, Appl

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18	373.8	7.5	180654	17	US-11-121-086-58	Sequence 58, Appl
19	372.6	7.5	167891	17	US-11-121-086-14	Sequence 14, Appl
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23	364	7.3	141121	10	US-10-995-561-13262	Sequence 13262, A
24	362.4	7.3	171427	17	US-11-112-908-60	Sequence 60, Appl
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64	340.4	6.8	179892	17	US-11-112-908-39	Sequence 39, Appl
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67	338.6	6.8	177623	17	US-11-112-908-41	Sequence 41, Appl
68	338	6.8	141121	10	US-10-995-561-13262	Sequence 13262, A
69	337.4	6.8	135019	11	US-10-849-438-11	Sequence 11, Appl
70	336.4	6.7	178024	10	US-10-330-773-698	Sequence 698, Appl
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72	335.6	6.7	171732	17	US-11-121-086-98	Sequence 98, Appl
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80	331.8	6.6	220895	10	US-10-775-169-88	Sequence 88, Appl
81	331.2	6.6	161994	17	US-11-112-908-57	Sequence 57, Appl
82	330.8	6.6	910	12	US-10-301-480-583016	Sequence 583016, A
83	330.8	6.6	910	12	US-10-301-480-1196425	Sequence 1196425, A
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Qy	2554	AAAAATGCTTCAATAAATATATGATAAAGAGACTTATATTTTTTCAAGCCATAGATCA	2613
Db	17440	AAAAAATAATACACACACACACAAAAAATCTGTTAATGCTTAACTACACAAAAATG	17499
Qy	2614	TTTCTCTGAAGCATCTTGGCGAAGTCATCCACCTGTTCTGAGAGTGGCGAGGTGAG	2673
Db	17500	AATCAGATAAATATGCAATTTATTTAGAGAACTGCATGTTGGTTCAGTCCCTGTCAG	17559
Qy	2674	GGGTGACCTATTGCTCTGCACTTACTCTTATCTCAGCTGTCCCTCCCACTTTCCAGGT	2733
Db	17560	GGGAATTCCAGCATGACCTCATCTGTTGAAGACAGACAACTCTTGTGTTTTATTT	17619
Qy	2734	TGCCAGACATGACAACTGCTATGACCGGCCAAGAGCTGGACAGCTGTAAATTTCTG	2793

Db 17620 TTTTAAGATGGATCTCACTCTGTTGCCGAGCTGGAGTGCAGTGGCATGATCTCAGCCCT 17679
Qy 2794 CTGGACAMCGGTACACCCACACTATTATCATCTGTGCTCTGTGCTGGCAATCACCCTGT 2853
Db 17680 CTGCCACCTCCACCTTCGGGTTCAAGAGATTCTCATGCTCCAGCCTCTCTAGTAGCTGA 17739
Qy 2854 AGCAGTAGGTTTATCCCTCTCTTGACCTATGAATCTCTAGTTGGTCTCTCAGTAGGCCGGG 2913
Db 17740 GATTACAGGCTGTGCTCCATGCCCAGCTAAATTTTATTTTATTTTACTAGAGATGAGGTT 17799
Qy 2914 GGAATAATAGTAACACAGCCATGATTTAGTGTAAATTTCTTGGTCTCTGGCAGTGT 2973
Db 17800 TCACCACTTTGGGAGCCG-----GTCTCAAACTCCTGACCTCAAGTGATCCAC 17849
Qy 2974 TCCTTTAATCCTCAGAACACACTATGGGATAGGTACAATATTCCTCATCTTAACAGATAA 3033
Db 17850 CCACCTCGGCTCCGAGTGCCTGGGATGACAGGTG-----CTGGTTCAGCAAC 17898
Qy 3034 GMAAACTGAGGCTCAGAAAGCTGAGCTATTGTGCCAAGATCACACAGCTTGTAAAGTGGTG 3093
Db 17899 TGTGTTTAGACATACATATTTATCTGCTCGTCCAGCATGGTCAGCCCTCCACTT----- 17954
Qy 3094 ACAGTTTGGTTTTTTTTGTGTTTGTAGACAGAGGTTCTTGTCTGTCAACCCAGGCA 3153
Db 17955 ---TTTAAATTTATTTATTTATTTTATTTTGTAGACAGAGTCTCACTCTGTGTCCAGGTT 18011
Qy 3154 TGAGCAGTGGTGCAACCATAGTCACTGACGCTCAACCTCCTGAGCTCAAGGATCT 3213
Db 18012 GGAGTCCAGTGGGTGATTTCCGCTCACTGCAACCTCTACTTCCAGGTTTCAGACAAATTC 18071
Qy 3214 GCTGACCTCAGCTCCCAAGTACCTGGGACTAGGCTGACAGCTGCACACAGCTGGCTTAAT 3273
Db 18072 TCTGCTCAGCTTCCGAGTACCTGGGATTACAGGCCGCTGCCACACACTAGTAAAT 18131
Qy 3274 TAAAAAAATTTTTTGTAGAGACTGGGTCTTACTAGCTTGGCAGGCTTGTCTTAAACTC 3333
Db 18132 TTTTGTGA--TTTTTAGTAGAGACAGGTTTCCACATGTTGGCCAGGCTGGTCTCGAACTC 18189
Qy 3334 CTGGCTCAAGCAATCCTCTACTCTTGGCATCCAAAGTGTCTGGGATTACAGGGGTGAGC 3393
Db 18190 CTGACCTCAGTGATTTCTCTGCTTGGCTCCGCTCCGAGTGTGAGATTACAGGTGTGAGC 18249
Qy 3394 CACCATGTGGGCTACTTATTTCTTTACATTTCCATCTTTCCAAATAGATGTAAAGTCCAC 3453
Db 18250 CACTGCACAGGCTTAAATTTTATTTATTTATTTATTTATTTATTTAGNAG----- 18304
Qy 3454 AGAACAGGATTAAGCTATTTCTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATC 3513
Db 18305 -----CTTAGTCTCACTCTGTTGCCAGGCTGGAGTGCAGT 18340
Qy 3514 ACCTCAACCTCCGTTGAGCTCACTGCNAACCTCTGCTCCCGGTTCAAGYGATTCTCCTG 3573
Db 18341 GGCATGCTCGGCTCACTGCATCCCA-----CCTCTGGGTTCAACGCCATTTCTCTG 18393
Qy 3574 CCTAAGCTCCTGAGTAGCTGGAAATACAGCGTGCACACCACTGCTTGGCTAAATTTTT 3633
Db 18394 CCTCAGCTCCGAGTAGCTGGGACTACAGGCCGCCACACCACTCCCGGCTAA--TTTT 18452
Qy 3634 GTATTTTAGCAGATGGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCCTGACC 3693
Db 18453 GTATTTTAGTAGATGGGGTTTCACTGTGTTAGCCAGGATAGTCTCGATCTCCTGACC 18512
Qy 3694 TCAAGTATCTGCTGCTCAGTCTCCCAAGTGTGGAAATATAGGCGTGAGTCACTGT 3753
Db 18513 TC--GTGATCGGCTCGCTCGGCTCCCAAGTGTGGGATTACTTATTTTGTGTTTTTGT 18570
Qy 3754 GCCTGGCCGATTAAGTCTATTTTCTTTTATTTG--CTATATCCCCAGATCTAGACAGTGT 3811
Db 18571 AGAGACAGGTTCTCACTGTGTTGCCAGGCTGGTCTTTGAACCTCTGATCTCAAGTATCT 18630
Qy 3812 CTGACATATAGTAGGTCTCAATAAATAATTTGATGAATGCACAGCCTAGATATAAATTT 3871
Db 18631 TCCACCTCAGTCTCTCAAAGGCTGGGATTACAGGGGTGAGCCACTGCACCCCACTTTC 18690

Qy 3872 CTTTTTCTTTTTTTTAAAAAATCTTGACAACTTTGCAGATAAATAACAATCTTGCATCT 3931
Db 18691 CCTCTACTTTTT-----GACGGTTTCTCTTCTGCTATGAATGT 18727
Qy 3932 GCTTTTTCACCTTATCACCTTGTATGACTTTTTCATATTGCTCAAACTTTATTTGTTAC 3991
Db 18728 GCATGTCAGTTGCTGCTTCTTAGAACTGATATTTACTTCTCCTCATCA----- 18780
Qy 3992 TGTTTTTCAATGTTTACTATTTTACTCACTCAATTAATATGGCTTAATTTGCTTTATACATC 4051
Db 18781 -----GCCATTTGGAGGAGTGGGACCGCTCAGATTATTGATCTGACCCATT 18828
Qy 4052 CTCCTGCTCCACTTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCC 4111
Db 18829 CTTTCGGAGGTTTCTTGGTGGTGTCTTCATCACCAGAACTGGAATCAGAAGATT 18888
Qy 4112 CCAGAGAAATACACACACACACACACTCAACACAGTTTTTTTTTTAAATGTTTCAACT 4171
Db 18889 CCATAGCCCTTTTTTTTCCCCACATCTTGTGTAAGCAGAGTTTGA-----AAAC 18941
Qy 4172 AAGACAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTTAAAAATAACTCAGTTGG 4231
Db 18942 AAAACCAAACTAAGCTATTCCCCAGAGAAATCTGTAATCAAAGATAAGCTCTGCCGG 19001
Qy 4232 GCACAGTCACTCAAGCCTGTAACACAGTACTTTTGGAAAGTCCAGGTGGTGGATCACTT 4291
Db 19002 GCACAGTGGCTCAGC-----CTTTTGGAGGCCAAGCGGGGATCACT 19047
Qy 4292 GAGGTGAGAAGTTTCAGAGCAGCCTGGTCAATATGGTGAACCCCTATCTCTACTAAAAAT 4351
Db 19048 GAGTTCAGAGTTCTAGACCTGCCAGGCCAATGTTAAACCTCATCTCTACTAAAAAT 19107
Qy 4352 ACAAATAATAGCTGGTGTAGTATGATGCTGTAGTCCAGCTACTCTGGAGGCTCAG 4411
Db 19108 ACAAATAATAGTATGCTGGTGGTGTAGTCTGTAGTCTCAGCTACCTGGAGGCTCAG 19167
Qy 4412 GCAGAGAAATGCTTGAACCTGGGAGGCAGAGGTTGCAAGTGGCCGAGATCCACCACTG 4471
Db 19168 GCAGAGAAATGCTTGAACCTGGGAAAGTAGAGGTTGCAAGTGGCCGAGATTCACCACTG 19227
Qy 4472 CACTCAGCCTGGGCGACACAGCAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531
Db 19228 CACTCAGCCTGGGCGAGCGAGTGAGACGACCTCACAAAAATTTTACATAAATAAATAA 19287
Qy 4532 GGATCGGAGAGAAACAAAA 4550
Db 19288 AAGTAAAAATAAAAAATACAA 19306

RESULT 2

US-10-960-414-12
; Sequence 12, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINSENSIUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; TITLE OF INVENTION: PROGNOSIS, AND DIAGNOSIS OF CANCERS
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 159440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-12

Query Match 8.5%; Score 424; DB 13; Length 159440;
Best Local Similarity 60.7%; Pred. No. 33;

Qy	3605	CGTGCACCA	CCACCATGCTTGGCTTAATTTT	TTTGTATATTTT	TATAGCAGAGATGGGTTT	TACCATG	3664
Db	25562	CACACGCC	CCCATATCTAGCTAATTT	-----	TATTTT	TTTGCAGATAGTTCTTGCAGTG	25617
Qy	3665	TTGCCCAGG	CTGCTCAAACTCCTGACCTCAAGTGTCTG	CGCTCAAGTGTCTG	CGCTCGCTCAGTCTCCCAAA	3724	
Db	25618	TTGCCCAGG	CTGCTTGAATCTCTGGGCTCAAGCAATCTT	CTCGCTTGGCTTCCGCTCCGAGC	25677		
Qy	3725	GTGCTGGAA	TTATPAGCGGTGAGTCACTGTG	CGCTGGCCGATTACTGTCTATTTT	CTTTATTT	3784	
Db	25678	GTGCTGAGAC	TACAGGCAAGACCGGTGCCAGCC-----	TTGCCCTATTACATCAACA	25732		
Qy	3785	GCTATATCC	CAGATCTAGAGCAGTGTCTGACATATAGT	AGTGTCTCAATAAATATGA	3844		
Db	25733	ACAGGGCTC	CACACAGAGTTTGCAATTTGAACAACA	CACTATATAACAGAAAAACAATGCATCT	25792		
Qy	3845	TGAATGCAC	AGCCTAGATATAAATCTTCTTTTCTTTT	TTTTAAAAACAATCTTGCACACTT	3904		
Db	25793	CTTTTTGT	CCCATGTTTAAACACACACACACACACACAC	ACACACACACACACACACACAC	25852		
Qy	3905	TGCAGAA	TAAATACAATCTTGCAATCTGCTTTT	TTCACTTATCACCTTGTATGACTTT--	3962		
Db	25853	ACACACACA	AGAAATACTGTTTAAATCTTTAAACAATAG	CATTTGGGATTTTGCATTTGA	25912		
Qy	3963	-TTCATATT	GGCTCAAACTTATTTGTTACTGTTTCTTTT	TTTCATTTACTTGTACTTATTTTAG-TCAC	4020		
Db	25913	ATAAGCA	TTTGTTTTGTAGTCTCAAAAGCTGTCTG	TATACAGAACAAATTAAGATCNA	25972		
Qy	4021	TGAATAAT	TGGCTTAATTTGCTTATACATCTCTGCT	CTCCACTTTAGAAGCCCAAAATTT	4080		
Db	25973	CAAA	TTGGGAGGAAATTTGGATAAATCTGAGTTAT	CTTGAATTTGTTTGTTTATATAT	26032		
Qy	4081	ACAAATCT	GATGAAGCTATGAACCTCTCTCCACAGAA	AAATACACACACACACACACACT	4140		
Db	26033	ATAAATATA	TATAATAATAATAATATGTTTAATGTAT	TATATATACAAATATAAAA	26092		
Qy	4141	CACACACAG	TTTTTTTTTAAATGTTTGCACATAAGACA	AGAAACCTGCAATTAGAGGATGTT	4200		
Db	26093	ATATATAA	ATAATATCTTTGTAGCCTTCAGACAAA	ACAGAGAACTTGGATGCCATGTGCT	26152		
Qy	4201	TGTT-----	-----CATATTAATTAATAATTA	AAAAAATACTCAGTTGGGC	4233		
Db	26153	ATCTGTGG	ATTAGGGGTGAGGTGGGAAAGAGAA	ACAGAAAAATAGAAAAGGCTAGGT	26212		
Qy	4234	ACAGTGA	CTCAAGCCTGTAACACAGTACTTTTGA	AGTCCAGGTGGGTGGATCACTTGA	4293		
Db	26213	GTGTGGCT	CATGGCTATAATCCACAGCACTTTTGG	GAGGCTGAGGCAGCGGATCACTGA	26272		
Qy	4294	GGTGAGA	AGTTTCAGACACAGCCTGGTCAATATG	TGGTGAACCCCTATCTCTACTAAAAA	TAC	4353	
Db	26273	GGTCAGAG	TTCAAGAACAGCCTGGTCAACATAGT	GAACCCCGCTCTACTAAAAA	TAC	26332	
Qy	4354	AAAAATP	AGCTGGGTGTAGTATGCAATGCTGT	PAGTCCAGCTATCTCGGAGGCTGAGGC	4413		
Db	26333	AAAAAT	TAGCTGGCATGTTGTGTGCGTAC	CTGTAGTCCAGCTACTCTCGGAGGCTGAGGC	26392		
Qy	4414	AAGAGAT	TGCTTGAACCTGGGAGGCAGAGGTTG	CAGTGCAGCCGAGATCCCACTGCA	4473		
Db	26393	ACGAGAA	TGCTGGAACCCGGGAGGCAGAGTTT	GCAGTGCAGTGCAGATCGCACCACTGCA	26452		
Qy	4474	CTCCAGC	CTGGGCGACACACGCGAGCTCTATCT	CAAAAAATAATAATAATAATAAAGG	4533		
Db	26453	TTGCAGC	CTGGGCACACAGACTGAGACTCTG	CTCTCAAAAAAATAATAATAATAAAGG	26512		
Qy	4534	ATCGGAG	AGAAAACAAACTTAATGA	4559			
Db	26513	ATAGAGG	AAAGAAAATAGAGAAA	26538			

RESULT 5
US-11-112-908-39/c
; Sequence 39, Application US/11112908
; Publication No. US20050260659A1

```

; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 179892
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-39

```

Query Match	8.3%;	Score 416.6;	DB 17;	Length 179892;
Best Local Similarity	54.4%;	Pred. No. 35;		
Matches 1334;	Conservative	2;	Mismatches 946;	Indels 171; Gaps 18;
Qy	2288	TTCAGGCCAGGCGGTGGCTCATGCCCTGTATCCAGCACTTTTGGGAGGCCGAGCGGG	2347	
Db	84959	TTTTGGCCAGGTGTGGTGGCTCACACCTTATATCCAGCACTTTTGGGAAGCCGAGGTGG	84900	
Qy	2348	CGGATCACTTGAGGTGAGAGTTCCAGACCCAGCCTGGCCAAATGTTGGTGAACCCCTGTCTC	2407	
Db	84899	CAGATCACTTGAGTTCAGGAGTTGGAGACCAAGCCTGGCCAAATGTTGGTGAACCCCTGTCTC	84840	
Qy	2408	TACTAAAAA-ATACAAAAATTAGCCGGACATGGTGGCGAGCCCTGTAAACCCAGCTACT	2466	
Db	84839	TACTAAAAATACAAAAAAATTAAACCGGTGTGGTGTGGCCCTGTAAATCCAGCTACT	84780	
Qy	2467	TGGGAGACTGA-----GTTGGAGGTTTTCAGTGAGCCAAAG	2500	
Db	84779	TGGGAGGCTGAGGCACGATAATCGCTTGAAACGAGTGGGTGAAGTTGCAGTGAGCCAAAG	84720	
Qy	2501	GTGGTGTCACTGTCTCAGCCTGGGTAAACAGAGCAACTCTGTCTC-----AAAA	2550	
Db	84719	AGCACAGCACTGTACTCCAGCCTGGAAGACAGAGCAAGCACTGTCTCAAAACAAAAACAA	84660	
Qy	2551	AAAAAAATGCTTTTCAATAAATATATGATAAAGACATTATATTTTTTCAAGCCATAGGA	2610	
Db	84659	AATAAAAAGCAATTATGGGCAATATTTGTATGATGTATGCTTTCATTCTCTTGGGA	84600	
Qy	2611	TCATTTCTCCTGAAGCATCTTGGGAAAGTCATCCCAACCTGTTCTTGAGAGTGGGCAGGT	2670	
Db	84599	GTATATACCCAGGAGTAGAAATGCTGGGTATATCGTAACTAAAGTTTAACTTTTGA	84540	
Qy	2671	GAGGCTGACCTATTGCTCTGCACATTACTCCTATCTCAGCTGCCTCC-----	2719	
Db	84539	ACTGCCAGACTCTTTCCCAAAGATTGCTTTTCTTCTTTTCTTCTTCTTCTTCTTCTT	84480	
Qy	2720	-----CAGTTTCCAGGTGTGTCGACACATGACAACCTGCTAYGACCAGG	2764	
Db	84479	TGTCAGACAGTGCTTATTGTGTGCCAGGCTGGTCTCAAACCTCTGGGCTCAAGCAGT	84420	
Qy	2765	CCAAGAAGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCACACCTATTTCAT	2824	
Db	84419	CCCTCTACCTCAGCCTCCCAAAGTGTGGGAATTACAGGCATGAGCCACTGTGCTCTGCTT	84360	
Qy	2825	ACTCGTGCTGCTGCTCGGCAATCACTGTAGCAGTAGGTTTATCCCTTCTTGGACCTATG	2884	
Db	84359	GCTTTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	84300	
Qy	2885	AATTCTA-GTTGGTCTCAGTAGGCCGGGGGAATAATAGTAAACAAACAGGCATGATTTA	2943	

Db 84299 TCACCAGGCTGGAGTACAGTGGTGCATCTCAGCTCACTGCAACCTCTGCCCTCCTGGGT 84240
Qy 2944 GTGTTAAATTTCTTGGTCTGGGCAAGTGTCTCTCTTTAATCCTCAGAAACAACTATGGGA 3003
Db 84239 TCAACGATTTCTCCTGCTAGCCTCTCAAGTACCTGGGATTAACAGCGCTGCATGCTACG 84180
Qy 3004 TAGGTACAATTTATCTCCTCACTTAACAGATAAGAAACTGAGGCTCAAGAGCTGAG----- 3058
Db 84179 CCCAGCTAATTTTGTATTTTGTATTTTAGTAGAGCGGGGTTTCGCCATGTTGGCCAGACTGG 84120
Qy 3059 -----CTATTTGCCCAAGATCACACAGCTTGT 3085
Db 84119 TCTTGGATTCCTGACCTCAGGTGATCCACCTGTCTTTGGCTCTCAAGTCTGGGATTAC 84060
Qy 3086 AAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTTGTAGAGACAGGGTCTTGTCTGTCTCA 3145
Db 84059 AGCGGTGAGCACTGCGCCCGGCCCTCTTTATTTTGTGAACAGAGGCTCGCTGTCTGTTG 84000
Qy 3146 CCAGGATGAGCACAGTGGTGCACCATAGGTCACTGCGAGCTCAACCTCCTGAGCTCA 3205
Db 83999 CCAGGCTGGAGTGCAGTGTATGATCTTGGATCACTGCNACTCTGCTCCTCTGGGCTCA 83940
Qy 3206 AGGATCTGCTGACCTCAGCCTCCCAAGTAGTGGGACTACGAGCTGCACCAACACGCC 3265
Db 83939 GGCAGTCT-CTCACCTCAGCCTCCTGAGTAGCTGGGACTACAGGCCACATGCCACTATGTC 83881
Qy 3266 TGCTAAATTAATAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGT 3325
Db 83880 CTGCTAATTTTGTATTTTTT---GAGAAACAGGGTTCTACCACTGTTACCCAGGCTGGTC 83824
Qy 3326 TTAACCTCCTGGCTTCAAGCAATCTCTACCTTGGCATCCCAAGCTGGGATTACAG 3385
Db 83823 TCCAACTCCTGGGCTCAAGTATCACTGCTCGGCTCCCAAGTGTGGGACTACAG 83764
Qy 3386 GGGTAGCCACCATTGTGCGGCTACTTATTTCTTTTACATTCATTCCTTCCAAATAGATGA 3445
Db 83763 CAGTGAGC-----CTGCTTTCTTTTAAAGTAAACTTTAATCAATACATTTAA 83716
Qy 3446 AGATCCACAGAACAGGATTTACTGCCTATTTCTTCTCTTTT-----TGNAGACAG 3501
Db 83715 GTAAATATTTAATAGGTATTTGTGTTTCTTTCTTTTCTTTTCTTGAGACAGAG 83656
Qy 3502 TCTCACTTCACTCACTCAACCT-----CGTTTCAGCTCACTGCAACCTCT 3546
Db 83655 TTTTGCTCTTTGTTGCCAGCTGGAGTGCAATGGCGCTATCTTGGCTCACCACAACCTCT 83596
Qy 3547 GCCTCCGGGTTCAAGATATCTCTGCTCAAGCTCCTGAGTGTGGAATTTACAAGCG 3606
Db 83595 GCCTCCTGGGTTCAAGTGAATCTCTGCTCAGCTCCAGAGTAGCTGGGATTTACAGGCA 83536
Qy 3607 TGCACACCACTGCTGGCTAATTTTGTATTTTGTAGCAGAGATGGGTTTACCATGTT 3666
Db 83535 TGTGCCACCAACCGCGGCTAA--TTTGTATTTTAGTAGAGCGGGTTTCTCTATGT 83478
Qy 3667 GCCAGGCTGCTCAAACTCTGACCTCAAGTATCTGCTGCCTCAGTCTCCC-CAGTCCC-AAAG 3725
Db 83477 GGTCAAGCTGCTCAAACTCCCACTCAGATGATCTGCCGCTCAGCTCCCAAG 83418
Qy 3726 TGTGGAATTTATAGGCTGAGTCACTGTGCTGCTGCGGATTTACTGTCTAT-----TTTC 3778
Db 83417 TGTGGGATTTACCGCTGAGCCACCGAGCCAGCTGTTCTTTCTTTCTTTCTTTCTGTTT 83358
Qy 3779 TTTATTTGCTATATCCCGAGATCTAGAGCAGTGTCTGACATATAGTAGGTGCTCAATAAT 3838
Db 83357 TTTTGAGACAAGTCTCCTCTTGTGCGCCAGGCTATAGTGCAGTGGTGCATCTTGGCT 83298
Qy 3839 AATTGATGAATGCACAGCTTAGATATAAACTTTCTTTTCTTTTCTTTTAAACAATCTGA 3898
Db 83297 CACAGCAACCTCCACCTCCTAGGTCAAGTATCTCTTGTGTGTCAGCTCCCAAG-TAGC 83239
Qy 3899 CACTTTGAGATAAATAAATCAATCTTGTGATTTCTGCTTTTCACTTATCACCTTGTATGA 3958
Db 83238 TGGGATTTACAGGACCCCGCCACCAACCGCGCTAAATTTTGTATTTTGTATTTTAGTAGATGGG 83179

Qy 3959 CTTTTTTCATATTGCC---TCAAAACCTTTATTTGTTACTGTTTTTTCATTTGTTACTATTATA 4015
Db 83178 TTTTTCATGTTGGCAGGCTGGTCTCAAACTCCCAACATCAGGTGATCCACCCACCTGC 83119
Qy 4016 GTCACTGAATAATATGGCTTAATTTTGTCTTATACATCTCTCTCTCCACTTTTGAAGGCCA 4075
Db 83118 CTCGCCCTCCCAAAGTGTCTGGGATTTACAGGAGTGAGCCACCGCGCCGGGCAATAAGTAT 83059
Qy 4076 AATTTACAAATCTGATGAAGCTATGAACCTCTCTCCAGAGAAATACACACACACAC 4135
Db 83058 TTTTAAAAAGCCATAGAACAATAAAGTGAATTTTAGCAAGCCTGTAAAAATAGAAGTTAC 82999
Qy 4136 ACACCTCACACACAGTTTTTTTTTAAATGTTTGCATCTAAGACAAGAAACCTGCATTAGAGG 4195
Db 82998 TATACAAAAGCAGTTCTTATCTATTAGTAGCAACAATTTGAAAA-----TTA 82950
Qy 4196 ATGTTTGTTCATATTAAATTTAAAAATACTAGTTGGGCACAGTCACTCAAGCTGTAAAC 4255
Db 82949 AAATTTTAAATTTTATTTAAAAATAGCATCA-----CAGGCCGGGTGCTGTAAATC 82899
Qy 4256 ACAGTACTTTGGAAGTCCAAGGTGGGTGATCAGTTGAGTGAGAGTTCGAGACCAAGC 4315
Db 82898 CTTGCAATTTGGGAGGCCAAAGGTAGCGGATCACCTGAGGTCAAGGTTCCAGACCAAGC 82839
Qy 4316 TGGTCAATATGTTGAAACCCCTATCTCTATAAAAAATACAAAAATTTAGCTGGGTGTAGTGA 4375
Db 82838 TGGCCAAACAGGTGAATTCCTTACTACAAACACAAAAATCAGTAGTTCGTGGTGG 82779
Qy 4376 TGCATGCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAAGAGAAATTTGTTGAACTGGG 4435
Db 82778 CGTATGCTGTAAATCCAGCTACTCGGAGGCTGAGGAGGAGAAATCGCTTGAACCCAGG 82719
Qy 4436 AGGCAGAGTTGCAGTGAGCCGAGATCCCACTGCTCAGCTCCAGCTCGGCCACACAGC 4495
Db 82718 AGGCGAGGTTGCAGTGAGCTGTTATTCGCCACCTGTACTCCAGCTCGGCCAACAGAGT 82659
Qy 4496 AGACTCTATCTCAAAAAATAAATAAATAAAGGATCGAGAGAAACAAAACTAAT 4555
Db 82658 AGATTCGCTCTCGAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 82599
Qy 4556 AAGATTCTCGAAGGTAAGCAGAGATACGTAAATATATGTAAATAAGTTTAAA 4608
Db 82598 TAAATAAATAAATAAGCATCAAAAAATAAACAATTTAGATAAATAAATAAATAA 82546

RESULT 6

US-10-330-773-500/c
; Sequence 500, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330, 773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 500
; LENGTH: 215974
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(215974)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-500

Query Match 8.3%; Score 413.6; DB 11; Length 215974;
Best Local Similarity 59.6%; Pred. No. 33;
Matches 847; Conservative 0; Mismatches 529; Indels 46; Gaps 7;

QY 3110 TTGTTGTTGTTTGTAGACAGGGTCTTGCTCTGTCAACCAGGCATGAGCACAGTGGTGA 3169
Db 4846 TGTCTTTTGTGTTGAGACAGGGTCTCGCTCTGTTGCCAGGCTGGAGTACAGTGGCACA 4787
QY 3170 ACCATAGTCACTGACAGCCTCAACCTCTGTAGCTCAAGGATCTGTGACCTCAGCCTCC 3229
Db 4786 ATCATGGCTCATTGGACGCTCAAACTCTCTGGGCTCAAAATGAGCCTCAACCTCAGCCTCC 4727
QY 3230 CAAATAGCTGGGACTACGAGCGTGCACACACCGCTGGCTAATTAATAAATAATTTTTTG 3289
Db 4726 TAAGTAGCTGGAACTACAGCATACATCACCCTCTAGCTAATTTTGTATTTTTT--- 4670
QY 3290 TAGAGACTGGGTCTTACTAGTTGGCCAGGCTTGTCTTAACTCTCTGGCTTCAAGCAATC 3349
Db 4669 -----GTCTCACTGTGTTGCCAGGCTGCTTCCAAATTCCTAGGCTCAAGCAATC 4620
QY 3350 CTCCTACCTTGGCATCCCAAGTCTGGGATTAACAGGGGTGAGCCACCATGTGCGGCTAC 3409
Db 4619 ACCTGCTTCAAGCCTCCCAAGTACTGGGATTAACAGACATGAGCCACGACCCAGCTTG 4560
QY 3410 TTATTTCTTTTACATCTCTTCCCAATAGAATGTAAGATCCACAGAACAGGGATTTACTG 3469
Db 4559 AAGAGTCTTTTATTAATTAATTAATTTTATTTTATTTTGTGATGAAG----- 4509
QY 3470 CCTATTTCTCTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCTCCGTTTC 3529
Db 4508 -----TCTCGCTCTGTTGCCAGGTTGGAGTACAGTGGCGCAATCTCGGCTC 4462
QY 3530 AGTCACTGCAACCTCTGCTCCGGGTTCAAGYGATTTCTCTGCTCAAGCCTCCTGAGT 3589
Db 4461 ACCGC---GCAACCTCTGCTCCAGGTTCCGGGATTTCTCTGCTCAGCCTCCCGAGT 4405
QY 3590 AGCTGGAATTAACAGCGTGCACCAACATGCTTGGCTAATTTTGTGATTTTAGCAGAGA 3649
Db 4404 AGCTGGATTAACAGCATGGCCACCAAGCCAGCTAA-TTTTGTGATTTTAGTAGAGA 4346
QY 3650 TGGGGTTTACCATGTGCCCCAGGCTGGTCTCAAACTCTCTGACCTCAAGTGTCTGCCGTG 3709
Db 4345 TAGGCTTTTCATCATGTGTCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCCACCCA 4286
QY 3710 CCTCAGTCTCCAAAGTCTGGAATTTATAGGCGTGAATCTAGTGTGCTGGCGGATTTACTG 3769
Db 4285 TCTCAGCTTCCCAAGTCTGGGATTTACAGGCATGACCCGACCTGCGCCGAAAGTATC 4226
QY 3770 TCTATTTCTTTATCTATATCCCGATCTAGACAGTGTCTGACATATAGTAGTGTGC 3829
Db 4225 TTTTAAAGTCTCTGATCT---CTAACCTCTGATAGTGGCTGTGATTTAGTAGGCAC 4169
QY 3830 TCAATAAATTAATGATGAATGACAGCCTAGATATAAACTTTCTTTTCTTTTAAAAA 3889
Db 4168 T---TAACACATTTGGAGATGAAGATATTAAACCATGGCATTTATCAATTACTCTCAGCTT 4112
QY 3890 CAATCTTGACAACTTTGCGAATAAATAACATCTGCAATTTGCTTTTTCATTTATCAC 3949
Db 4111 AAATGCTTTGCCCTCAAGCCACGAGCTGGTAGTGGCAGAGTTGGAATGCAACACAAAT 4052
QY 3950 TTGTTATGATCTTTTTCATATGCTCAAACTTTATTTGTTACTGTTTTCATTTGTTACT 4009
Db 4051 TTGTTGATTCACAAATCTTTGCCCTTTCCACAAACAGAGCCCTACATGTCCCTTTACA 3992
QY 4010 ATTTTAGTCACTGAATAATATGCTTAAATTTGCTTATACATCTCTCTGCTCCACTTTAGA 4069
Db 3991 TATTTTTCAGGTGTACATTATCTTTCCAGCATTTGTGAAC-TCCTAGTGAAGCCTTAGATC 3933
QY 4070 AGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCCCGACAGAAATACACAC 4129
Db 3932 TCACATAATAGCAATGACCTCTCTAGCTGTATTTTATGAGTCTTATGATGTGCCAGGC 3873
QY 4130 ACACACACACTTCACACACAGTTTTTTTTTAAATGCTTTTGCAACTAAGACAAAGAACTGCA 4189
Db 3872 ATTGCAATTTAGCACTTCACACATATGATCTCATTTAAATTTTCAACAATTCCTCATGAGAT 3813
QY 4190 TAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTCAGTTGGGCACAGTGAATCAAGCCT 4249

Db 3812 TGGCACTATTATTATGGCTTTTAAACAGAAAGAAACAGGCCAGCATGTGGCTCATGCC 3753
QY 4250 GTAACCCACAGTACTTTTGAAGTCCAAGTGGGTGATCACTTTGAGTGAAGATTTGCGAGA 4309
Db 3752 ATAATCTTAGACACTTTGGAGGCTGAGGTGGGTTGATCACCTGAGTCAAGGATTTCAAGA 3693
QY 4310 CCAGCCTGGTCAATATGTTGTAACCCCTATCTCTACTAAAAATACAAAAATTAAGCTGGGTG 4369
Db 3692 CCAACCTGGCCAAACATAGTGAACCCCATCTCTACTAAAAATACAAAAATTAGCCGGCA 3633
QY 4370 TAGTGATGATCCCTGTAGTCCAGCTACTCGGAGGCTGAGGCAAGAGATTTGCTTGA 4429
Db 3632 TGGTGGCGCGTCTGTTAATCCAGCTACTCGGAGGCTGAGACAGGAGATTTGCTTGA 3573
QY 4430 CCTGGAGGCGAGAGTTCAGTGAGCCGAGATCCACCACTGCACCTCCAGCCTGGSCGAC 4489
Db 3572 CCCAGGAGCGGAGGTTGAGTGAGCAGAGATTCAGCTGTTGCACCTCCAGCCTGGAGAC 3513
QY 4490 ACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531
Db 3512 AGAGCAAGACTCCGCTCTCAAAAAAGAAACAGAGAGGAACAGA 3471

RESULT 7
US-10-330-773-122
; Sequence 122, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 348101
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(348101)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-122

Query Match 8.1%; Score 406.2; DB 11; Length 348101;
Best Local Similarity 58.2%; Pred. No. 27;
Matches 895; Conservative 1; Mismatches 579; Indels 62; Gaps 8;

QY 3029 GATAAGAAACCTGAGGCTCAGAAGGCTGAGCTATTTGCCAAGATCACACAGCTTGTAAAG 3088
Db 97262 GATTACAGCGGTGAGCCACCGCGCCGCCACATTTCTTATTTCTAATGAATGAAT 97321
QY 3089 TGGTACACAGTTTGGGTTTTTTTTTTTGTGTTAGACAGAGGCTCTGCTCTGCACCC 3148
Db 97322 TACCAATCTTTTATTTCTTTTCTTTTGTGAGATGAGTCTTGCACTATCGCCC 97381
QY 3149 AGGCATGACACAGTGGTGCACACCATAGTGTACTCGAGCTCAACCTCTCTAGCTCAAGG 3208
Db 97382 GGGCTAGATTTGCATGGCATGCTCTCGGCTCACTGCAACCTCTGCTCCAGGTTCAAGT 97441
QY 3209 GATCTGCTGACCTCAGCCTCCCAAGTGTGGACTACGAGGTGCACACACACCGCTGG 3268
Db 97442 GATTCCTGCTCAGCCTCCCAATAGTGGATTCAGGGGTGTGTACCCAGCCTGG 97501
QY 3269 CTAATTAATAAATAATTTTTTTGTAGAGACTGGGCTTTACTACGTGGCCAGGCTTGTCTTA 3328
Db 97502 CTAATTTTTTGTG-TTTTTAGTAGACGGAGTTTCACTATGTTGCCAGGCTGGTGTG 97560
QY 3329 AACTCCTGGCTTCAAGCAATTCCTCTACCTTGGCATCCCAAGTGTGGATTCAGGGG 3388

QY 1391 ACTGCACTCCAACTGGGCAACAGACGAAGACTCCATCTCAAAAAAATAAATAAATAT 1450
D 1392 CTTCCCAAGTAGCTGGGATTAACAGGTGGCCACCATCAGCCCGAGCTAATTTTGTATTTT 33628
QY 1451 CAGGCCCTAGCTGGGTGGCAATGCTCCCTGTGTAATCTTCTAGCTGAGGGGTAGGGTCCCAAG- 1509
D 1452 ATCATGCCATTTGCAAGTCCAGGCTGGGTGATAGAGCGAGACTCTGTCTCARATAAATAAT 32529
QY 1510 ---AAGAAGAAGAAAAGAAAGAGATATATATATATATACACACACAAAGATATA 1566
D 1511 TCCACCTATCTCGGCCCTCCCTAAGTCTGGGATTAACAGGTGGCCACCGCACCTGGCC 33508
QY 1567 AACTTTTATATATAAAGTTTTTCATTTAAAAAATAAATAAATAAATAAATAAATAAATAA 1626
D 1568 ATATTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCCACTGTGGCCCGAGCTGG 33448
QY 1627 TACCAAGTTCTGGGTGCAACGGTCTTACAGAGAGGACGCTGGCAGGGGTACAGGAGGA 1686
D 1628 TCTCAAACTCTAAGCTCAAGCAATCTGCTTGGCTTCCCAAAATGCTGGGACTAC 33388
QY 1687 GGTGGGACCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1746
D 1688 AGGCATATGCCACTGCACAGACAGGAAATTAGGTTGAAGAGACAGAACTGAAGTTT 33328
QY 1747 AACTCTGGCTATGTCTTTCTGAGTGGCCCGCCGCMCAGCGGCATCAGCCCTCGGGCG 1806
D 1748 TCTGTGACCACTGCCCTTGTGTCACACCCACATCTCTGATCACAGAGACCGGTGCT 33268
QY 1807 TGTGGAGTTCCGCAAAATGATCAAGTGGTGTATCCCGGGAGTGACCCCTTTTGGAA 1866
D 1808 TGGGATCATGCTCCCTCTGGCTTAAACTTTTCCAAAGGGTTTTCACAC- ---TCAGAAT 33212
QY 1867 ACAACACTACGGCTGCTACTGTGGCTTGGGGGCTCAGGCACCCCGTGGATGACTGG 1926
D 1868 AAAATCCAAACTCTTCACTTAGCTTGTGAGTTCCCGCCATCCCGCTCATTCATCTCTTTG 33152
QY 1927 ACAAGTAAGTATCCGCTCGAGGAAATTTGAGTGCCTCGCGGGGGGGGGTGGGAC 1986
D 1928 TTTTCTCTTGTATTTTTTTTCTTAGAGATGGAGTCCCGCTCTGTGGCCAGGCTGGACTG 33092
QY 1987 AGCCCAAGGATCTCAGAGGATATACAAAGGGGACTTGCATATCTGCTAAGGATAACATAT 2046
D 1988 CAGTGGCGTATCTGGCTCACTACAGCTCCGCTTCCCGGATTCAGGCCATCTCTCTGC 33032
QY 2047 TTTCACTCTTGTCAAAATAAATAATGTTTCAAGAGACGCTGTAGGCAAGCACCCC 2106
D 2048 CTCGCTCTCCAGAGYAGCTGGGACTACAGGGCCCTGCGCCATGCTGGCTTAATTTTGT 32972
QY 2107 GTTAGAGATGGAAACAAATCACCGACGTGCAAAACAGTGGCGGATGCTGCCCTCCAGTGG 2166
D 2108 TTTTGTATTTTGTAGAGACAGGGTTTCAACA-TGTTAGCCAGGATGCTGTGATCTCC 32913
QY 2167 AGAATGTAGCAACAGTAAACATCACAGCAACTATCCAGTGTCAATTTCTAGCAGTGGTT 2226
D 2168 TGAACCTCGTATCG- ---CTCGCTCAGCTCCCAAGTGTGGGATTAACAGGCTGA 32858
QY 2227 GTCACTGACCTTCTGAATACAGGATTTTACTGTATCTTGTCAACCATGTTAAAAATCGC 2286
D 2228 GCCACACACCTT- ---GCCAGGCCACTTACCT 32829
QY 2287 TTTTCCAGGCGGCGGTGGCTCATGCCCTGTATCCAGCACTTTTGGGAGGCGGAGGGCG 2346
D 2288 CTACTAGCCGGCAGAGTGGCTCATGTCTGTATCCAGCACTTTTGGGAGGCGAAGGCG 32769
QY 2347 GCGGATCACTTGAAGTTCAGAGTTCAGAGCCAGCTGGCCAAACATGGTGAACCTGTCT 2406
D 2348 GCAGATCAACTGTGGTCAGAGTTTTCAGAGCCACCTGGCCCAACATGGCGGAAACCCATCT 32709
QY 2407 CTACTAAAAATAAAAAATTTAGCCGGACATGGTGGCGAGCGCTGTAAACCCAGCTACT 2466
D 2408 CTATTTAAAAATAAAAAACTTAGCCGGGATGTGGCAGTTGCTGTATATCCAGCTACT 32649

QY 2467 TGGGAGACT- ---GAGTTGGAGGTTTTTCACTGAGGCCAAG 2500
D 2468 CGGAGGCTAAGGAGGAGGAATCACTTGAACCTTGGAGGTAGAGTTGCGTAAAGCCAAAG 32589
QY 2501 GTCTGTCTACTGTCTGTCAGGCTGGGTAAACAGCAACTCTGTCTCAAAAAAATAAATAAATG 2560
D 2502 ATCATGCCATTTGCAAGTCCAGGCTGGGTGATAGAGCGAGACTCTGTCTCARATAAATAAT 32529
QY 2561 CTTTCAATATAATATATATAAAGGACTTATATTTTTTCAAGCCATAGAGTCAATTTCTCC 2620
D 2562 GAAACAAATTAATCTATCTCATATCCATCCCTGTCTCTAGACTATTGGCYGCTGATCTCC 32469
QY 2621 TGAAGCATCTTGGGAAAGTCAATCCCACTGTCTGAGAGTGGGACAGGTGAGGCTGAC 2680
D 2622 AGAACAGAACTTTAGTAGGCTTTTCAATAACCCCTCCCAACATATCTTCCCTTTAATGA 32409
QY 2681 CTATTGCTCTGCATTTACTCTCTAGCTGTCCCTCCCACTTTCCAGGTGCTGCCAGA 2740
D 2682 TAAATCAGGATCCCTGATATATTCATCCCAAAAGCAAAACCTATATATTTTCTTCCAGA 32349
QY 2741 CACATGACAACTGTCTAYGACCAAGCCCAAGAGCTGGACAGCTGTAAATTTTCTGTGGACA 2800
D 2742 CAACCTTCCCAAGTGTGTATATTTTACCTGTGGGATTTTGTCCCTATTAG 32289
QY 2801 MMCGTACACCCACACCTATTCTATCTCTGCTCGGCTCGGCAATCACTGTAGCAGTA 2860
D 2802 ACCGAAATGGATGTGAGATGACAGAGGCTTATTTGTTTGTATAT-TGCTGCTGACGC 32230
QY 2861 GGTATTCCCTTCTTGTGACTATGAAATTTCTAGTTGGTTCTCAGTAGGCGGGGGGAAATA 2920
D 2862 GCAGTAGGATTTTATAGAAAGGACAGATAGTGGCTACAATGGACTGGTAGTCTA 32170
QY 2921 ATAGTAAACACAGCCATGATTTAGTGTAAATTTTCTGTTCTGGGCAGTGTCTCTTTA 2980
D 2922 GTATTGCTCACTCACTTGGCTTTAGCAGGCTACTTAACCTGGGGTTTAGTGTGCTCAT 32110
QY 2981 ATCTCTCAGAACAACTATGGGATAGGTACAATATCTCTACTTAAACAGATGAAGAACT 3040
D 2982 CT- ---ATAATAGGAAATAACAGTCTCTACTACTCAAGTTGTCTAAGATT 32062
QY 3041 GAGGCTCAGAGGCTGAGCTATTTGCCCAAGATCACAGCTTGTAAAGTGTGACAGTTT 3100
D 3042 CAGTCAGTGAATATTTAATCACTGGTTTAAAGACATATATATATATATATATATATTT 32002
QY 3101 GGGTTTTTTTTTGTGTTTGTAGAGACAGGCTGTCTGTCTCACCAGGCGATCAGCAC 3160
D 3102 TTTTTTTTTTTTTTTTTTTTTTTTGTAGACA--GTCTACTGTCTGCCAGGCTGAGTGC 31944
QY 3161 AGTGTGCAACCATAGGTCACTGACGCTCAACCTCTCTGAGCTCAAGGATCTGTGACC 3220
D 3162 AGTGGCGTATCTTGGCTCACTGCAAGCTCCACCTCCCGGGTTCTATGCCATTTCTCTGCC 31884
QY 3221 TCAGCTCCCAAGTGTGGGACTACAGAGCTGACACACCGCTGCGCTGCTAATTAATAA 3280
D 3222 TCAGCTCCCGAGTAGCTGGGACTACAGCGCCGCCACCGCCACCTAATTTTGT 31824
QY 3281 ATTTTTTTGTAGAGACTGGTCTTACTAGTTGGCCAGGCTGTCTTAACTCTCTGGCTT 3340
D 3282 ATTTTTAT-TAGAGACGGGTTTACCAATTTTAGCCAGATGGTCTCTATCTCTGACT 31765
QY 3341 CAAGCAATCTCTACCTTGGCATCCCAAGTGTGGGATTAACAGGGGTGAGCCACCATG 3400
D 3342 C--GTGATCCGCGCTCTCGCTCCCAAGTGTGGGATTAACAGGCTGAGCCACCGC 31707
QY 3401 TCGGCTACTTATTTCTTTTCAATTCATCTTTTCCAAATAGAATGTAAAGATCCACAGACAG 3460
D 3402 CTGGCCCTTTTTTTTTT- --- 31690
QY 3461 GGATTACTGCCTATTTTCTCTCTCTTTTGTAGACAGAGTCTCACTTCTATCTCACTCAA 3520
D 3462 -GTTTGTGTAGACAGAGTCCCGCTCTGTCTATGACGCTGGAGTGCAGTGTGGCTATC- -- 31633
QY 3521 CTTCCGTTTCAAGTCACTGCAACCTCTGCTCCCGGGTTCAAGYGATTTCTCTGCTTAAGC 3580

Qy	2333	GGAGGCCGAGCGGGCGGATCACTTGAGGTCAGGAGTTCGAGCCAGCCTCGGCCAACATG	2392
Db	26867	AGAGGCCAACACAGGCGGATCACCTGAGGTCAGGAGTTCGAGCTAGCCTGACCAACATG	26926
Qy	2393	GTGAACCCCTGTCTCTACTAATAAATAACAAAATTAGCCGACATGTTGGCGAGCGCCTG	2452
Db	26927	GAGAACCCCTCTCTACTATAAAAA--TACAAAATTAGCCGGCGTAGTGCCACATGCTTTG	26984
Qy	2453	TAACCCAGCTACTCTGGGAGACT-----GAGTTGGAGGT	2486
Db	26985	TAATCTTAGCTACTCTGGGAGGCTGAGCGAGGAATCGCTTGAAACCGGGAGTCAAGAGT	27044
Qy	2487	TTCAAGTGAGCAAGGTCGTCTCACTGCTGCTCCAGCCTGGGTAAAC-AGAGCAACTCTGTCT	2545
Db	27045	TGCTGTGAGCGAGATCAGGCCATTGCATCCAGCCTGGCAACAGAGCAAACTCCGT	27104
Qy	2546	CAAAAAAATAATGCTTTCATAATAATATGATAAAGGACTTATATTTTTCAAGCCA	2605
Db	27105	CTCAAAAAAAGAAAGAAAAACACTGATTTAGACCAACTGCCTCGTTTTACAGATAGA	27164
Qy	2606	TAGGATCATTTCTCCAGACATCTTTGGCGAAGTCATCCCAACCTGTTCCCGAGAGTGG	2665
Db	27165	GAGGTCGACCCCTAGAGAAGGTGAGTCCAGGTCATCCAGGAGGTAGACTCTTTTCTCTCC	27224
Qy	2666	CAGGTGAGGCTGACACTATTGCTCTGCATCTCACTCTATCTCAGCTGTCCCTCCCACTTT	2725
Db	27225	AGCTCAGAGCTTTCAACCTTTAAATGTGATCAAAATCACTTGGCAGTCTCTGTTAATGT	27284
Qy	2726	CCAGGTGCTGCC-----AGACACATGACAACTGTGTAGCAGGCGCAAGAGCTGGACA	2779
Db	27285	GCAGATTCTGATTTGGTAGGTTGCAGGAAGCCTGCGATTTGTTATTTGTTGTTCTT	27344
Qy	2780	GCTGTAAATTTCTGCTGGACAMMCGGTACACCCACACTATTTCATCTCTGCTCTGCT	2839
Db	27345	TGTTTGAGATGGAAATTCACTCTGTTGCCCCAGGCTGAGTGCAATGCGCACTATCTCGC	27404
Qy	2840	CGGCAATCACTGTAGCAGTAGGTTTAT-----CCCTCTCTTGACCT	2881
Db	27405	TCAGTCAACCTCTGCTCCGGTTTCAAGCGATCTCTGCTCAGCTCCCGAGTAGC	27464
Qy	2882	ATGAATTTCTAGTTGGTTCTCAGTAGGCGGGGGAAATAATAGTAACAACAGCCATGAT	2941
Db	27465	TGGGATTACAGGCATGTGCCACTATGCTCGGCTAAATTTGTATTTTAGTAGAGA-CAGG	27523
Qy	2942	TAGTGTAAATTTCTTGGTCTCGGCAGTGTCTCCTTTAATCCTCAGAACACACTATGG	3001
Db	27524	GTTTCTCCATGTTGGTCAAGCTGGTCTTGAACTCTCTGACCTCAGGTGATCTGCCCACTC	27583
Qy	3002	GATAGGTACAATTTATCTCTACTTTAACAGATAAGAAAACTGAGGCTCAGAAAGCTGAGCTA	3061
Db	27584	AGCTCCCAAGTCTCTGGATGACAGCGGTGAGCCACTCGGCCACGCGAGATTGTGTCAT	27643
Qy	3062	TTTGCCCAAGATCACACAGCTTGTAAGTGGTGACAGTTTGG-----GTTTT	3107
Db	27644	TCTTAACAAGCTCCAGGGGATGCCAATACTGTGAGTTGGGACACACTTGATTTTTTTTT	27703
Qy	3108	TTTTTGTGTTGTTTAGAGACAGGCTCTGCTCTGTACCCAGGCAATGAGCACAGTGGTG	3167
Db	27704	GTTTTTGTGTTTTTTTAGACAGGGTCTCACTCTGTCTCTCCAGGCTGAGTGCAGTGGCA	27763
Qy	3168	CAACCATAGTCACTGCAGCCTCAACCTCTGAGCTCAAGGATCTGTGACCTCAGGCT	3227
Db	27764	GGTTCCTCGGCTCAATGCAACCTCCGCTCTCTGGTTCAAGTGATTTCTGTGCTCAGCT	27823
Qy	3228	CCCAAGTAGCTGGGACTACGAGCGTGACACCAACGCTGGCTAAATAAAAAATTTTTT	3287
Db	27824	CCCGAGTAGCTGGATTACAGGCTTGAGTTACCATGCTGGCTAAATTTTTTTTATTTT	27883
Qy	3288	TGTAGACATGGGTCTTACTAGCTGGCCAGGCTGTCTTAACCTCTCGGCTTCAAGCAA	3347
Db	27884	-GTAGAGACAGGTTTCCCATGTTGCCGAGACTGCTCTCCAACTCTCGGCTCAATTTGA	27942

3348	Qy	TCTCTCTACCTTGGGATCCCAAAGTCTGGGATTAACAGGGGTGAGCCACCAATGTCGGCT	3407
27943	Db	 TCCACATACCTCAACT--CATAGTGTCTGGGATTAACAGGTGTAAAGCCACTGTGTCTGTCT	28000
3408	Qy	ACTTATTTCTTTACATTCATCTTTCCAAATAGAAATGTAAGATCCACAGAACAGGGATTAC	3467
28001	Db	 TGTTTTTATTAATTTTT-----ATTTT	28022
3468	Qy	TGCTATTATTTCTTCTCTTTTGTGAGACAGAGTCTCACCTTCATCACTCAACCTCCGT	3527
28023	Db	 TTATTTTTGAGATAGGGTCTCACTGTGCCCAGGCTGGAGTGCAATGGCAATC-----	28077
3528	Qy	TCAGTCTACTGCAACCTCTGGCTCCCGGGTTCAAGYGAATCTCTGCGCTCAAGCCTCTGA	3587
28078	Db	 ATGGCTCCCTGAGCCTCAAACTCTGGGATCAAGTGAATCTCCACCTCAGCCTCTCCAA	28137
3588	Qy	GTAGCTGGNAATTACAAGCGTGCACCAACCATGCTGGCTAAATTTTT--TGTATTTTTAGCA	3645
28138	Db	 GTAGCTGGGACTACAGATGGGAAACACCACTGCTGTCTAAATTTTTTAAAAAATGTTTGTGA	28197
3646	Qy	GAGATGGGGTTTTTACATGTTTGCCCAGGCTGGTCTCAAACTCCCTGACCTCAAGTGAATCTG	3705
28198	Db	 GAGATGGGGTCTCCCTATGTTTGCCCAGGCTGGTCTTAAACTACTGACCTCAAGTGAATCT	28257
3706	Qy	CCTGCTCAGTCTCCCAAGTCTGGAAATATAGCGGTGAGTCACTGTGCTGCG-----	3760
28258	Db	 CTTGCTTGGCCTCCCAAGTACTAGGATTTTCAGTTGTGAGCCACCATACCCAGCTGGGA	28317
3761	Qy	----CGATTACTGTCTATTTTCTTTATTCCTATATCCCCAGATCTAGAGCAGTGTCTGACA	3817
28318	Db	 CCACACTGAATAGCAAGGCTCTGTCTAACTCTTCAGCAGACACATTTCTCCCTCATACCA	28377
3818	Qy	TATAGTAGTGTCTCAATAAATAATGATGAATGCACAGCCTAGATATATAAACTTTCTTTT	3877
28378	Db	 CCTGGTAAGTGAATCACTGTAACCTCTCAATGGCAGGACAGGCTCTTGTTCAATTTATGT	28437
3878	Qy	CTTTTTTAAAACAATCTTGACACTTTTGCAG--AATAAATACAATCTTGCAATCTCTGCTT	3935
28438	Db	 GCCCTCAACCACTTACCTACACAGTTTCCCGGCACACAGTGAGGGCTTAATTAACACCC	28497
3936	Qy	TTTCACCTTACACCTGTTATGACTTTTTCATATTCCTTCAAACTTTATTTGTTACTGTT	3995
28498	Db	 ACTGACTCTAGTGTGTTTCAGGTTCTCAGCAAAAGTGCCAAACACTCTTGAGCAAAAACTT	28557
3996	Qy	TTTTTCATTGTTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTTATACATCTCTCC	4055
28558	Db	 GTTCAAGGCTGGGCACAGTAGCTCATGCTATGATCCAGCACCTTTGGAAAGCTGAGGTG	28617
4056	Qy	TGCTCCACTTTAGAGGCCAAATTTACAAATCTGTATGAAGCTATGAACCTCTCCCCAG	4115
28618	Db	 GGAGGACTGCTTGAGCCCAAGGATTTTGAGACTG-----CCTGGGTGA	28660
4116	Qy	AGAAATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCACCTAAGA	4175
28661	Db	 CATAGTAAGACTGTCATCTCAAAAAACAAAAACCTTATTCAAAAACATTTTCTTGCAATGC	28720
4176	Qy	CAAGAAACCTGCATTAGAGGATGTTTGTTCATATTAATTAATAAATAAATCACTCAGTTGGGCAC	4235
28721	Db	 TTCTTTGTGACACACACTGGAGAAAGCACTTTTCATAAATAGATTTGTGGGCCAGATGT	28780
4236	Qy	AGTGACTCAAGCCTGTAACCACTGACTTTTGGAAAGTCCAAGGTGGGTGGATCACTTGAGG	4295
28781	Db	 GGTGGCTCATGCTGTATATCACAGCACCTTTGGAGGCCGAGCGGGGATCACTCTGAGG	28840
4296	Qy	TGAGAAGTTTCGAGACAGCGCTGGTCAATATATGGTGAACCCCTATCTCTACTAAAAATACAA	4355
28841	Db	 TCAGGAGTTTCGAGACAGCGTTTGGCCAAACATGATAAAACCCCGTCTCTACTAAAAATAC-A	28899
4356	Qy	AAATTAGCTGGGTGTAGTGCATGCTGCTGTAGTCCAGCTACTCGGAGGCTCAGGCCAA	4415
28900	Db	 AAATTAGCTGGACATGGTGACACAGCCTGTAAATCCCACTACTCTCGGAGGCTCAGGCAG	28959
4416	Qy	GAGAAATTGCTTGAACCTCGGAGGCAGAGGTTGCAATGAGCCGAGATCCCACTCGCACT	4475

Db 28960 GAGAAATGGCTTGAACCTGGGAGCGGAGGCTACAGTGAGCCAAGATCATGCGCACTGCACT 29019
Qy 4476 CGAGCCTGGCGACACAGCGAGACTTACTCAAAAAAATAAATAAATAA 4531
Db 29020 CCACCCCTGGGTGACAGAGTGAGACTGTGCTCAAAAAAATAAATAAATAA 29075

RESULT 11

US-11-114-798-58
; Sequence 58, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 58
; LENGTH: 318488
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-58

Query Match 7.8%; Score 387.6; DB 18; Length 318488;
Best Local Similarity 53.6%; Pred. No. 42;
Matches 1252; Conservative 3; Mismatches 937; Indels 144; Gaps 16;

Qy 2273 ATGTTAAATCGCTTTCAGGCGAGCGGGTGGCTCATGCCCTGTAAATCCAGCACTTTG 2332
Db 84122 ATTTTAAATAGTTATCTGTTGGCCAGCATGGTGGCTTGTGCCCTATAATCCCAGCACTTAG 84181
Qy 2333 GGAGGCGGAGCGGGCGGATCACTTCAGGTGAGAGTTCGAGACCAAGCCTGGCCAAACATG 2392
Db 84182 AGAGGCCAAGACAGCGGATCACTTCAGGTGAGAGTTCGAGACTAGCCTGACCAACATG 84241
Qy 2393 GTGAAACCCCTGCTCTACTATAAATAATACAAATATAGCCGACATGGTGGCGAGCGCCTG 2452
Db 84242 GAGAAACCCCTCTCTACTATAAATAA--TACAAATATAGCCGGCGTAGTGGCACATGCTTG 84299
Qy 2453 TAACCCAGCTACTTGGGAGACT-----GAGTTGGAGGT 2486
Db 84300 TAATCTAGCTACTCGGGAGGCTGAGGCGAGGAGAAATCGGTTGAACCCGGGAGTCAAGGT 84359
Qy 2487 TTCAGTGAGCAAGTCTGCTACTGCTCCAGCCTGGGTAAAC-AGAGCAACTCTGTCT 2545
Db 84360 TGGTGTAGCCGAGATCAGGCCATTGCATCCAGCCTGGGCAACAGAGCAAACTCCGT 84419
Qy 2546 CAAAAAATAAATGCTTTCAATAATAATATATGATAAAGAGCTATATATTTTTCAGGCA 2605
Db 84420 CTCAAAAAATAAAGAAAAAACAACCTGATTTAGACCAACTGCTCGTTTACAGATAGA 84479
Qy 2606 TAGGATCATTTCTCCTGAGACATCTGGCGAGTCAATCCCACTGTTCTCGAGTGGG 2665
Db 84480 GAGGGTGACGCTAGAGAGGTCAGCTCCAGGTCATCCAGGAGGTTAGAGCTCTTTCCTCC 84539
Qy 2666 CAGGTGAGGCTGACCTATTGCTCTGCACCTACTCTATCTCAGCTGTCCTCCCACTTT 2725
Db 84540 AGCTCAGAGCTTTTCAAACTTTAATGTGATACAAATCACTTGGCAGTTCTTGTAAATGT 84599
Qy 2726 CCAGGTGCTGCC-----AGACACATGACAACTGTCTAYGACCAGGCCAAGAGCTGGACA 2779
||||| |||

84600 GCAGATTCGTGATTTGGTAGTTGCGAGGAGCTGCGATTTGTATTCTTTGTTGTTCTT 84659
Qy 2780 GCTGTAAATTTCTGCTGACACAMMCGTACACCAACCTATTTCATCTCTGCTCTGGCT 2839
Db 84660 TGTTTGAGATGGAATTTCACTCTTGTGTCAGGCTGGAGTCAATGGCACTATCTCGC 84719
Qy 2840 CGGCAATCACCTGTAGCAGTAGGTTTAT-----CCCTTCCTTTGACCT 2881
Db 84720 TCACCTGCAACCTCTGCCCTTCGGTTTCAAGCGATTCTCTGCTCAGCGCTCCGAGTAGC 84779
Qy 2882 ATGAATTTCTAGTTGGTTCTCAGTAGCGCGGGGAAATAATAGTAACAACACCATGATT 2941
Db 84780 TGGGATTACAGGCATGTGCCACTATGCTGGCTAAATTTGTATTTTATAGTAGAGA-CAGG 84838
Qy 2942 TAGTGTAAATTTTCTGTCGCGAGTGTCTCTTTAAATCCTCAGAACAACTATG 3001
Db 84839 GTTCTCCATGTTGTCAGGCTGGTCTTGAACCTCTGACCTCAGGTGATCTGCCACCTC 84898
Qy 3002 GATAGGTACAAATTTATCCTCACTTAAACAGATAAGAAAACTGAGGCTCAGAAAGCTGAGCTA 3061
Db 84899 AGCCTCCCAAGTGTGGATGACAGGCTGAGCCACTGCGCCAGCCGAGATTTGTCTAT 84958
Qy 3062 TTGCCCCAAGATCACACAGCTTTGTAAGTGGTGACAGTTTG-----GTTTT 3107
Db 84959 TCTTAAACAGCTCCAGGGGATGCCAATACTGTCAAGTTGGGACCACTTGATTTT 85018
Qy 3108 TTTTGTGTTGTTTAGAGACAGGCTTGTCTCTGTCACCCAGGATGAGCAGTGGTG 3167
Db 85019 GTTTTGTGTTTGTGAGACAGGCTCACTCTGTCTTCCAGGCTGGAGTGCAGTGGCA 85078
Qy 3168 CAACCATAGGTCACCTGACGCTCAACCTCTGAGCTCAAGGATCTGTGACCTCAGCT 3227
Db 85079 GGTTCCTGCTCAATGCAACCTCCGCTCTCGGTTCAAGTGTCTTGTGCTCAGCT 85138
Qy 3228 CCCAAGTAGCTGGAGTACAGGCTGACCAACCTCCGCTCTCGGTTCAAGTGTCTTGTGCT 3287
Db 85139 CCCGAGTAGCTGGGATACAGGCTTGAAGTACCATGCTGCTGCTAAATTTTATTTT 85198
Qy 3288 TGTAGAGACTGGTCTTACTAGTTGGCAGGCTTGTCTTAACTCTCTGGCTTCAAGCAA 3347
Db 85199 -GTAGAGAGAGTTTACCATGTTGCCAGACTGGTCTCCAACTCTCTGGCTCAATGA 85257
Qy 3348 TCCTCTACCTTGGCATCCCAAGTGTGGGATTAACAGGCTGAGCCACCATGTGCGCT 3407
Db 85258 TCCACATACCTCAACT--CATAGTCTGGGATTAACAGGTGTAAGCCACTGTGCTGTCT 85315
Qy 3408 ACTTATTTCTTACATTCATCTTTCCAAATAGATGTAAGATCCACAGAACAGGATTAAC 3467
Db 85316 TGTTTTTATTTATTTT-----ATTTT 85337
Qy 3468 TGCCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCTCCGT 3527
Db 85338 TTATTTTGTAGATAGGTTCTACTGTTGCCAGGCTGGAGTCAATGGCAATC----- 85392
Qy 3528 TCAGCTCACTGCAACCTCTGCTCCCGGTTCAAGYGATTCTCTGCTTAAGCTCTCTGA 3587
Db 85393 ATGGCTCTCCGAGCTCAAACTCTCTGGATCAAGTGTCTCCCACTCAGCTCTCCAA 85452
Qy 3588 GTAGCTGGAATTAACAGGCTGACACCATGCTGGCTAAATTTT--TGTATTTTACGA 3645
Db 85453 GTAGCTGGGACTACAGATGGGAAACACCACTGCTGCTAAATTTTAAAAAATGTTTGT 85512
Qy 3646 GAGATGGGTTTACACTGTTGCCAGGCTGCTCAAACTCCTGACCTCAAGTGTATCTG 3705
Db 85513 GAGATGGGTTCTCCCTATGTTGCCAGGCTGGTCTTAACTACTGACCTCAAGTGTCTCT 85572
Qy 3706 CTTGCTCAGTCTCCCAAGTGTGGAATTAATAGGCTGAGTCACTGTGCTTGGC----- 3760
Db 85573 CTTGCTTGGCTCCCAAGTACTAGGATTTTCAAGTTGTGAGCCACCACTACCCAGCTGGGA 85632
Qy 3761 ---CGATTTACTGTCTATTTTCTTTTATTTGCTATATCCCGAGATCTAGACAGTGTCTGACA 3817
Db 85633 CCACACTGAATAGCAAGGCTCTCTGCTAACTCCTTCAGCAGACACATTTCTCCCTCATACCA 85692

QY 3818 TATAGTAGTGCTCAATAAATAATGATGAATGCACAGCCTAGATATAAATCTTCTTTT 3877
Db 85693 CTTGGTAAGTGATCACTGTAAATCTTCAATGGCAAGGACAGGCTCTTGTTCATTTATGT 85752
QY 3878 CTTTTTTAAACAATCTTGACAACTTTTGAG--AATAAATAAATCTTGTCAATCTGTCTT 3935
Db 85753 GCCCTCAACCACTACCTACCAAGTCCCGGCACACAGTGAAGGCTTAATTAACACC 85812
QY 3936 TTTCACTTATCACTTGTGTTAAGACTTTTTCATATGCTCAAAACCTTTATTTGTTACTGTT 3995
Db 85813 ACTGACTCTAGGTGGTTTCAAGTTCTTAGCAAAAGTGCAAAACCTTTGAGCAAAAACCTT 85872
QY 3996 TTTTCATTTTACTATTTTGTGCTCACTGAATAATATGGCTTAATTTGCTTATACATCCTCC 4055
Db 85873 GTTCAAGGCTGGGCACAGTAGTCACTGCTTATGATCCAGCACTTTTGGAAAGGCTGAGGTG 85932
QY 4056 TGCTCCACTTTAGAAAGCCAAATTTTACAAATCTGTATGAAGCTATGAACCTCTCCCCAG 4115
Db 85933 GGAGGACTGCTTGAGCCAGGAGTTTGAGACCTG-----CCTGGGTGA 85975
QY 4116 AGAAATACACACACACACACACTCACACAGTCTTCTTAAATGTTTGAACCTAAGA 4175
Db 85976 CATAGTAAGACTGCTCTTACAAAACCAAAACCTTATTCAAAAACATTTCTCGCATGC 86035
QY 4176 CAAGAAACCTGCTATGAGGATGTTTCTCATATTAATTAATAATTAACAGTTGGGCAC 4235
Db 86036 TTCTTTGTGACAGACACTGGAGAAAGCACTTTTTCATAATGATGTTTGGGCCAGATGT 86095
QY 4236 AGTGACTCAAGCCTGTAAACACACAGTACTTTTGAAGTCCAAAGTGGGTGATCACTTGAGG 4295
Db 86096 GGTGGCTCATGCTGTAAATCACAGCACTTTGGGAGCGGAGGCGGATCACCTTGAGG 86155
QY 4296 TGAGAAGTTGCGAGACCAAGCTGTGTAATATGTTGTAACCTTATCTCTAATAAAATACAA 4355
Db 86156 TCAGGAGTTGCGAGACCAAGCTTGGCCAAACATGATAAAACCCGCTCTCTACTAAAAATAC-A 86214
QY 4356 AAATTTAGCTGGGTGTAGTGATGATGCTGCTAGTCCAGCTACTCGGAGGCTGAGGCAA 4415
Db 86215 AAATTTAGCTGGACATGGTGACACAGCTGTAAATCCAGCTACTCGGAGGCTGAGGCAG 86274
QY 4416 GAGAAATGCTTGAACCTGGGAGGACAGAGTTTGCAGTGAGCGAGATCCCAACCACTGCACT 4475
Db 86275 GAGAAATGCTTGAACCTGGGAGGAGGCTACAGTGAGCAAGATCATGCGCACTGCACT 86334
QY 4476 CCAGCTGGGCGACACAGCAGACTCTATCTCAAAAAATAAATAAATAAATAA 4531
Db 86335 CCACCTGGGTGACAGAGTGAGACTGTGCTCAAAAAATAAATAAATAAATAA 86390

RESULT 12
US-11-121-086-14/c
; Sequence 14, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121.086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 167891
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-14

Query Match 7.7%; Score 384.8; DB 17; Length 167891;
Best Local Similarity 53.8%; Pred. No. 71;

Matches 1239; Conservative 3; Mismatches 910; Indels 150; Gaps 16;
QY 2292 GCCAGAGGCGGTGCTCATGCTGTATATCCAGACACTTTGGGAGCGCGAGCGGCGGA 2351
Db 61654 GCCAGAGCGGTGCTCACCCCTGTATCCAGACACTTTGGGAGCGCGAGCGGCGGA 61595
QY 2352 TCACCTTGAAGTTCAGAGTTCGAGACAGCCTGGCCAAACATGTTGAAACCTCTCTACT 2411
Db 61594 TCACCTGAGTTCGAGTTCGAGACAGCCTGGCCAAACATGTTGAAACCTCTCTACT 61535
QY 2412 AAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2471
Db 61534 AAAAAA--TACAAAAATTAGCCAGCATAGTGGTACATGCTGTAACTCCAGCTACTTGGGA 61477
QY 2472 GACTGAGT--TGGAGTTCAGTGAGCCAAAGTGTGCTGCTGCTCCAGCCTGGTAAAC 2530
Db 61476 GGTGAGTTCAGGAGAAATGCTTGAACCTGGGAGGAGAGGTTTCGGTGAGCGAGATGTC 61417
QY 2531 AGAGCAACTCTGCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 2590
Db 61416 GCATTGCACTCCAGCCTGGGCAACAGAGC--AAACTCCGCTCAAAAAATAAATAAATAA 61358
QY 2591 TATTTTTTCAAGCCATAGATCATTTCTCTGAAGCATCTTGGCGAAGTCACTCCCACT 2650
Db 61357 AAAAAAGACACAGATGGGAGGAGGAGTGAAGAGAGGTTGATTAATGATGACAAATA 61298
QY 2651 GTTCTGAGAGTGGGAGGCTGAGGCTGACCTATTTGCTCTGCACCTACTCTCTACTCAGC 2710
Db 61297 TATTTTGTATACAAAGATGAAGACCACTTACTGTTTCAATAGATCAGTAGATGATTATGT 61238
QY 2711 TGTCCCTCCCACTTCCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAAGGCAAGA 2770
Db 61237 TATCATTAATTTGATGGTGCATTCCTCAATTTAGTGAATAAATAAATAAATAAATAA 61178
QY 2771 AGCTGGACAGCTGTAAATTTCTGTGGACAMMCCGTACACCCACACCTTATTCATCTCGT 2830
Db 61177 TAAAGAAAAGATAAATAATTTTCAAGT--GATGGATATTTCAATTTACCTGATGATTATAT 61119
QY 2831 GCTCTGGCTGGCACTACCTGTAGCAGTGTGTTTATCCCTTCTTGACCTATGATTCCT 2890
Db 61118 GAATGTATCAAAATTTACATGTACCGTCCAAAAATATG-----TACATCA 61074
QY 2891 AGTTGGTTCTCAGTAGGCGGGGGAATAATAGTAACAACAGCCATGATTTAGTGTAA 2950
Db 61073 AATTTGTATCAACAAAAATAAATCAATCAATATAGGACACAGATGAACCCAGATG 61014
QY 2951 TTTCTTGGTCTGGGAGTGTCTCTTTTAACTCTCAGAACACACTATGGGATAGGTAC 3010
Db 61013 AAGTACGTGGGGAGGCTCTGAAAGGATAGGTATCAACAATA-----GGAGCTTC 60964
QY 3011 AATTATCTCACTTAACAGATAAAGAAACTGAGGCTCAGAGGCTGAGCTATTTGCCCAA 3070
Db 60963 TGTCTTCAATGAGATGAAGTGTGCCACTCTCTGCGCCATGGAGGCTTTTACTCAGCTCAT 60904
QY 3071 GATCACACAGCTTGTAAAGTGTGACAGTTTGGGTTTTTTTTTTTGTGTTTGTAGACAG 3130
Db 60903 CAAGTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGTTTGTGAGACGG 60844
QY 3131 GGTCTTGTCTGTCAACCCAGGATGAGCAGTGTGTGCAACCATAGGTGCTCTGAGCCTC 3190
Db 60843 AGTCTCACTCTGTGCGCCAGGCTGGAGTGCAATGGCAGATCTCGGCTTACTGCAACCTG 60784
QY 3191 AACCTCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTAGGAC 3250
Db 60783 CACCTCCAGGTTCAAGCGATTTCTCTGCTCAGCCTCAGAGTAGCTGGGATTTACAGGC 60724
QY 3251 GTGCAACCAACGCTGCTAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 3310
Db 60723 ACCCACTACCGCCAGCTAATTTTGTACTTTTA--GTAGAGACGGGTTTCCACATG 60666
QY 3311 TTGGCCAGGCTTGTCTTAACTCTGGCTTCAAGCAATCTCTCTACCTTGGCATCCCAA 3370
Db 60665 TTGGTCAGACTGTCTTGAACCTCTGACCTCAAGCATTTCCACCTCGGCTCGGCTCCCAA 60606

QY 3371 GTGCTGGGATTAACAGGGGTGAGCCACCATGTGGGCTACTTAATTTCTTTACATCTC 3430
Db |||||
60605 GTGCTGGGATTAACAGGCATGAGCCACCGTGGCCGGCTTTTCTTTCTTGAGAT-- 60548
QY 3431 TTCCAATAGAATGAAGATCCACAGAACAGGGAATTAAGTCTCTTTCTTTT 3490
Db |||||
60547 -----GGAGTCTCACTC 60536
QY 3491 TTGAGACAGAGTCTCACTTATCATCACCTCAACCTCGTTCAGCTCACTGCAACCTCGCCT 3550
Db |||||
60535 TGTGGCCAGGCTGGAGTGAGTGGTGAATCTCG-----GCTCACTGCAACCTCTGCCT 60481
QY 3551 CCGGGTTCAAGYGATTCTCTGCTTAAGCTCCTCGAGTAGCTGGAATTAACAAGCGTGCA 3610
Db |||||
60480 CCGGGTTCAAGCGAATCTCTGCTCAGCTCCCAAGTAGCAGGATTCAGAGGTGCA 60421
QY 3611 CCACCATGCTGGCTAAATTTTGTATTTTATAGCAGAGATGGGTTTACCATGTTGCC 3670
Db |||||
60420 CCACCACGACGAGCTAA--TTTTGTATTTTATTAGACGCGGATTTTCAACATGTTGCC 60362
QY 3671 AGGCTGGTCTCAAACTCCTGACCTCAAGTATCTGCTGCCCTCAGTCTCCCAAGTGCTG 3730
Db |||||
60361 AGGCTGGTCTCAACTCTTGACCTCAGGTGATCTCCACCTTAACCTCCCATAGTGTG 60302
QY 3731 GAATTATA-----GGCGTAGTCACTGTGCTGCCCTGGCGGATTAAGTCTC 3771
Db |||||
60301 GAATTACAGGTGTGAGCTGGGATTACAGGTGTGAGCCACCGCACCGGCCCATCAAGTGT 60242
QY 3772 TATTTTCTTTATTTGCTATATCCCAAGATCTAGAGCAGTGTCTGA----- 3815
Db |||||
60241 TGTTCACAGGTTTATGAGGCTTTGGCCAGGAGCGGTGCTCATGCCGTGAACCCGCAAC 60182
QY 3816 -----CATATAGTAGTGCTCAATAATAATATGATGATGCACAGCCTAGAT 3862
Db |||||
60181 ACTTTGAGAGGCTCATGTAGGAGGATCACTTGAGCAGGAGTTCAAGACCAGCCTGGGC 60122
QY 3863 ATAAACTTTCTTTTCTTTTAAACCAATCTTGACAACTTTTGACAGATAATAACAATC 3922
Db |||||
60121 ATATACTGAGACCCCATCTACAAAAACCCCTTATTTTAAATTAATAAAAAATTTT 60062
QY 3923 TTGCATTTGCTTTT--TTCACTTATACCTTTGATGACCTTTTTCATATTTGCCCTCAAACT 3981
Db |||||
60061 TTTTCTTTTGTAGATGAGTCTTGCTCTGTGGCCAACTGGAATGCAATGGCGCGATCTC 60002
QY 3982 TTATTTGTTACTGTTTTTCTATTTTACTATTTTAGTCACTGAATATATGCTTAAATTTG 4041
Db |||||
60001 AGCTCACTGCAACTCTGCTCTCCCGGTTCAAGCAATTTCTTCTCAGCCTCTTGTAGTAC 59942
QY 4042 CTTATACATCTCTCTCCACTTTTGAAGGGCCAAATTTTACAAATCTGATGAAAG----- 4096
Db |||||
59941 TGGGATGACAGGCAGGCACCACTACGCTGGGTAAATTTTGTATTTTAAATAGACACAA 59882
QY 4097 -----CTATGAACCTCTCTCCAGAGAAATACACACACACACACACACACAGT 4150
Db |||||
59881 GTTTCACCATGTTGGCTAGGCTGGTCTCAAACTCTGACCTCAAGTGATCCACCCACCTC 59822
QY 4151 TTTTCTTTTAAATGTTTCAACTAAGACAAACCTGCAATAGAGGATGTTTGTTCATATT 4210
Db |||||
59821 ATCCCTCCCACTTGTGGGATTAACAGCGTGAGTCACTGCTAGTGGGTCCCTAAAAATTTT 59762
QY 4211 AATTA--AAATAACTCAGTTGGGCAGTGACTCAAGCCTGTAACACACAGTACTTTGGAA 4269
Db |||||
59761 ATTAAATTAATAACATGGCGGGGTGGTGGCTCATGCTGCAATCCAGACACTTTGGA 59702
QY 4270 GTCCAAAGTGGTGGATCACTTGTAGGTGAGAGTTTCAGACACGAGCTGTGTAATATGGTG 4329
Db |||||
59701 GGTGAGGGGGGGGAATCACTGAGTTTCAAGAGTTTCAAGACCGGCTGCATAAACATGGTG 59642
QY 4330 AAACCTATCTCTACTAAATAACAAATATAGCTGGGTAGTGTGATGATGCCTGTAGT 4389
Db |||||
59641 AAACCTGTCTCTAC--AAAAACAAAAATTAGTGGGTATGATGCGGATACCTGTAAAT 59583

QY 4390 CCAGCTACTCGGAGGCTGAGCGAAGAAATTTGCTGAACCTGGAGCGAGGTTGCA 4449
Db |||||
59582 TCCAGCTACTCGGAAGTTGAAGCAGGAGAAATCGCTTGAACCCAGAGCAGAGTTGCA 59523
QY 4450 GTGAGCCGAGATCCCACTGCTGCTCAGCTCCAGCTGGCGACACAGGAGACTCTATCTCAA 4509
Db |||||
59522 GTGAGCCGAGATCAAGCCTTGCCTCAACTGGCAACAGAGCAAGGCTGTCTCAAAA 59463
QY 4510 AAAAAATAAATAAATAAATAA 4531
Db |||||
59462 CAACAACAACAAGAAATAA 59441

RESULT 13
US-11-121-086-33/c
; Sequence 33, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; PRIOR FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-33

Query Match 7.7%; Score 384.2; DB 17; Length 154548;
Best Local Similarity 59.4%; Pred. No. 76;
Matches 861; Conservative 1; Mismatches 524; Indels 63; Gaps 10;

QY 3085 TAAAGTGTGACAGTTTGGGTTTTTTTTTTTGTGTTGTTTGTAGACAGAGGTTCTGCTC-TGT 3143
Db |||||
72006 TTAGTCTGTTTATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 71947
QY 3144 CACCCAGCATGAGCAGATGGTGCACATAGGTCACTGACGCTCAACCTCCTGAGCT 3203
Db |||||
71946 CACCCAGCGTGGAGTGCAGTGGTGCATCTCGGCTCACTGCACAACTCTGCTCCTGGGT 71887
QY 3204 CAGGGATCTGCTGACCTCAGCTCCCAAGTAGTGGGACTACGAGCGTGACACACCAG 3263
Db |||||
71886 CAAGCAATTTCTCTGCTCAGCTCCCAAGTAACTGGGATTACAGGCGTGACACACCACA 71827
QY 3264 CTTGGCTAAATTAATAAATAAATTTTGTAGAGACTGGGTCTTTACTAGTGGCCAGGCTTG 3323
Db |||||
71826 CCCG--GCTAATTTTGTATTTGTAGAGCGAGTTTCAACATGTCGGCAGTCTGG 71769
QY 3324 TCTTAACTCTGCTGCTCAAGCAATCTCTCACTTGGCATCCCAAGTGTGGGATTAC 3383
Db |||||
71768 TCACCACTCTCTGACCTCAGGTGATCTGACTGCTCGCTCCGAAAGTGTGGGATTAC 71709
QY 3384 AGGGTGAACCACTGCGGCTACTTATTTTCTTATCTTCACTCTTCCAAATAGAATG 3443
Db |||||
71708 AGCGTGAAGTCAACAGCTGCGCAATTTAGTCT----- 71673
QY 3444 TAAGATCCACAGACAGGATTTACTGCTCTTTCTTCTTTTGTAGACAGATGTC 3503
Db |||||
71672 -----GAAAAATTTTCTTTTCTTTTGTAGCTCTTGGTCTGCCCC 71625
QY 3504 TCATTTCACTCACTCAACTCCGTTTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 3563
Db |||||
71624 AGGCTGGAGTACAGTGGGCTGATCTCAGCTCACTGACGCTCCATCTCCAGACTTAGGC 71565
QY 3564 GATTTCTCTGCTAAGCTCTCTGAGTAGTGAATTAAGGCTGACACCATCTGCTGG 3623
Db |||||
71564 GATTTCTCTGCTCAGCTCTCTGAGTAGTGGGATTACAGGACGCGCCACCCAG 71505

QY	3624	CTAATTTTGTATTTTACACAGATGGGTTTACCATGTGTCAGGCTGGTCTCAA	3683
Db	71504	C-AAATTTTGTATTTTGTAGATAGATGGGTTTACCAATGTGGCCAGGCTGGTCTGA	71446
QY	3684	ACTCTGACCTCAAGTGATCTGCTGCTCAGTCTCCAAAGTCTGGAATATAGGCT	3743
Db	71445	ATTCTCACCTCAAGTGATCCGCTGCTGGCTCCAAAGGCTGGGTTATAGCAT	71386
QY	3744	GAGTCACTGTGCTGGCC-----GATTACTGCTATTTTCTTTATTTGCTATATCCCA	3796
Db	71385	GAGCCACTGCACCTGGCCTAGCTCTTATAAATGTGCCATTTATTTATCATTTAAGGA	71326
QY	3797	GATCTAGACAGCTGTCTGACATATAGTAGTGTCTCAATAAATTAATTTGATG-AATGCACAG	3855
Db	71325	TGTATAGGGAGATCATTTGAAGACCTAGAGTTTGTAAATATATAGAGGACCAAACTTTA	71266
QY	3856	CCTAGATATAAATCTTCTTTCTTTTAAACAATCTTGACAACTTTGCAGATAAA	3915
Db	71265	CCGTAACCTCTAAAAGCCTCCACCTGGTCTGAGAACTAAATGGACATAAGGCATTAGC	71206
QY	3916	TACAATCTTGCAATCTGCTTTTTCACCTATACCTTTGTTATGACTTTTTCATATTCGCTC	3975
Db	71205	AGGAGAAAAGTATACAGATTTTACATGTGCATAGGAACCCCATGGGAAAATGAAGACC	71146
QY	3976	AAACCTTTATGTACTGTTTTCATTTGTTACTATTTTGTACTCTACCTGAATAATATG-GCT	4034
Db	71145	TAAAGAAGTGACAAAATCTAAGTGCTTATGTACTAGGTTGAACCCAGAGAAATTTGGA	71086
QY	4035	TAATTTGCTTATACATCTCTGCTCCACTTTAGAAGGCCAAAATTTACAAATCTGATGAA	4094
Db	71085	AAAGTAAGTCAATATATATGGGAGACCAAGGAAGATGAGTTATTTTACAAATGATTT	71026
QY	4095	AGTATGAACCTCTCCCCAGAGAAATACACACACACACACACTCACACACAGTTTTT	4154
Db	71025	TGTACAGAAATGTCT-----TAGCCTCCATTCGCTCTCTGTGGTCAGAATGTTG	70976
QY	4155	TTTTATGTTTGAACCTAAGACAAAGAACCTGCATTAGAGATGTTGTTGCATATTAAT	4214
Db	70975	CTTTCTCTCTGTACATAGAGGGCATCTTTTCAAGGGAGTTTGTCTTGTATTTCAAG	70916
QY	4215	AAAAATAACTCAGTTG---GGCACAGTGACTCAAGCCTGTAACACACAGACTTTTGGAGT	4271
Db	70915	AAGGGAGGTCAGAGGCCAGATGAGTGGCTCAGGCTTAATCCAGACACTTTGGGAGG	70856
QY	4272	CCAAGTGGGTGGATCACTTTGAGTGAGAAATTCGAGACACAGCCTGGTCAATATGTTGAA	4331
Db	70855	CCGAGTGGGTGAATCATTTGAGGCCAGGAGTTTGAACCCAGCCTGGCCCAACATGTTGAA	70796
QY	4332	ACCTATCTCTACTTAAATAACAAAATTAAGCTGGGTGATGATGCATGCCCTGTAGTCC	4391
Db	70795	ACCTTGTCTCAACTTAAAACTTACAAAATTAAGC-CAGTGTGGTGGTGGGTCCTGTAAATCC	70737
QY	4392	CAGTACTCGGGAGGCTGAGGCAAGAGAAATTTGCTTGAACCTGGGAGGACAGAGTTGCAGT	4451
Db	70736	GAGCTACTCCAGAGGCTGAGGCAAGAGAAATCGCTTGAACCCGGAGGTGGAGTTGCAGT	70677
QY	4452	GAGCCGAGATCCCAACCACTGCATCCAGCCTGGGGACACAGCGAGACTCTATCTCAAAA	4511
Db	70676	GAGCAGAGATCGGCCCACTGGACTCTAGCCTGGGGACAGCGAGACTCAGTCTCAAAA	70617
QY	4512	AAATAAATA 4520	
Db	70616	AAAAAATTA 70608	

RESULT 14

US-10-960-414-12/c
; Sequence 12, Application US/10960414
; Publication NO. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH

; APPLICANT: VEGA, VINSSENSUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; CURRENT FILING DATE: 2004-10-06
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 159440
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-960-414-12

Query Match	7.6%;	Score 381.4;	DB 13;	Length 159440;
Best Local Similarity	54.7%;	Pred. No. 79;		
Matches 1051;	Conservative	2;	Mismatches 773;	Indels 97;
Gaps	11;			
QY	3106	TTTTTTTGTGTTGTAGACAGGGTCTTCTCTGTCAACCAGGCATGAGCAGATGG	3165	
Db	72512	TATTTCTTTTCTTTTTTGAGACGGAGTCTGCTCTTTTGACAGGCTGGAGTGCAGTGG	72453	
QY	3166	TGCAACCATAGTCACTGCAGCCTCAACCTCCTGAGCTCAAGGATCTGCTGACCTCAGC	3225	
Db	72452	CACAGTCTCGGCCCACTGCAACCTCTGCTTCCAGGTTCAAGCGATTCTTTGCCTCTGC	72393	
QY	3226	CTCCCAAGTAGTGGGACTACGAGCGTGCACACACGCTGGCTAAATTTAAAAAATTTT	3285	
Db	72392	CTCCCGAGTAGCTGGGATTACAGGTTGTGTCCATCGCTGGCTAAATTTTGTATTTT	72333	
QY	3286	TTT-GTAGAGACTGGGTCTTACTAGTGTGGCCAGGCTGTCTTAAACTCCTGGCTTCAAG	3344	
Db	72332	TTTAGTAGAGACGGGTTTCATGTGTTGCCAGGCTGCTCTCA-----AAG	72286	
QY	3345	CAATCCTCTACTTGGCATCCAAAGTCTCGGATTAACAGGGTGAGCCACCATGTGCG	3404	
Db	72285	TTATCCACCACCTCAGCCTCCAAAGTCTAGGATTACGGGCATGAGCACCCTGCCCG	72226	
QY	3405	GCTACTTATTTCTTACATTCCATCTTCCATAGATTAAGATCCACAGAACAGGGAT	3464	
Db	72225	GCCTTTTTTTTTTTTTTTTT-----T	72205	
QY	3465	TACTGCCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCATTCTCATCACCTCAACCTC	3524	
Db	72204	TTTGAGATGGAGTCTCCTCTTTTCTACTTAGGCTGGAGTGCAGTGCATGATC-----	72153	
QY	3525	CGTTCAGTCTCACTCAAACTCTGCTCCCGGTTTCAAGTGATTTCTCTGCCCTAAGCCTCC	3584	
Db	72152	---TTGGCTTACTGCAAACTCTGCTCTCCAGGCTCAAGCAATTTCTCTGCCCTCAGCCTCC	72096	
QY	3585	TGAGTAGCTGGAATTTACAGCGTGCACCAACCATGCTTGGCTAATTTTGTATTTTATAGC	3644	
Db	72095	AGAGTAGCTGGGATTGCGAGCACCCACTACCAACCCAGCTAA-TTTTGTATTTTATGT	72037	
QY	3645	AGAGATGGGGTTTTTACCATTGTTGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGATCT	3704	
Db	72036	AGAGACAGAAATTTACCATTGTTGTCCAGGCTGCTCTCAAACTCCTGACCTCAGTGTTC	71977	
QY	3705	GCTGCCCTCAGTCTCCCAAAGTCTGGAATTAAGCGTGAGTCACTGTGCTGCCGCGAT	3764	
Db	71976	ACCCACCTTGGCTCTCCAAAGAGCTGGGATTACAGGTGTGAGCCACAGCTCTCGACCC--A	71919	
QY	3765	TACTGCTATTTTCTTTTATTTGCTATATCCCGAGATCTAGAGCAGTGTCTGACATATAGTA	3824	
Db	71918	CAAAGCTCTTTCTTATTTTCATCCAAATAGCCATTACTTCTGGGCTAGAGATAAATG	71859	
QY	3825	GGTGTCTCAATAAATAATTGATGAATGCACAGCCTAGATATAAACTTTCTTTTCTTTT	3884	
Db	71858	GGTTTTTCAAGGCTAGCAGTTGAGTCAATTGCTTCTCTTAGAGGAGACTTTCTTCTCCTC	71799	
QY	3885	TAAAAAATCTTTGACAACTTTTCAGAAATAAATAAATCTTGTGATTTCTGCTTTTCACTTA	3944	
Db	71798	CA---GACATGGCCAGTTTAAAAACCAACCAAGTTGCTATGTCCAGAGTGGCAGAAAAGATG	71743	

QY 3945 TCACCTTGTATGACTTTTTCATATTTGCCTCAAACTTTATTTGTTACTGTTTTCATTG 4004
Db 71742 ATAAATGGCTCACATCCTCAGCATTTACCGTCTGCCAGGAATGCCGACTTTATGGCCAT 71683
QY 4005 TTACTATTTTAGTCACTGAATAATATGGCTTAATTTGCTTTATACATCTCTCTGCTCCACT 4064
Db 71682 CAGCAGAGTGGCAGCACTGTCTCTGGAGAAAGGTGCTTTACTAGTCCCTTTTGTGC 71623
QY 4065 TTAGAGGGCCAAATTTTACAAATCTGATGAAGCTATGAACCTCTCTCCAGAGAAATACA 4124
Db 71622 ATGAGGGTACTGAGCTCAGAGACAGACATACTTCCCTAAGGTTTACAGAGTGTGTGT 71563
QY 4125 CACACACACACACTCACACAGATTTTTTTTTTAATGTTTGCAACTAAGACAAGAAACC 4184
Db 71562 GGCAGAGTCAGATTAGATACAGCTCTCTCCAGAGTCTGTAATCACCTGCCCTTTT 71503
QY 4185 TGCATTAGAGGATGTTGTTTCAATTT-----AATTAATAATACTCAGTTGGGCACAG 4237
Db 71502 TTTTTTTTTTTTTTTTTTTTTTTTACATTATAGAGAAATTTTAAACATAGAGCTGGGCGCAG 71443
QY 4238 TGAATCAAGCTGTAACCAAGTACTTTGGAAGTCCAAAGTGGTGATCACTTGAGTG 4297
Db 71442 TGGCTTGTGCTGTAAATCCAGACACTTTGGGGGGCGAGCGGGTAGATCACTTGAGGTC 71383
QY 4298 AGAAGTTTCAGACACGCTGGTCAATATGCTGAACCCCTATCTCTACTAAAAATACAAAA 4357
Db 71382 AGAGTTTCAGACCACTCTGGCCAAATGTTGTAATCACCGTCTCTACTAAAAATACAAAA 71323
QY 4358 ATTAGCTGGGTGATGATGATGCTAGTCCAGTCTCCAGTCTCGGAGGCTGAGGCAAGA 4417
Db 71322 ATTAGTGGGTATGGTGGTGCACACCTGTAGTCCAGTACTCAGGAGGCTGAGGTGGGA 71263
QY 4418 GAATTCCTTGAACCTGGGAGGAGAGGTTGCAGTGAGCGCGAGATCCACCACTGCACTCC 4477
Db 71262 GAATTCCTTGAACCTGGGAGGAGGAGGTTGCAGTGAGCTGAGATCGGGCACTTGCACTCC 71203
QY 4478 AGCTGGGGCACACAGCGACTCTATCTCAAAAAATAAATAAATAAAGGATCG 4537
Db 71202 AGCTGGGCAACAGATGAGACTCTGTTTCAAAAAAACCCNAATAAACAACACAAAAA 71143
QY 4538 GAGAGAAAACAAACTAATAAGATTCCTG-----AAGGTAAAGCAGAGATAGCTAA 4586
Db 71142 CATATAGAGAAATAGTAAATGAATGCTGGCATACTTAAACCGCTCAACAAATGTCA 71083
QY 4587 ATTATATGTAATAAGTTTAAATGCATTTTAAGTAACTTATTTATTTTGGTTAT 4646
Db 71082 ATACTGCTGGGCATGTTGGCTCAAGCTGTGATCTTAGCACTTTGGAAGGCCAAGGCTGG 71023
QY 4647 AAAAGTAAACAGCCAA-----AAGTAATGCAACTTCAAAKCTPACATAAATATCTAT 4699
Db 71022 AGGATTCGCTGAGCCAGGAGTTCAAAACGCTTAGGCACATGTTGAAACCTAATCTC 70963
QY 4700 TATGAAAAGTGGAGGATCTATAATCTCTACTACCCAAAGATAACCAAGTTACATATCT 4759
Db 70962 TACAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 70903
QY 4760 CCAGATTTTGGGCATACACTAGCTTTTATTTTGGGAAATTTTCCATGTGCAGGCAT 4819
Db 70902 CTACTTGGGAAGCTGATGTGAGAAGATTCGTTGAATCCAGGAGGTCGAGGGTGCAGTAAG 70843
QY 4820 ACCTAATTTTCTAAATGCTATGTAGTATTCATTTAAGGATGTTTCCATAATTTTAA 4879
Db 70842 ATGAGATTGCGCACCTTACTCCAGCTGGAGTCTGTATCAAAAAAATACACAGCTAGA 70783
QY 4880 ATACATGCTTTAAAGTAGAGAAACTAGTTGGGCATGGTGGCTCAGCCT-GTATCCCGAG 4938
Db 70782 GTCTGTATCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 70723
QY 4939 CACTTTGGAGGCGGAGGCAATGATCACTTGGAGTCCGGAGTTTGACACCAAGCTGGA 4998
Db 70722 CACTTTGGAGGCGGAGGCGGAGTCACTCAGGTGCGGAGTTTGAGACCAAGCTGAC 70663

QY 4999 CAA 5001
Db 70662 CAA 70660

RESULT 15
US-10-960-414-490
; Sequence 490, Application US/10960414
; Publication No. US20060074565A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, LANCE D.
; APPLICANT: GEORGE, JOSH
; APPLICANT: VEGA, VINSENISUS B.
; TITLE OF INVENTION: METHODS, SYSTEMS, AND COMPOSITIONS FOR CLASSIFICATION,
; PROGNOSIS, AND DIAGNOSIS OF CANCERS
; FILE REFERENCE: 38271-76067
; CURRENT APPLICATION NUMBER: US/10/960,414
; NUMBER OF SEQ ID NOS: 500
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 490
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-960-414-490

Query Match 7.6%; Score 377.8; DB 13; Length 174009;
Best Local Similarity 58.7%; Pred. No. 79;
Matches 837; Conservative 1; Mismatches 493; Indels 94; Gaps 7;

QY 3105 TTTTTTTTGTGTTTGTAGACACAGGGTCTTGTCTGTCAACCCAGGCATGACACAGTG 3164
Db 120941 TTTTTTTTTTTTTTTTGTGAGATAGTCTCACTCTGTGCGCCAGGCTGGAGTACAGTG 121000
QY 3165 GTGCAACATAGGTCACTGACGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCAG 3224
Db 121001 GCGAGATCTCACTGCTCACAGCAGCTCTGCTCCCGGTGGAAAGCGATTTTCTGCTCAG 121050
QY 3225 CCTCCAAAGTAGCTGGGACTACGAGCGTGACACACCGCTGGCTAATTAATAAAATTT 3284
Db 121061 CTTCTGATTAGCTGGGACCAAGGCATCAGCCATGCGCCAGCTAATTTTGTGA--TT 121118
QY 3285 TTTTGTAGAGACTGGGTCTTACTAGCTTTGGCAGGCTTGTCTTAAACTCTGCTTCAAG 3344
Db 121119 TTTTGTAGAGACAGGGTCTCACTATATTGGCCAGGCTGTCTCTCAAACTCTGACCTCAA 121178
QY 3345 CAATCTCTACCTGGGATCCCAAGTCTGGGATTTACAGGGTGAGCCACCATGTGCG 3404
Db 121179 AGATCCGCCACCTTTGGCTTCCCAAGTCTGGGATTTGAGCGCTGAGCGCGTGCCTG 121238
QY 3405 GCTACTTATTTCTTTACATTTCCATCTTTTCCAATAGAATGTAAGATCCACAGAACAGGAT 3464
Db 121239 GC-----CTGAATCTTTAATTTTATTTAATAATTTGATTTAATCTTTT 121281
QY 3465 TACTGCTCTATTTCTTCTTCTTTTGTAGACAGAGTCTCACTTTCATCCTCAACCTC 3524
Db 121282 TTTTTTTTTTTTGTAGACAGAGTCTGCTCTGTGCGCCAGGCTGGAGTGGTGCA 121341
QY 3525 CGTTGAGTCACTGCAACTCTGCTCCCGGGTTCAAGVATTTCTCTGCTGCTTAAGCTCC 3584
Db 121342 ATCTCGGCTCACTCAAGCTCTGCTCCAGGTTTCCACACATTTCTCTACCTCAGCTCC 121401
QY 3585 TGAGTAGCTGGAATTTACAAGGCTGCACCACTGCTGCTAA--TTTTTCTATTATTTTA 3642
Db 121402 CGAGTAGCTGGAGCTTACAGGCGCTGCGCCACAGCTGGCTGCTAATTTTTTTTGTATTTTA 121461
QY 3643 GCAGAGATGGGTTTTTACCATGTTTCCAGGCTGGTCTCTCAAACTCTGACCTCAAGTGT 3702
Db 121462 GTAGAGACGGGTTTTTACGTTGTTAGCCAGGATGATCTTGATCTACTGACCTC--GTGAT 121519
QY 3703 CTGCTGCTCAGTCTCCCAAGTCTGGAATTTATAGGCTGAGTCACTGCTGCTGCGCG 3762
Db 121520 CTGCTGCTGCGCTCCCAAGTCTGGGATTTACAGGCTGAGCCACCGTGCC----- 121573

```
QY 3763 ATTACTGCTATTTCTTTATTCCTATATCCCCAGATCTAGACGAGTCTGCACATATAG 3822
Db 121574 -----CAGCTTAAATTTTGATT 121590
QY 3823 TAGGTGCTCAATAAATAATGTGAATGCACAGCCTAGATATAAACTTTCTTTCTTTT 3882
Db 121591 TAAATAACCATATTTGTTATTTGAACAGCACAATTTTCATACCTTAAGTTTTTATTTGTAATGA 121650
QY 3883 TTTTAAACAATCTTTGCAAACTTTTGCAGAAATAAATAACAATCTTGCATTTCTTTTCACT 3942
Db 121651 TTTCAAAGTGAGGCTAATGGGTTTTTATTTGTAGATTCAAAAACAAGTTTTTATTTAG 121710
QY 3943 TATCACTCTGTTATGACTTTTTCATATTCGCTCAAACTTTTATTTGTTATGTTCTTTTTCAT 4002
Db 121711 ATTCAAAGTGAGGCTAATGGGAACAAGATTATTCAGCAGCAGTTTGTGGGATATTTGGCT 121770
QY 4003 TGTACTATTTTATGCTCACTGAATAATATGGCTTTAAATTTGCTTATACATCTCTCGTCCA 4062
Db 121771 GAAAGGAAATTTTCAGAGCACAACCTGTCATACGTTTGTGAGGATACATGAAAGGCCA 121830
QY 4063 CTTTAGAAGGCCAAATTTTCAAAATCTGATGAAAGCTATGAACCTCTCCCCAGAGAAATA 4122
Db 121831 CTTCACTGTGACCAGCATTCATATGT-----ATAAGACATTTGCAATATATTAGCATA 121882
QY 4123 CACACACACACACACTCACACAGTTTTCTTAAATGTTTTCACACTAAGACAGAAA 4182
Db 121883 CATGGACATATGTGAAAAATCAAAAAGATTTGCTTCCAATTTTATGAGCTAAAGGGAAAA 121942
QY 4183 CTGCACTTAGAGGATGTTTCTTCATATTTAATTAATAAATACTCAGTTGGGCACAGTGACT 4242
Db 121943 AGCAATTCAG-----TAAAAATAACAGCTGTTGGCCAGGCACAGTGGCT 121988
QY 4243 CAAGCTGTAAACACAGTACTTTGGAGTCCAAAGTGGGTGGATCACTTTGAGGTGAAG 4302
Db 121989 CATGCTCTGCAATACCAGCACTTTGGGAGCTGGAAGGGGAGATCACCTGAGGTTCAGGAG 122048
QY 4303 TTCGAGACAGCTGCTCAATATGTTGAAACCTTCTCTACTTAAAAATACAAAAATTAG 4362
Db 122049 TTCGAAACAGCTGCGCAACATGCGCAACCTCTCTCTACTTAAAAATACAAAAATTAG 122108
QY 4363 CTGGGTGTAGTATGATGCTGCTAGTCCAGCTACTCGGGAGGCTGAGGCAAGAGAAAT 4422
Db 122109 CCGGGCGCAGTGTGGGCGCTGTAAATCCAGCGACTCGGGAGCTTGAGGCAAGAAATC 122168
QY 4423 GCTTGAACCTGGAGGAGGAGTTGCAGTGAGCGGAGATCCCACTGCACTCCAGCCT 4482
Db 122169 ACTTGAACCTTAGGAGGCGGAGTCTACAGTGAGCTGAGATTGTGTCACTTACACTCCAGCCT 122228
QY 4483 GGGCGACAGCAGCACTCTATCTCAAAAAATAAATAAATAAAA 4527
Db 122229 GGGTGACAGAGTGAGACTCTATCTCAAAAAATAAATAAATAA 122273
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RESULT 16

US-10-995-561-13303

; Sequence 13303, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995,561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 13303

; LENGTH: 201990

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(201990)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-4)
US-10-995-561-13303

Query Match 7.5%; Score 376.8; DB 10; Length 201990;

Best Local Similarity 59.5%; Pred. No. 72;

Matches 842; Conservative 4; Mismatches 501; Indels 67; Gaps 10;

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QY 3104 TTTTGTGTTGTTGTTGTTTGTAGAGACAGGCTTTGCTCTGTCTACCCAGGATGAGACAGT 3163
Db 33667 TATTTATTTATTTATTTTGTGRRACGGATCTCGCTCTGTGGCCAGGCTGAGTGCACT 33726
QY 3164 GGTGCAACCATAGTCACTGACAGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCA 3223
Db 33727 GCGTGATCTTGGCTCACTGCAACCTCGCCCTCTGGGTTAAGCAATTTCTCTG-CTCA 33785
QY 3224 GCTCCCCAAGTAGCTGGGACTACGAGCGGTGACACCAAGCTGCTTAATTAATAAAATTT 3283
Db 33786 TCCTCCCGAGTAGCAGGATTTACAGGCATGTGCCACCAAGCCAGCTAATTTTGTGTA--T 33843
QY 3284 TTTTGTAGACTGGGCTTTACTAGTTGGCCAGGCTTGTCTTAAACTCTCTGGCTTCAA 3343
Db 33844 TTTTAGTAGACGGGGTTTTCACCATCTTGGCCAGGCTGGTCTTGAACCTTCTGACCTC-- 33901
QY 3344 GCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATACAGGGGTGAGCCACCATGTGC 3403
Db 33902 GTGATCCAACTCGCTCGGCTCCCAAGTGTGGGATTTACAGCGGTGAGCCACCATGCCT 33961
QY 3404 GGCTACTTATTTCTTTTACATTTCCATCTTTTCCAAATAGAATGTAAAGATCCACAGAA 3463
Db 33962 GGC--CTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 34019
QY 3464 TTACTGCTATTTTCTTCTCTCTTTCTTTTGTAGACAGAGTCTCACTTCATCACTCAACCT 3523
Db 34020 TGGAGTGAATGGTGTGGTCTT----- 34041
QY 3524 CGTTTCAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYGATTTCTCTGCTCAAGCCCTC 3583
Db 34042 -----GGCTCACTGCAACCTCGGCTCCAGGTTCCAGGATTTCTCTGCTCAGTCTC 34095
QY 3584 CTGAGTAGCTGGAATTAACAAGGTCACACCATGCTTGGCTAAATTTTTTGTATTTTTAG 3643
Db 34096 CCAAGTAGCTGAGATTACAGGCATGCGCCACACACCGCCGGCTAA-TTTTTGTATTTTTTCA 34154
QY 3644 CAGAGATGGGGTTTACCATGTTGCCAGGCTGGCTCAAACTCCTGACCTCAAGGATC 3703
Db 34155 TAGAGGTGGGGTTTCAACATGTTGGCCAGGCTGATCTAGAACTCCTGATCTCAGGTGATC 34214
QY 3704 TGCCTGCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGAGTCACTGTGCTGGCCGA 3763
Db 34215 CACCCACCTCAGTCTCCCAAGTGTGAGATTACAGTCTGAGCCACCATGCTGGCCAC 34274
QY 3764 TTACTGTCTATTTTCTTTATTTGCTATATCCCCAGATCTTAGACAGTGTCTGACATATAGT 3823
Db 34275 ACCCGGTTTATTTGCAT--TTGCTTTCTAATAGAGAAATCAACCCAGTAAACAAATGAAT 34332
QY 3824 AGGTGCTCAATAAATAATTGATGAATGCACAGCTAGATATAAACTTTCTTTTCTTTT 3883
Db 34333 ATTGTAGCAAACTGGGGGTGGGTTGGGAAGGAAAGTAGTTCCTCTCTAATAAATAAAC 34392
QY 3884 TTTAAAAAATCTTGACAACCTTTTGCAGAAATAAATAACAATCTTGCAATTTCTGTTTTCAC 3943
Db 34393 TTGCTGATATTTGTTGAAAGTCATTGCTTACTCATCTTGTATAGATAAGTCAACA 34452
QY 3944 ATCACTTGTGTATGACTTTTTTCAATGTGCTCAAACTTTATTTGTTACTGTTTTTTCA 4003
Db 34453 ATGAGTGGTATCAGGGTTTCAGGGTTTCCCTCCTGAGACACACATGGAATGAACCGTGT 34512
QY 4004 GTTACTATTTTATGCTCACTGAATAATATGCTTTAAATTTGCTTTATACATCTCTGCTCCAC 4063
Db 34513 GTGGGATGCTGTTTAAAGAAAAACAAGAACCATGTG---TTGGAACAACCTTAAGTAT 34569
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Qy	4064	TTTTAGAGGCCAAATTTACAAATCTGATGAAGAGCTATGAACCTCTCCCCAGAGAATAC	4123
Db	34570	TGAGCGGTGGAGGATTTGCTGAAATTTGTGGACTACTATGCAGTCAATTACC----	34625
Qy	4124	ACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGGCAACTAAGACAAGAAAC	4183
Db	34626	TGAAAAATGTTTCCATGATATGGCAGGATGTTTATGCTATAGAANAATTTAAGACGCCAG	34685
Qy	4184	CTGCATTAGAGGATGTTTGTTCATATTAATTTAAAAATAACTCAGTTTGGCACACAGTCTC	4243
Db	34686	CTTCAAAGTAAAGTATAAAACCTAAATTTGGTCAAACA-----GGCTGGCGCAGTGGCTC	34739
Qy	4244	AAGCCTGTAACACACAGTACTTTGGGAAGTCCAAGTGGGTGGATCACTTGAGTGAGAGT	4303
Db	34740	ACAGCTGTATCTCGACACTTTTGGGAGGCCGAGGACGGTGGGTCTTGGAGGTCAAGGAGT	34799
Qy	4304	TCGAGACCAAGCCTGGTCAATATGGTGAACCCCTATCTCTACTTAAAAATACAAAAATTAGC	4363
Db	34800	TCGAGACCACTCTGGCCAGTATGGCGAGACCCCATCTCTACTTAAAAATACAAAACTAGC	34859
Qy	4364	TGGGTGTAGTATGCATGCCCTGTAGTCCACAGCTACTTCGGGAGGCTGAGGCAAGAAATTG	4423
Db	34860	TGGGTATGGTGGCTCATGCCCTGTAAATCCACAGTACTTCAGGGGTCTGAGGCAAGAGGATCA	34919
Qy	4424	CTTTGAACCTGGGAGGCAGAGTTGCAGTGCAGCGAGATCCACCACTGCACCTCCAGCCTG	4483
Db	34920	CTTTGAACCTGGGAGGCGAGGTTGTAGCGAGCGAGATTGTGCCACTTCGACTCCAGCCTG	34979
Qy	4484	GGCGACACGCGAGACTCTATCTCAAAAAATAA	4517
Db	34980	GGCAATAGAGCGAGACTCTGTCTCAAAAAATAA	35013

RESULT 17

```

RES011 17
US-11-114-798-49
; Sequence 49, Application US/1114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 49
; LENGTH: 121736
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-49

```

Query Match 7.5%; Score 375; DB 18; Length 121736;
Best Local Similarity 54.1%; Pred. No. 1.1e+02;
Matches 1251: Conservative 1; Mismatches 881; Indels 178;

Qy	2312	GCTGTAAATCCCAAGCACTTTTGGAGAGCCGAGGGCGGATCACTTGTAGGTCAGAGATTC	2371
Db	17745	GCCTATAATCCCAAGCACTTTTGGAGAGCCGAGGGGTGGATCACTTGTAGATCAGAGATTC	17804
Qy	2372	GAGACCAAGCCTGCCCAACATGGTGAACCCCTGTCTTCTATAAAAAATCAAAAAATTAGCC	2431
Db	17805	CAGACCAAGCCTGCCCAACATGGTGAACCCCTGTCTTCT-AAAAATACAAAGATTAGCT	17863
Qy	2432	GGACATGGTGGCGAGCGCCTGTAAACCCACAGTACTTGGGA-----	2471

17864	Db		GGCGTCTGGCATGCACCTGAGTTCCAGCTACTCAGGAAGTCAAGCAGGAGAAATCTC	17923
2472	Qy	-----GACTGAGTTGGAGGTTTCAGTGAGCCAAAGTTCGTGTCACCTGCTGTCCAGCCTGG	2525	
17924	Db		TTGAACTCTGGAGGTGGAGGTTGCAGTAAGCTGAGACCATGCCATCTGCATCCAGCCTGG	17983
2526	Qy	GTAAACAGACA--ACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATGATAAAA	2583	
17984	Db		GCTACAGAGCAAGACTCTGTCTCAAAAAAATAAATAAATAAATAAATAAATAAATAA	18043
2584	Qy	-----GGACTTATATTTTCAAGCCATAGGATCATTTCTCTCTGAA	2624	
18044	Db		AAGTACCTACTGATGCCAGCTTCATGTGAATCCAAAGAAATAATATCTGATATTGGCAC	18103
2625	Qy	GCATCTTG-----GGAGTCTATCTCCCACTCT	2652	
18104	Db		AGCCCTTGACATCAGAAATACCTTCAGCCCTCAGGAAGCAATTTCTGCATCTCTCAGT	18163
2653	Qy		TCTGAGAGTGGCAGGTGAGGCTGACCTATTTGCTCTGCATTTACTCTATCTCAGCTG	2712
18164	Db		TTCTAGTGAGACAAATTAAGGCTCCATCAAGTCAAGTCACTCTGGTCTCTAGGCTCGAC	18223
2713	Qy		TCCCTCCCACCTTCAGGTGCTGCCAGACACATGACACTGCTATGACACGAGCCCAAGAG	2772
18224	Db		ACCATGAATGCATGAGCAGGTGAGATAAAGAGACACCCCCAAGAACTACAGATGCAGAG	18283
2773	Qy		CTGACAGCTGTAAATTTCTGTGGACAMWCGTACACCCACACCTATTATCTACTCTGTCG	2832
18284	Db		CAAGATTGCTTTCTTTTCTCTCTTTTATAGAAAGACTCTCATGTGCCACCCAG	18343
2833	Qy		TCTGGCTCGGCAATACCTGTAGCAGTAGTTTATCCCTTCTTGACCTAT-----GA	2885
18344	Db		GCAAGATCATAGTCACTTTAACTCGAAGTCTCTGGCTCAAGTGAAGTCCATCCAGA	18403
2886	Qy		ATTCTAGTTGGTTCTCAGTAGGCCGGGGGAAATTAATAGTAACACAGCCATGATTAGT	2945
18404	Db		CTCCTGAGTAGCTGGGACTATAGCGCATGCCATCTCTGCCATCTCACCAGGTGCCAGC	18463
2946	Qy		GTATAATTTCTTGGTCTCGGCGAGTCTCTTTTAACTCCTCAGAACACACTATGGGATA	3005
18464	Db		AGTATTCTCTTTCTTTTCTCTTTTCTCTTTTCTCTCTCTCTCTCTCTCTCTCTCTCT	18523
3006	Qy		GGTACAATTATCTCACTTAAACAGATAGAAAACTGAGGCTCAGAGGCTGAGCTATTTG	3065
18524	Db		TTTCTCTTTCTCTTTTCTCTTTCTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	18583
3066	Qy		CCAAGATCACAGCTTGTAAGTGGTGACAGTTTGGGTTTT-----TTTTTGTGTGTG	3120
18584	Db		CTTTCTCTCTTTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTT	18643
3121	Qy		TTAGACAGAGGTTCTTCTCTGTCACCCAGCATGACACAGTGGTGCAACCATAGGTCA	3180
18644	Db		TTTTTGACAGAGTCTTGTCTGTGTGCCAAGCTGGAGTGCACTGGCAGCATCTCAGCTCA	18703
3181	Qy		CTCAGCCTCAACCTCTCAGCTCAAGGATCTGTGACCTCAGGCTCCCAAGTAGCTGG	3240
18704	Db		CTGCAATCTCCGCTCTCTGGTTCAAGCATTTCTATGCCTCAGCCCACTGATAGCTGG	18763
3241	Qy		GACTACAGCGGTGCACCAACGCGCTGGCTAAATTAATAAATAATTTTTTGTAGAGACTGG	3300
18764	Db		GACTACAGGTGCGTGCACCAACGCGCTGCCTAAATTTTGTGA--TTTTTAGTAGACAGGG	18821
3301	Qy		TCTTACTAGTTGGCCAGGCTGTCTTAACTCTCGGCTTCAAGCAATCTCTCACTCTG	3360
18822	Db		TTTTCAACATGTTGGCCAGGCTGGTCTCGAACTCTCGAATCTCAGTGTATCCACCCACCTCG	18881
3361	Qy		GCATCCCAAGTCTCGGATTAACAGGGGTGAGCCACCATGTGCGGCTACTTTCTTTTA	3420
18882	Db		GCCTCCCAAAGTCTGGGATTAAGGTATAGCCACCATGCCCCGCTATTCTCTTTTGT	18941
3421	Qy		CATTCCATCTTTTCCAATAGAAATTAAGATCCACAGAACAGGGAATTACTGCCTATTTTCTT	3480

Db	18942	TGTTGTTGTTGT-----TGTTTTTTT	18965
Qy	3481	CTTTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCTCAACCTCCGTTCCAGTCACTGCA	3540
Db	18963	TGAGGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGCAGTGTAACTCTCAGCTCACTGAA	19022
Qy	3541	ACCTCTGCTCCCGGGTTCAAGYGATTCCTCGCTTAAGCCTCCTGAGTAGCTGGAATTA	3600
Db	19023	ACCTCTGCTCCCTGGGTTCAAGTGAATCTCATATCTCAGCCTCCTAAATAGCTGGCATTA	19082
Qy	3601	CAAGCGTGCACCAACCATGCTTGGCTAAATTTTTTGATATTTTAGCAGAGATGGGTTTTTAC	3660
Db	19083	CAGCTCCACCAACAGCCCTGGCTAA-TTTTTGATATTTTAGTAGACAGAGATTTTCAAC	19141
Qy	3661	CATGTTGCCAGGCTGCTCAAACTCCTGAACCTCAAGTGATCTGCTGCTCACTGCTCC	3720
Db	19142	CATGTTGGCCAGGCTGCTCGAACTCCTGACCTCAGTGTGATCTGCCACCTTGGCCCTCC	19201
Qy	3721	CAAAAGTCTGGAATTAATAGCGGTGAGTCACTGTGCGCTGGCCGATTACTGTCTATTTTCTT	3780
Db	19202	CAAAGCGCTGGATTTACAGTGGTGGCCACCACTGGCCCCCAGCAGTATTACTTTATA	19261
Qy	3781	TATTGCTATATCCCCAGATCTAGAGCAGTGTCTGCACATATAGTAGGTGCTCAATAAATAA	3840
Db	19262	AGCCTCTAGTGACATACTGGGCCCTCTCTGGACAACTTT-----CTTA	19303
Qy	3841	TTGATGAATGCACAGCTAGATATAAACTTTCTTTTCTTTTATAAACAATCTTGACA	3900
Db	19304	TTCCCAACAACAGCTCACATCATGACACACTCTGAGCCCTTTTTCTAGGCTGGACACCTG	19363
Qy	3901	ACTTTGCAGAAATAACAATCTTGCAATCTGCTTTTTTCACTTATCACCTTGTATGACT	3960
Db	19364	GCCTGGAAGGTCTCTGCGCCTCCCCACGCCACTCACCCCAACGAGCTATGAGCTTC	19423
Qy	3961	TTTTCATATTGCTCAAAACCTTTATTGTACTGTTTTTTCATTTGTTACTATTTTAGTC--	4018
Db	19424	CCCATCTGGGAAGCTGCCCCCTGCTTTTGAAGCCAAAGAACACTGTGGAAGGAGTTTCTCCCA	19483
Qy	4019	-ACTGAAATAATATGGCTTAAATTTTGTCTATATACCTCTCTGCTCCACTTTAGAAAGGCCAAA	4077
Db	19484	GCCCTTAGGATGGTCTTAAGAAAGGAGGTGCTTAGGAGAGTCCCCACAGGCAGAGGCC	19543
Qy	4078	TTTACAAATCTGATGAAGCTATGAACCTCTCCCCAGAGAAATACACACACACACAC	4137
Db	19544	TGCAGACCCACAGACTCAGCTGGGCTCCTGCTAACCA-----TTTCAGAAATACAGAT	19596
Qy	4138	ACTCACACAGATTTTTTTTTTAATGTTGCAACTRAGACAAGAAACCTGCAATTAGAGAT	4197
Db	19597	TTTTAGAAAAGTTTGTTTTTCTCTTAACTATAAAGTGCACAC-----TGC	19644
Qy	4198	GTTTGTTTCATATTAATTTAAAAATAAATCAAGTTGGGCACAGTCACTCAAGCCTGTAAACCAC	4257
Db	19645	TTTGTTGTTTAAAAAATAAATAAATAAAGCCAAAGCGCATGGCTCACACCTGTAATACC	19704
Qy	4258	AGTACTTTGGAAGTCCAAGGTGGGTGGATCACTTGAGGTGAGAGTTGAGACACAGCCTG	4317
Db	19705	AGCACTTTGGGAGGCTCAGGTGAGTGGATCAC--GAGGTCAAGAGATTGAGACCACTCTG	19762
Qy	4318	GTCAATATGGTGAACCCCTATCTCTACTAAAAATAC-AAAAATTAGCTGGGTGATGAT	4376
Db	19763	GCCAACTGGTGAACCCCATCTCTACTAAAGTACAAAAAATTAGCCGGGTGTAGTGGC	19822
Qy	4377	GCATGCTGTAGTCCCAGCTACTCGGAGGCTCAGGCAAGAGAAATGTTGTGAACCTGGGA	4436
Db	19823	GGGCGCCTGTAGTCCCAGCTACTCAGGAGGCTCAGGACAGGAAATCACTTGAACCCAGGA	19882
Qy	4437	GGCAGAGTTGCAGTGAGCGCAGATCCCAACCTGCACCTCCAGCCTGGCGACACAGCGA	4496
Db	19883	GGTGAGGTTTGCAGTGHAGCCGAGATTTGGCCACTGCACCTCCAGCCT-AGCGATGGAGTGA	19941
Qy	4497	GACTCTATCTCAAAAAAATAAATAAATAAAA	4527
Db	19942	GACTTCCATCTCAAAAAAATAAATAAATAAAA	19972

```

RESULT 18
US-11-121-086-58
; Sequence 58, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 58
; LENGTH: 180654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-58

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Db 19942 GACTCCATCTCAGAAAAATAATAATAAAAAA 19972

Db	154318	ACAGTGGTATTTCTAAATAGCTTATCTCTGTACATATTTCTCCAGCCTCATAAACAAGTT	1543737
Qy	3823	TAGGTGCTCAATAAATAATTTGATGAAT--GCACGCCTAGATATATAAATCTTTCTTTTCTT	3880
Db	154378	TACTATTTTAAGCTGTGCTCTTTGGTTCAGCTGAGCATGGTGATGAAAGCCCTTCCCA	154437
Qy	3881	TTTTTAAACA-ATCTTGACAACCTTTGCAGAAATAAATAACAATCTTGCAATCTGCTTTTTC	3939
Db	154438	TGAAAAGTTTCATGGGAACCTCTTGAAGCCCTTAGGCCAAGCACTAACCCAGACCTCAT	154497
Qy	3940	ACTTATCACCTTGTTTATGACTTTTTTCATATTGCGCTCAAAACCTTTATGTACTGTTTTTT	3999
Db	154498	GGTAAGCCCAATATGCATATGGATGAAACTGTGTAGTTACAGCTGGACTGACAGTTCOA	154557
Qy	4000	CATTGTTACTATTTTAGTCACTGAAATAATATGGCTTAATTTGCTTTATACATCCTCCTGCT	4059
Db	154558	AGCTG-CAGAGCAGTGTAGATCAGATCACCTTTGCGTGGATTAGAAAGGTGCCCT	154616
Qy	4060	CCACTTTAGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTCTCTCCACAGAA	4119
Db	154617	TCTCTAGTGCACACAGTTCACACACCAGTACTCATCTTGGTAAGTGGAGTACAGATAG	154676
Qy	4120	ATACACACACACACACACTCACACACAGTTTTTTTTTAATGTTTGCACATAACACAG	4179
Db	154677	ATTTCACCCCTCACTTGCACCTGAACAGGATATCCTTT--TGCTGGGTGCAATCTCTAT	154734
Qy	4180	AAACCTGCATTAGAGGATGTTTGTTCATATTAATTTAAAAATAAATCACTGCTGGGCACAGT	4239
Db	154735	GGTCCTTACACAGCAGCCGT-----TAAGAAGTGTACCGGCGAGGACGGCT	154782
Qy	4240	ACTCAAGCCTGTAAACACAGTACTTTTGAAGTCCAAGGTGGGTGGATCACTTTGAGGTGAG	4299
Db	154783	GTTACACGCTGTAATCCCAACACTTTTGAAGCGCAGGACGGCTGATCAC-AGAGGTGAG	154841
Qy	4300	AAGTTTGGAGCAGCGCTGGTCAATATGTTGAAAACCTATCTCTACTATAAATAACAAAAAT	4359
Db	154842	GAGTTTGAGACAGCGCTGGCCAAACATGTTGAAAACCCCGTCTCTACTATAAATAATGAAAAT	154901
Qy	4360	TAGCTGGGTGTAGTATGATCATGCTGCCTGTAGTCCCAGCTACTCGGAGGCTGAGGCAGAGA	4419
Db	154902	TATCCGGGCATTTGGTGGCAGGCACCTGTAAATCCAGCTACTCGAGAGCTGAGGCAGGAGA	154961
Qy	4420	ATTGCTTTGAACCTGGGAGGCAGAGGTTGCAGTGAAGCCAGAGATCCCAACCACTGCATCCAG	4479
Db	154962	ATCGCTTGAACCTGGAGGTGGAGGCTGCAGTGAAGCCAGGATTTGGCCACTGCATCCAG	155021
Qy	4480	CCTGGCGAC-ACAGCGAGACTCTATCTCAAAAAATAAATAA	4521
Db	155022	CCTGGCAACAAAGACGAAATCTGTCTCTCAAAAAAGAAAA	155064

RESULT 19

RESOLUTION 19
US-11-121-086-14

US-11-121-086-14
: Sequence 14. Application US/11121086; sequence 14, Application US/111
: Publication No. US20050266459A1

; PUBLICATION NO. US20050266459A1
 : GENERAL INFORMATION:

: GENERAL INFORMATION: TIM S.
 : APPLICANT: POULSEN.

APPLICANT: FOULSEN, TIM S.
APPLICANT: NIELSEN, KIRST

REFLECTIONS. NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

FILE OF INVENTION: NOCTECTIC ACID PROBES A
; FILE REFERENCE: 09138.6000-00000

; FILE REFERENCE: 09138.0000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086

CURRENT FILING DATE: 2005-05-04

; PRIOR APPLICATION NUMBER: 60/567,570

; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 14

; LENGTH: 167891

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-121-086-14

Query Match	7.5%	Score 372.6;	DB 17;	Length 167891;
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[illegible]

Dn	53231	-----AATTATACACAAATGATGGCTGGCGGGTG	53262
Qy	4240	ACTCAAGCCGTGAACACAGTACTTTGGAAGTCCAAAGGTGGGTGATCACTTTGAGGTGAG	4299
Dn	53263	GCTCTTGCCTGTAAATCCAGCACTTTGGGAGGCCAAGCGAGTTGGATCAC--GAGGTCTAG	53320
Qy	4300	AAGTTCGAGACCAAGCTGGTCAATATGTTGGAACCCCTATCTCTACTTAAATAAATA-CAAAAA	4358
Dn	53321	GAGTTCAAGACCAAGCTGGCCCAATATGGTGAACCCCTGTGTCTACTTAAATAAATAAATA	53380
Qy	4359	TTAGCTGGGTGTAGTGATGATGCCCTGTAGTCCAGCTACTCTGGGAGGCTGAGGCAAGAG	4418
Dn	53381	TTAGCTGGGTGTAGTGGTGGCACCTGTAGTCCAGCTACTTGGGAAGCTGAGACAGGAG	53440
Qy	4419	AATTGCTTGAACCTGGGAGCGACAGGTTGCAAGTGAGCGGAGATCCCACTGCACTCCA	4478
Dn	53441	AATTGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGTGCAGTGCAGCACTGCCTCCA	53500
Qy	4479	GCCTGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAAGGATCGG	4538
Dn	53501	GCCTGGCGAACAGAGTAAGACTCTGTCTCAAAAAATAAATAAATAAAGGAAAG	53560
Qy	4539	AGAGAAACAAACCTAATAAGATTCTCTGAAGGTAAGCAGAGATACGTA	4585
Dn	53561	AAAGACGCAATGATAAATAATTAGCAGAAAAAGACAAATAAACAGATA	53607
RESULT 20			
US-10-995-561-13256/c			
; Sequence 13256, Application US/10995561			
; Publication No. US20050272054A1			
; GENERAL INFORMATION:			
; APPLICANT: CARGILL, Michele et al.			
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH			
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF			
; TITLE OF INVENTION: DETECTION AND USES THEREOF			
; FILE REFERENCE: CL001559			
; CURRENT APPLICATION NUMBER: US/10/995, 561			
; NUMBER OF SEQ ID NOS: 85702			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 13256			
; LENGTH: 55826			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-995-561-13256			
Query Match 7.4%; Score 369.6; DB 10; Length 55826;			
Best Local Similarity 53.4%; Pred. No. 2.1e+02;			
Matches 1255; Conservative 6; Mismatches 925; Indels 164; Gaps 17;			
Qy	2276	TTAAAAATCCGTTTCAGGCCAGCGGGTGGTGGTCCGCTGATGATCCAGCACTTTGGGA	2335
Dn	16289	TTTTAAAAAGAAATGTAAGCCGGGTGGTGGCTCACACCTATAATCCAGCACTTTGGGA	16230
Qy	2336	GGCGAGCGCGGGATCACTTCGAGGTCAGAGTTTCAGACCAAGCTGGCCAAACATGGTG	2395
Dn	16229	GGCCAAAGACAGGTGGATCA--TAAGGTTCAGAGTTTGGAGCAACCTGGACCAACATGGTG	16172
Qy	2396	AAACCCCTGTCTCTACTAAAAAATACAAAAATTAGCCGGACATGGTGGCGAGCCCTGTAA	2455
Dn	16171	AAACCCCATCTCTAAACAAAGATACAAAAAATTAGCCGGCATAGTCCCGGTGTCCTGTAA	16112
Qy	2456	CCCAGCTACTTGGGAGACT-----GAGTTGAGGTTTC	2489
Dn	16111	TCCAGCTACTTGGGAGGCTGAGCGAGGAGAATCGCTTGAACCCGGGAGCGAGGTTGC	16052
Qy	2490	AGTGAGCCAAAGGTGCTGCTACTGCTGCCAGCTGGGTAAACAGAGCAACTCTGCTC---	2546
Dn	16051	AGTGAGCCGAGATYGCACCATTTGCACTCCAGCATGGGCAACAGGGCGAGNCTCCGTCTCA	15992
Qy	2547	-----AAAAAATAAATGCTTTTCAATAAATATATGATAAAGACTTATATTTTCAAG	2602

Dn	15991	AAAAAAAAAAAAAAAAWGAAATGTGACTTAGTGAGTTTAAAAATCAGTACCTCTGTAATAACG	15932
Qy	2603	CCATAGGATCATTTCTCTGAAGCATCTTTGGGAAG-----TCATCCCCACCTGTTCTCT	2656
Dn	15931	TGCGATAATCTTTCATAGTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA	15872
Qy	2657	GAGAGTGGCAGGTGAGGGCTGACCTATTTGCTCTGCACCTTACTCTCTCTCTCTCTCTCTCT	2716
Dn	15871	GCTGATGTGCAATTTGAGGATAATTTCCAGGGCTAAATAATTTCTCTCTGCAATAAGTTAT	15812
Qy	2717	TCCCATTTTCCAGGTGCTGCCAGACACATGACAACTGTATGACACGAGGCCAAGAGCT--	2774
Dn	15811	TCAGGCAATTTTGAGCACAAGAGTGAGCCTTCTTGTCTAATAATTTTCCAAAAAGAAAAATA	15752
Qy	2775	--GGACAGCTGTAAATTTCTGCTGCACAMMCGTACACCCACACCTATTTTATCATCTGTCG	2832
Dn	15751	AATGTGACTTGTAAACAGAAATTTGATATCTTCCCTCCCTAAATAATTTTCTTTTTTTTT	15692
Qy	2833	TCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTCTTCCCTTACCTTATGAATTTCT	2892
Dn	15691	TTGACACRGAGTCTCACTCTTTCACCCAGGCCGAGTGAGTGGCGCTATCTTGGCTCAC	15632
Qy	2893	TTGGTTCTCAGTAGCCCGG-----GGGAAT 2919	
Dn	15631	TGCAAGCTCGGCACCCCGGTTTCATGCCATTTCTCTCGCTCAGCCTCCCGAGTAGTGGT	15572
Qy	2920	AATAGTAACACAGCCATGATTTAGTGTAAATTTTCTTGGTTCTGGGAGTGC-TCCCTT 2978	
Dn	15571	ACTACAGGCACCCGCCACACCGCGGTAAATTTTGTATTTTGTAGTAGACGGGGTT	15512
Qy	2979	TAACTCTCAGAACAACTATGGGATAGTACAATTTATCTCTCACTTAAACAGATAAGAAAA	3038
Dn	15511	TCATCTGTGTAGCCAGGATGGTCTTGTAT---CTCCTGACCTCGTGATCCCGCCCTT	15455
Qy	3039	CTGAGGCTCAGAAAGCTGAGCTATTTGGCCAAAGATCACACAGCTTGTAGTGGTGACAGT	3098
Dn	15454	GGCCTCCCAAAGTGTGGGATTAACAGGRTGAGCCACTGCGCCCGGCTCCCTAAATAAT	15395
Qy	3099	TTGGGTTTTTTTTTGTGTGTAGACAGGGTCTTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	3158
Dn	15394	TTAATCATTAATTTTTTTTTTTTTTTTGTAGACAGAGTCTTGTCTGTCTGTCTGTCTGTCT	15335
Qy	3159	ACAGTGGTGCAACCATAGTCACTGAGCCTCAACCTCTCTGAGCTCAAGGGATCTGCTGA	3218
Dn	15334	GCAGTGGAGCAATCTCAGCTTACCACACCTCCGCTCCCGGTTCAAGTGATTTCTCTG	15275
Qy	3219	CCTAGCCTCCCAAGTAGCTGGGACTACGAGGCTGCACACACCGCTGGCTTAATTAATA	3278
Dn	15274	CCTAGCCTCTCAAGTAGCTGGGACTACAGGCAATGCACCAACCATGCTGGCTTAATTTTG	15215
Qy	3279	AAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTTAAACTCTCTGC	3338
Dn	15214	TA--TTTTTAGTATATACAGGGTTTCACTCTGTAGCCAGGCTGGTCTCTCAAACTCTG--	15159
Qy	3339	TTCAAGCAATCTCTCTACCTTGGCATCCCAAAGTCTGGGATTACAGGGGTGAGCCACA	3398
Dn	15158	ATCTTGTGATCGCCTGCTCGCTCCAAAGTCTCGGATTACAGGTGTGAGCGCCA	15099
Qy	3399	TGTGGGCTACTTATTTCTTTTACATTCATCTTTTCAATAGAAATGTAGATCCACAGAAC	3458
Dn	15098	CACCTGGCCAACTTTTTTTTTT-----15077	
Qy	3459	AGGGATTACTGCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACTTCATCACTC	3518
Dn	15076	-----TTTTTGAGTGGAGTCTTGTCTGTCTCACCAGCTGGAGTCACT	15032
Qy	3519	AACCTCCGTTACGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYATTTCTCTGCTAA	3578
Dn	15031	GGCATGATCTGGCTCACTGTAAGCTCTGCTCTCTGAGTTTACGCCATTTCTCTGCTCA	14972
Qy	3579	GCCTCTGAGTAGCTGGAATTAACAGCTGACCAACCATGCTTGGCTAATTTTTTGTATT	3638
Dn	14971	GCCTACCAAGTAGCTGCGACTACAGGTGCCACCCGCTAATTTTTTGTATT	14912

QY	1620	TTCACTTTACAGGTTCTCGGTCCCAACGGTCTTTCAGAGGAGCGAGCTGSCAGGGGTCAAG	1679	QY	2672	AGGGTGACCTATTGCTCTGCACCTTACTCTATCTCAGCTGTCCCTCCACCTTTCCAGGT	2731
Db	114284	AGCTATCTCTGCTTCCTGCTTCCCAAGTGCT---GGGATACAGGTGTGAACACCTTG	114340	Db	115296	CTGGATATTTTGCCTGCCATGATTTTATTAATCTGAACACAACCCCGTGAGGTAGAAAT	115355
QY	1680	GGAGGACGTGGGACCCGAGGAGCAGAGGACAGTGTGTCCCGGGGTGCTGGCAGAC	1739	QY	2732	GCTGCCAGACACA---TGACAACTGTCTAYGACCAGGCCAAGAAGCTGGACAGCTGTAAA	2787
Db	114341	GCCAACTTCCTGCTTCTTAAACATCCTTACCTGTAAAGTCATTAGGGAGTTCAAGTCTTCA	114400	Db	115356	TAGCACCAAGCTCACCTGGGTGAACCTGAGTCTGTCTGACCTGCGTCTTTTCAGCCATGTCTC	115415
QY	1740	CGATTTGAACCTGGGTATGCTCTTCTTGAGTGGCGCCGCCGACAGCGGCATCACCCCT	1799	QY	2788	TTTCTGCTGGACAMMCCGTACACCCACACCTATTTCATCTCGTCTCTGGCTCGGCAATC	2847
Db	114401	GCATTTAGTTTGTGCTGCCAGTCTCTTCTGCTGACACAGGCAATAAATGCCTCACTTCGG	114460	Db	115416	TGAAAACCTACTTTTCTGCAGACCCCCACCCCTGAACCTAGAGGTACTGTAGGCTCTAAT	115475
QY	1800	CGGCGGTGTGGAGTTCCCAAAATGATCAAGTGGGTGATCCGGGGAGTGACCCCTTY	1859	QY	2848	ACCTGTAGCAGTAGGTTTATCCCTTCTTGACCTATGAATTTCTAGTTGTTTCTCAGTAGG	2907
Db	114461	CTTGTGTAATCCAGCGTCT---AGTGTTTGTTTGTGTTTCTGCTGTGCTGCGTAA	114518	Db	115476	TCTTAATCGCCTCAGATCATCCACAAGTTCTGACACCTGAGATTTGAGCCCGTGGTCTTG	115535
QY	1860	TTGGAATPACAACTACGCTGCTACTGTGTGGCTTGGGGGCTCAGGCACCCCGGTGGAT	1919	QY	2908	CGGGGGGAAATAAATAGTAACAACAGCCATGATTTTAGTGTGTTAATTTTCTGTTTCTGGGC	2967
Db	114519	GCAGACCAAGTTTCAGTTGGGTAAACAGCTAGGATTTCTAAAGGTTTAAAGGAAGCAAGTGAA	114578	Db	115536	CAGACAGATCCCGCGGTAAACCAAGGGCTTCTCTTTAGCCTTCTTCCAATCACCTGCCA	115595
QY	1920	GAAGTGAACAAGTAAGTATCCGCTGCAGGAAATTTGGAGTCCCTGCGGGGGCGGGGT	1979	QY	2968	AGTGTCTCTTTAACTCTCAGAACAACTAGGTAGGTACAATTTCTCTCACTTA--	3025
Db	114579	CTTTGTTTGGCTTTTTCACCTACACACAGAGATTAACCAAGTACAGGGAGTAAAGTCCCA	114638	Db	115596	ATTGCCCTTCCCAATCCTGCTGGACTGACTCTCAGAT--GCTACAGTGACACTGCTTCAGA	115654
QY	1980	GGGCACACGCCCAAGGATCTCACGAGGCATACAAAGGGGACTTGCATATCTGCTAAGGAT	2039	QY	3026	-----ACAGATAAGAAAACTGAGCCTCAGAAAGCTGAGCTATTTGCCCAAGATCA	3075
Db	114639	TTTTTACAGGCTGTATATGAGAGACCTGTGTGCACTGTCAGACAGCTGCTGCTCCGGGT	114698	Db	115655	GGAGTGACATATATACATATAATATATAATAATAATAATAATAATAATAATAATAATA	115714
QY	2040	AACATATTTTCACTCTTGTCAATTAACAAATATGTTTCAAGAGGACCCCTGTAGCGAAC	2099	QY	3076	CACAGCTTGTAAAGTGGTGACAGTTTGGGTTTTTTTTTGTGTTGTTTGTAGACACAGGCT	3135
Db	114699	AGAAAGTCTTGCTTAAAGATCAAAACAATCAGTATGT-----	114735	Db	115715	AACAAGAAATATATAAAATATATATTTCAITTTACTTATTTATTTTGTAGATGAAGTCT	115774
QY	2100	GCACCCGTTAGAGATGGAACAATGACCGACGTGCAACACAGTGGCGAGTGTGCCCTC	2159	QY	3136	TCGCTGTCTCACCCGCGCATGAGCAGGTGGTGCACCATAGGTACTCTGCAGGCTCAACCT	3195
Db	114736	-----CACTATGAGTTCTCTCTGACCC	114757	Db	115775	CGCTCTGTACCCAGCGCTGGAGTGCAATGGTGCAATCTCAGCTCACTGCACACTCGCCT	115834
QY	2160	CAGTGGCAGAATGTAGCAACAGTAACATCACAGCACTATCCACGTGTCTTTCTAGC	2219	QY	3196	CCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACAGAGCTGCA	3255
Db	114758	AGAGCTCTTGCAGGCTGAGGGAACATCTGTCCAGAGTGTCTTTATGGAGAATTC	114817	Db	115835	TCGTGATTCAGTGATTTCTCTGCTCAGCCTCTCGAGTAGCTGGGACTACAGCCATGCG	115894
QY	2220	AGTGGTTGTCACTGCACCTTCTGAATACAGGATTTTACTGTATTTCTTGCAACCATGTTAA	2279	QY	3256	CCACACGCGCTGGCTTAATAAAAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGC	3315
Db	114818	TAGGTTGGTCCATTAGGGAATAATGTCCCAAGGAACATTGATTTCTTACCATATAAGAA	114877	Db	115895	CCACCACGCCACAGCTAAATTTTGTGA--GTTTTAGTAGAGACGGGTTTTCCACATGTGGC	115952
QY	2280	AAATCGCTTTTCAGCCAGGCGCGGTGCTCATCGCTGTAAATCCAGCACTTTGGGAGGC	2339	QY	3316	CAGGCTGTCTTAAACTCTCGCTTCAAGCAATCTCTACCTTGGCATCCCAAGTAGTCT	3375
Db	114878	TACATACCCAGGCGGGCGTGGTGGCTCACGCTGTAAATCCAGCACTTTGGGAGGCC	114937	Db	115953	CAGGATGTCTCGATCTCTTGACCTCATG--ATCTGCCACCTTGTCTCTCCCAAGTGTCT	116010
QY	2340	GAGCGGGCGGATCACCTTGAGGTGAGGATTCGAGACCCAGCTGGCCAACATGGTGAAC	2399	QY	3376	GGGATTACAGGGGTGAGCCACCATGTGCGGTACTTATTTCTTTTACATTTCCATCTTTTCCA	3435
Db	114938	AGGGCGGCGGATCAC--GAGGTGAGGAGATCGAGACCATCTCTGGCTAACACGGTGAAG	114995	Db	116011	GGGATTATAGGCGTGAGCCAGTGTCGCGGCTATTTCTTTT-----ATTTTTATTTTTTA	116065
QY	2400	CTGTCTCTATAAAAAATACAAAAATTAGCCGACATGTTGCGAGCGCTGTAAACCC	2459	QY	3436	ATAGAATGTAGATCCACAGAACAGGATTAAGTGTCTATTTTCTTTCTTTTCTTTTGTAG	3495
Db	114996	CTGTCTCTATAAAAAATACAAAAATTAGTGGGATGTTGGGAGCACTTATAGTCCC	115055	Db	116066	TTTATTTTATTTTTTTTAGACAGGTTGTCTGTCTCACCAGGCTGGAGTGCAGTGAT	116125
QY	2460	AGCTACTTGGAGACT-----GAGTTGGAGTTTCACTG	2493	QY	3496	ACAGAGTCTCACTTCTCATCACTCAACCTCCGTTACAGTCACTGCACCTCTGCCTCCCGG	3555
Db	115056	AGCTACTTGGAGGCTGAGCGAGGAGAAATGGCTGAACCTTGGAGCGCGAGCTTGCAGTG	115115	Db	116126	GCAAA-----CATGCTCACTGCAGCCTCAACCTCTCGG	116158
QY	2494	AGCCAAGGTGTGTCACTGTGTCCAGCGCTGGGTAAACAGA--GCAACTCTGTCTCAAAA	2551	QY	3556	GTTCAGYGATTTCTCTGCTAAGCCTCTGAGTAGCTGGAAATTAACAGCGTGCACACC	3615
Db	115116	AGCGGAGACTGCGCCACTGCATCCAGCTTGGGTGACAGAGTGAGACTCTGTCTCAAAA	115175	Db	116159	GCTCAAAATGAGCCTCCACCTTGGCCTCTTGTGACGTGGGACTATAGTGTGCTGCACC	116218
QY	2552	AAAAAATGCTTTCAATAATATATATAAAGACCTTATATTTTTTCAAGCCATAGGAT	2611	QY	3616	ATGCTTGGCTAATTT-----TTTTGTATTTTAGCAGAGATGGGTTTTTACCATGTTGCC	3669
Db	115176	AAAAAATAAAGAAATATATACACCTCACTCCCACTTTTGTGAGACCTGAGAAAGCAG	115235	Db	116219	ATGCCAGCAAAATTTTCATATTTTAAATTTATGTAGAAACAGAGTCTCACCTTTGTGCC	116278
QY	2612	CAITTTCTCTGAAGCATCTTGGCGAGTCACTCCCACTTCTCTGAGAGTGGCAGGTG	2671	QY	3670	CAGGCTGTCTCAAACTCTCTGACCTCAAGTGTATCTGCTGCTGCTCAGTCTCTCCCAAGTGTCT	3729
Db	115236	TAGGACAGTAATGACGATGAATAGTACTTCTTTTATTTTCTACTATGACGCTCTGTG	115295	Db	116279	CA-GCTGTCTCAAACTCTCTGGATTCAGGCCATCTCCACCTTGGCCTCCCAAGTGTCT	116337
				QY	3730	GGAAATATAGGCGTGAGTCACTGTGCTGGCC	3761

Db	116338	GAGATT-CAGGATGAGCCACTGCACCTGGCC	116368	Db	11612	GCTGAGGCTCAAGTTAAAGTGGAGCAGCAGCTGAGCTGTACCAGGTGAGGACATGAGC	11671
RESULT 22							
US-10-995-561-13296							
; Sequence 13296, Application US/10995561							
; Publication No. US20050272054A1							
; GENERAL INFORMATION:							
; APPLICANT: CARGILL, Michele et al.							
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH							
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF							
; FILE REFERENCE: CL001559							
; CURRENT APPLICATION NUMBER: US/10/995,561							
; CURRENT FILING DATE: 2004-11-24							
; NUMBER OF SEQ ID NOS: 85702							
; SOFTWARE: FastSeq for Windows Version 4.0							
; SEQ ID NO 13296							
; LENGTH: 35770							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
; FEATURE:							
; NAME/KEY: misc_feature							
; LOCATION: (1)...(35770)							
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-							
US-10-995-561-13296							
Query Match 7.4%; Score 367.8; DB 10; Length 35770;							
Best Local Similarity 53.2%; Pred. No. 3.1e+02;							
Matches 1223; Conservative 11; Mismatches 914; Indels 153; Gaps 16;							
QY	2292	GGCCAGCGCGGTGCTCATGCTGTAAATCCAGCACTTTGGGAGCGCGGCGGA	2351	QY	2292	GGCCAGCGCGGTGCTCATGCTGTAAATCCAGCACTTTGGGAGCGCGGCGGA	2351
Db	11031	GGCTGGCGTGGTGTACACCTGTAAATCCAGCACTTTGGGAGCGCGGCGGA	11090	Db	11031	GGCTGGCGTGGTGTACACCTGTAAATCCAGCACTTTGGGAGCGCGGCGGA	11090
QY	2352	TCACTTGAGTTCAGGAGTTTCAGTACGAGCGCTGCGCAACATGTTGAAACCTGTCTCTACT	2411	QY	2352	TCACTTGAGTTCAGGAGTTTCAGTACGAGCGCTGCGCAACATGTTGAAACCTGTCTCTACT	2411
Db	11091	TCAC--GAGGTACAGGAGTCGAGACCATCTCTGCGCAACATGTTGAAACCTCTCTACT	11148	Db	11091	TCAC--GAGGTACAGGAGTCGAGACCATCTCTGCGCAACATGTTGAAACCTCTCTACT	11148
QY	2412	AAAAATACAAAAATTAGCCGACATGTTGGCGAGCGCTGTAAACCCAGCTACTTTGGGA	2471	QY	2412	AAAAATACAAAAATTAGCCGACATGTTGGCGAGCGCTGTAAACCCAGCTACTTTGGGA	2471
Db	11149	AAAAATACAAAAATTAGCTGGCGATGTTGGCATGHCCTTTAGTCCAGCTGCTCGGGA	11207	Db	11149	AAAAATACAAAAATTAGCTGGCGATGTTGGCATGHCCTTTAGTCCAGCTGCTCGGGA	11207
QY	2472	GACTGAGTTGAGGTTTCAGTGAGCGCAAGTCTGTCTGCTGCTCCAGCTGGGTAACA	2531	QY	2472	GACTGAGTTGAGGTTTCAGTGAGCGCAAGTCTGTCTGCTGCTCCAGCTGGGTAACA	2531
Db	11208	GGCTGAG--GCAGGAAATTGCTTGAACCTTGAGCGGAGGTTGCAGTGACGAGATT	11265	Db	11208	GGCTGAG--GCAGGAAATTGCTTGAACCTTGAGCGGAGGTTGCAGTGACGAGATT	11265
QY	2532	GAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATATATAAAGGACTTAT	2591	QY	2532	GAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATATATAAAGGACTTAT	2591
Db	11266	GGCCCACTGCACCTCAAGCTGGTGACAGCGAGTCTCCGTCTCAAAAAAATAAATA	11325	Db	11266	GGCCCACTGCACCTCAAGCTGGTGACAGCGAGTCTCCGTCTCAAAAAAATAAATA	11325
QY	2592	ATTTTTCAGCCATAGGATCATTTCTCTGAGCATCTTGGGGAAGTATCCCCACCTG	2651	QY	2592	ATTTTTCAGCCATAGGATCATTTCTCTGAGCATCTTGGGGAAGTATCCCCACCTG	2651
Db	11326	ATTCTTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGGTATCAG	11385	Db	11326	ATTCTTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAGGTATCAG	11385
QY	2652	TTCTCAGAGTGGCGAGGTGAGGCTGACCTATTGTCTGCACTTACTCTCTCAGCT	2711	QY	2652	TTCTCAGAGTGGCGAGGTGAGGCTGACCTATTGTCTGCACTTACTCTCTCAGCT	2711
Db	11386	AGACTGACTCCACCCAGAGCTGTACGCTCAAAACTC-----CTAGAGTT	11431	Db	11386	AGACTGACTCCACCCAGAGCTGTACGCTCAAAACTC-----CTAGAGTT	11431
QY	2712	GTCCCTCCCACTTTCCAGGTGTGCCAGACATGACAACTGCTAYGACCGGCCAAGAA	2771	QY	2712	GTCCCTCCCACTTTCCAGGTGTGCCAGACATGACAACTGCTAYGACCGGCCAAGAA	2771
Db	11432	GGGAGCACCAAGTCCCTCACCTCTGCCAAACCCCTGATCKCCTCATTTCTCCCT	11491	Db	11432	GGGAGCACCAAGTCCCTCACCTCTGCCAAACCCCTGATCKCCTCATTTCTCCCT	11491
QY	2772	GCTGGACAGCTGTAAATTTCTGCTGGACAMCCGTACACCCACCTATTCATCTCGTG	2831	QY	2772	GCTGGACAGCTGTAAATTTCTGCTGGACAMCCGTACACCCACCTATTCATCTCGTG	2831
Db	11492	GCTAGAAATCTATGACAAGTTCAAGCAGAGTACACACGATATATATGTTCTTCAACAC	11551	Db	11492	GCTAGAAATCTATGACAAGTTCAAGCAGAGTACACACGATATATATGTTCTTCAACAC	11551
QY	2832	CTCTGGCTCGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTCCCTATGAAATTCTA	2891	QY	2832	CTCTGGCTCGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTTCCCTATGAAATTCTA	2891
Db	11552	ATCAGAGCTCCGAGAGCGGTACTGAAACCCGTGTTGCTCTCCCGGGCAGAGCTGTCT	11611	Db	11552	ATCAGAGCTCCGAGAGCGGTACTGAAACCCGTGTTGCTCTCCCGGGCAGAGCTGTCT	11611
QY	2892	GTTGGTTCTCAGTAGGCGGGGAAATAATAGTAACAACAGCCATGATTTAGTGTAAAT	2951	QY	2892	GTTGGTTCTCAGTAGGCGGGGAAATAATAGTAACAACAGCCATGATTTAGTGTAAAT	2951


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Db 114879 TGCTGTATCCAGACATTTGGAGCCGAGAGAGATGATCACCCTGAGTCAAGAGTT 114820
Qy 4305 CGAGACAGCCTGGTCAATATGTTGAACCCCTATCTCTACTATAAATAACAAAA-TTAGC 4363
Db 114819 CGAGACAGCCTGGCCAAACATGTTGAGAGCCCATCTCTACTATAAATACTACAAAAATTTAGC 114760
Qy 4364 TGGGTGTAGTGATGCATGCTGCTGTAGTCCAGCTACTCGGAGGCTGAGCGAGAGATTG 4423
Db 114759 CAGGTGTGGTGGTACGTGTCTGTAGTCCAGCTACTCAGAAGGCTAAGCGAGGAAATCA 114700
Qy 4424 CTTGAACCTGGGAGGAGAGGTTGCAGTGAGCCGAGATCCACCACTGCACTCCAGCCTG 4483
Db 114699 TTTGAACCCGGAAGTGGAGGTTGCAGTGAGCTGAATACACCA-----CTCCAACTG 114645
Qy 4484 GCGACACACGAGACTCTATCTCAAAAAATAAATAATAA 4525
Db 114644 GCGACAGAGCAAGACGTTGTCTCAACAACAACAACAAA 114603

RESULT 25
US-10-995-561-13274/c
; Sequence 13274, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13274
; LENGTH: 415117
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(415117)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13274

Query Match 7.28; Score 362.2; DB 10; Length 415117;
Best Local Similarity 56.48; Pred. No. 57;
Matches 825; Conservative 2; Mismatches 605; Indels 31; Gaps 7;

Qy 3098 TTTGGGTTTTTTTTTTGTTGTTTGTAGACAGGGTCTTGCTCTGTCAACCCAGGCATGAG 3157
Db 326605 TGTGTTGTTAAATTTTTTTTTTTCCAGACAGGGTCTACATGTCACCCAGGCTGGG 326546
Qy 3158 CACAGTGGTCAACCATPAGTCTACTGAGCCTCAACCTCTGAGCTCAAGGGATCTGCTG 3217
Db 326545 TGCAGTGACACGATCTCGGTTCACTGCAACCTCCACCTCCAGGTTTAAAGTGATCTCCT 326486
Qy 3218 ACCTCAGCCTCCCACTAGCTGGGACTACAGCGGTGCACACACACCGCTGGCTAAATAA 3277
Db 326485 GCCTCAGCCTCCCAAGTAGCTGGGATGACAGGTGTGCACCACTGCTGAGCTAAATTTT 326426
Qy 3278 AAAATTTTTTTGTAGAGACTGGGTCTTACTACGTGTGGCCAGGCTGTGCTTAAACTCTGG 3337
Db 326425 GTA--TTTTTAGTAGAGATGGGGTTTACCATGTTGCTGAGCTTAAGTGATCACCCTGC 326368
Qy 3338 CTTCAAGCAATCTCTTACTCTGGCATCCCAAGTGTGGGATTAAGGGGTGAGCCACC 3397
Db 326367 CT-----AAGCCTCCCAACTGGGCTT-----ACAGCATGAGCCACCATGCCCCAGCAAAA 326319
Qy 3398 ATGTGGGCTACTATTCTTTTACATTCATCTTTCCATAGTAATGTAAGATCCACAGAA 3457
Db 326318 AAAAACGGTTTATCTATTTCATTTCTTTATTTATTTATTTATTTATTTATTTATTTA 326259
Qy 3458 CAGGGATTACTGCTATTTTCTTCTTCTTTTGTGAGACAGAGTCTCACTTCATCACCT 3517
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Db 326258 CTTACTTATTTATTTATTTTGTGAGGAGAGTCTCACTCTGTTGCCAGGCTGGAATGCA 326199
Qy 3518 CAACCTCCGTTCCAGTCTCACTGCAACCTCTGCTCCCGGGTTCGAAGTATCTCTGCTCA 3577
Db 326198 GTGGCAGCATCTCGCTCATTTGCAACCTCTGCTCTCAAGTTTCAAGCGATTTCTCTGCTC 326139
Qy 3578 AGCCTCTCGTGTAGTGTGGAAATTTACAGGCTGCACACCATGCTTGCTGCTAAATTTTGTAT 3637
Db 326138 AGCTTCCCAAGTAGCTGAGATTACAGGCACACACACACACTGCTGCTAA--TTTTTCTAT 326080
Qy 3638 TTTTAGCAGAGATGGGTTTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTCAA 3697
Db 326079 TTTTAGTAGAGATGGGTTTCCGCATGTTGGCCAGGCTGGTTTCGATCTCTGACCTCAG 326020
Qy 3698 GTGATCTGCTGCTGCTCACTCTCCAAAGTGTGGAATTTATAGGCTGTAGTCTACTGTGCT 3757
Db 326019 GTGATCTGCCGCTCGGCTCCCAAGTGCAGGATTTACAGGCATGAGCCACGAAGCC 325960
Qy 3758 GGCGGATTACTGTCTATTTTCTTTATTTGCTATATCCCGAGATCTAGAGCAGTGTCTGACA 3817
Db 325959 GGCCCCCGGCCCAAAATTTTTAAATG-----AGGACTTTGGGACGGATGCTCA 325909
Qy 3818 TATAGTAGGTGCTCAATAAATAATTGATGAATGCACAGCTAGATATAAACTTTCTTTTT 3877
Db 325908 CTCAACTGTCACTTATTTATCTCATTTTAAAAAATCTAAATCTTTTATAAATGAAACTTA 325849
Qy 3878 CTTTTTTTAAACAATCTTGACAACCTTTGCAGATAAATAACAATCTTGATCTCTGCTTT 3937
Db 325848 GGGTGGCAAGCATACTTGTTCAGAAATAATACACCTAGTAAATAAGGAGAGGCTGTG 325789
Qy 3938 TCACATTATCACCTTGTGTATGACTTTTTCATATGCTCTCAACCTTTATTGTTACTGT 3997
Db 325788 AAAGTAATTGACAGAGAGAAATATTTGGCTTCAACACTGACAGAGAGAAAGTAGAGT 325729
Qy 3998 TTCATTGTTACTATTTTAGTCTCACTGAATAATAATGCTTAAATTTGCTTATPACATCCT 4057
Db 325728 TAGAGGAAAAAACAARAATAATGCCATATAGTGTACTCTTAGGTTACTAGGGCATA 325669
Qy 4058 CTCACATTTAGAGGCCAAATTTACAATCTGATGAAGCTATGAACCTCTCCCCAGAG 4117
Db 325668 GTAGTACTTTTATAAACAACAGCAGGAAAGATAATTTGAAATTCATTTATCTTTA 325609
Qy 4118 AAATACACACACACACACTCAACACAGTTTTTTTTTTAATGTTTGCAACTAAGACA 4177
Db 325608 GAGCATCTGTATGTGAATACTATAAACA-----GACCCATGTGAAGGTGTCTAGAA 325556
Qy 4178 AGAAACCTGCATPAGAGGATGTTTGTTCATATTAATTAATAATAACTAGTTGGGCACAG 4237
Db 325555 GGGCCCTTCACACAAAGATTCAATGCTGGGATAGAGATATAGATTGGCCAGCGCTGG 325496
Qy 4238 TGACTCAAGCCTGTAAACACAGTACTTTTGGAGTCCAAGGTGGGTGGATCACTTGAGGTG 4297
Db 325495 TGGCTCACACCTGTAATCCAGCACTTTTGGGAGCGGAGACAGGAGATCACTGAGGTG 325436
Qy 4298 AGAAGTTGAGACACAGCCTGGTCAATATGTTGCAAAACCTTATCTCTACTAAAAATACAAA 4357
Db 325435 AGAGTTTGAGACAGCCTGGCCAAATGCGCAACCCCGTCTCTACTAAAAATACAAA 325376
Qy 4358 ATTAGCTGGGTGTAGTGATGTCATGCTGTAGTCCAGGCTACTCGGAGGCTGAGGCAAGA 4417
Db 325375 ATTAGCCATGTGTGTGGCATGCACCTGTAGTCCAGCTACTTTGGAGGCTGAGGCAGGA 325316
Qy 4418 GAATTTGCTGAACCTGGGAGCAGAGGTTGCAAGTGCAGCGAGATCCCA--CCACTGCACCTC 4476
Db 325315 GAACCACTTGAACCTTTGGGAGGTGAGACTGTCAGTGAGCCCAAGATCGACCCCACTGCACTC 325256
Qy 4477 CAGCTGGGCGACACAGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAGGATC 4536
Db 325255 CAGCTGGGAGACAGCGAGACTCCATCTCAAAACAACAACAACAACAACAACAACA 325196
Qy 4537 GGAGAGAAACAACAATAATAAGA 4559
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; LENGTH: 35962
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-234

Query Match      7.2%; Score 361.6; DB 10; Length 35962;
Best Local Similarity 58.9%; Pred. No. 3.5e+02;
Matches 844; Conservative 1; Mismatches 460; Indels 127; Gaps 8;

QY 3104 TTTTGTGTTGTTGTTAGACAGGGGTTGCTCTGTCACCCAGGATGAGCAGT 3163
D 3142 TTTTGTGTTGTTGTTAGACAGAGTCTCATCTGTTACCCAGGCTGAAGTGCAGT 33083
QY 3164 GGTGCAACCATAGTCTAGTGCAGCCTCAACCTCTGAGCTCAAGGATCTGCTGACTCA 3223
D 33082 GGTGCGATCTCAGGTCACTGCAACCTCTTCCCGGGGGTCAAGATATTCTCTGCTCA 33023
QY 3224 GCCTCCCAAGTAGCTGGGACTAGGAGCTGCACACACAGCCTGGCTTAATAAAAAATT 3283
D 33022 GCCTCTGAGTAGTCTGAGATTACAGGTGATGCACACGCCCATCTAATTTTGTGTA--T 32965
QY 3284 TTTTGTAGAGACTGGGTCTTACTAGCTTGGCCAGGCTTGTCTTAACTCTCGGCTTCAA 3343
D 32964 TTTTAGTACAGACGGGGTTTCATCAGCTTGGCCAGGCCAGTTTCGAACTACTGACCTCAA 32905
QY 3344 GCAATCTCTACTTGGCATCCCAAGTCTGGGATTACAGGGTGAGCCACCATGTGC 3403
D 32904 GTGATCGGCTGCTCATCTCCCAAGTCTGGGATTACAGCGGTGAGCCACCACTCC 32845
QY 3404 GGCTACTATTCTTTACATTCCTATCTTCCCAATAGAAATGTAAGATCCACAGAACAGGA 3463
D 32844 AGCAGGAATTTCTTTTGTGAGACAAG-- 32809
QY 3464 TTACTGCTAATTTCTCTCTTTTGTGAGACAGAGTCTACTTCATCACCCTCAACCT 3523
D 32808 --TTTCGCTCTGTGTCAGGCTGGAGTGAATGTTGTGATCTCGTCTCAATGCAACCT 32751
QY 3524 CCGTTCAGCTCACTGCNAACCTCTGCTCCGGGTTCAAGVGATTCCTCGCTCAAGCCCTC 3583
D 32750 CCG-----CTCCGGGGTTCAAGAAATTCCTCGCTCAGCCCTC 32713
QY 3584 CTGAGTAGCTGGAATTACAGCGTGACACCACTGCTTGCTGAATTTTGTGATTTTGTAG 3643
D 32712 CTGAGTAGCTGGGATTAGAGCATGTGCCACACCGCCGGCTAATTTT--TACTTTGG 32655
QY 3644 CAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTCAAACTCTCGACTCAAGTGATC 3703
D 32654 TAGAGACAGGGTTTCTCCATGTTAGTCAGGCTGGTCTGAACTCCCGACCTCAGGTGATC 32595
QY 3704 TGCTGCTCAGTCTCCCAAGTCTGGAAATTATAGCGTGAGTCACTGTGCTGGCCGA 3763
D 32594 TGCCACTTCGGCTCCCAAGTCTGGGATTACAGCGGTGAGCCACTGTGCCCGC--- 32538
QY 3764 TTACTGTCTAATTTCTTTATTGCTATATCCCAAGATCTAGACAGTGTCTGACATAGT 3823
D 32537 -----CTAGCCAGGAATTTCTTAAAGGCT 32514
QY 3824 AGGTGCTCAATAAATTGATGAATGACAGGCTAGATATAAACTTTCTTTTCTTTT 3883
D 32513 GGCTGCTTTTAAAGAACTCTACCAATGAATCTGAT-----TTTTTTTTTTT 32468
QY 3884 TTAATAACAATCTTGACAACCTTTTCAGAAATAAATAACAATCTTGCTTTTTCACATT 3943
D 32467 TTTACCCCGAGAGACACGGTCTCCCTCTATTGCCCAAAATTGGAATGCGAGTGTGTTTC 32408
QY 3944 ATCACTTGTATTGACTTTTTCATATTGCTTCAACCTTTTATTGTTTACTGTTTTCATT 4003
D 32407 ATGGCTCACCGCAGCTCGACTCTTTGGCTCCAGTGGGAGCTTGGCTAATTTTAAATT 32348
QY 4004 GTTACTAATTTTAGTCACTGAATTAATATGGCTTAATTTGCTTATACATCTCTGCTCCAC 4063
D 32347 TCTGTAGAGGTAAGATCTCTACTAGATTGCAACAGCTGGGTTTCGAAAC-----TCCTGAC 32296
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QY 4064 TTTAGAAGCCAAATTTTACAAATCTGATGAAGCTATGAACCTCTCTCCACAGAAATAC 4123
D 32295 CTCAGGTGATCCACCTGCTCGGCTCCCAAAGTCTGGGATTACAAGCACAG----- 32242
QY 4124 ACACACACACACACACTCACACACAGTTTTTTTTTTAATGTTTTCGAACTAAGACAAGAAC 4183
D 32241 -----CCACAGCACCTGGCCTCCATTTTGCACCTTTGAATGGATCTTTAACCTGTGCA 32190
QY 4184 CTGCATTAGAGGATGTTGTTTCATATTAAATTTAAATAAATCACTCAGTTGGGCACAGTACTC 4243
D 32189 TGATTTTATATCATGCAATGATCATTTAGAAAATAATGGTTTGGCTGGGCACGGTGGCTC 32130
QY 4244 AAGCCTGTAACACACAGTACTTTTGAAGTCCAAAGTGGGTGGATCACTTGGAGTGAAGCT 4303
D 32129 ACACCTGTAATCCAGCATTTTGGAGGGTGGTGGCCAGATCATTTTGAAGTCAGGAGT 32070
QY 4304 TCGAGACAGCCTGGTCAATATGTTGAACCCCTATCTCTACTAAAAATAACAAAAATTAGC 4363
D 32069 TCAAGACCAAGCTGGCTTAACATGGTGAACCTCCTCTACTAAAAATAACAAAAATTATT 32010
QY 4364 TGGGTGTAGTATGATGCTGCTAGTCCAGTACTCGGAGGCTGAGGCAAGAAATTG 4423
D 32009 CACTTGTGTGGTGCATGCCCTGTAATCCAGCTACTCAGGAGGCTGAGGCAAGAAATTG 31950
QY 4424 CTTGAACCTGGAGCAGAGGTTGCAGTGAGCCGAGATCCCACTGCACTGCCAGCCTG 4483
D 31949 CTTAAACCTGGAGGTGAGGTTGTAGTGAGCCGAGATCATGCCACTACACTCCAGCCTA 31890
QY 4484 GCGCACACGCGAGACTCTATCTCAAAAAATAAATAAATAAATAAAGGAT 4535
D 31889 GACAAACACAGCAAGACTCTGTGCAAAAAACAAACAAAAAGAAATAATTGAT 31838
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RESULT 28
US-10-995-561-13308/c
; Sequence 13308, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 13308
; LENGTH: 148935
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13308
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Query Match      7.2%; Score 360.2; DB 10; Length 148935;
Best Local Similarity 59.1%; Pred. No. 1.3e+02;
Matches 897; Conservative 2; Mismatches 500; Indels 118; Gaps 12;
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QY 3073 TCACACAGCTTGTAGTGGTGACAGTTCCTGTTTGGGTTTTTTTTTGTGTTTGTAGACAGGG 3132
D 44221 TCTTATATATAGCATATAGTAGGATTGTTTTTGTGTTTTTTTTTTTGTGAGATGGAG 44162
QY 3133 TCTTCTCCTC-TGTCACCCAGGCATGAGCAGTGGTGGCAACCATAGTCACTCGAGCCTCA 3191
D 44161 TTTTGTCTTGTGTTGCCAGGCTGGAGTGCATGGTGCATCTCAGCTCACTACACCTCT 44102
QY 3192 ACCTCCTGAGCTCAAGGATCTGTCAGCTCAGCCTCCCAAGTAGTGGGACTACGAGCG 3251
D 44101 GTCACCCAGGTTCAAGCATTTCTCTGCTCAGCCTCCTGGGTAGTGGGATTACAGGCA 44042
QY 3252 TGCACCAACCGCTGGCTAATTAATAAAAAATTTTTTTGTAGAGACTGGGCTTACTACCT 3311
D 44041 TGCACCACTACACCAAGCTAATGTTTGTGTA--TTTTTAGTAGAGTTGGGTTTCCACCATGT 43984
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QY 4049 ATCTCTCTGCTCCACCTTTAGAGGCCAAATTTTACAAATCTGATGAAGCTATGAACCCCTC 4108
Db 10538 AATTTTGTATTTTGTAGTAGAGATGGGGTTTACCATGTTTGGCCAGGCTGATCTCGAACT 10597
QY 4109 TCCCCAGAGAAATACACACACACACACACTCACACAGTGTCTTTTAAATGTTTGA 4168
Db 10598 TCTGACCTCAAGTGATCCACCCTCGGCTCCCAAGTGTGGGACTACAGGCGTGAG 10657
QY 4169 ACTAAGCAAGAAACCTGCAATAGAGAGTGTGTTTCATATTAATTA 4216
Db 10658 CCACAGCACCTGGCTGTTCACTCTATCATATTAATTCAGTCAATAAATGCAAAATATTTAAAAA 10717
QY 4217 ---AATAACTCAGTTGGGCACAGTGAATCAAGCCTGTAACACAGTACTTTGGAGTCC 4273
Db 10718 ACTAATTTCTAGCTGGGGCGAGTGGCTCATGCCCTGTAATCCACGACCTTTGGGAGGCC 10777
QY 4274 AAGGTGGGTGGATCACTTGAAGGTGAGAAAGTTCAGAGCCAGCCTGGTCAATATGTTGAAAC 4333
Db 10778 AAGCAGGCAGATTTGCTGAGGTGAGGATTCAGAGTTCAGAGCCAGCCTGGCCAAACATGTTGAAAC 10837
QY 4334 CTTATCTCTACTAAAAATACAAAAATTTAGCTGGGTGTAGTGATGCAATGTTAGTCCCA 4393
Db 10838 CTTGCTCTACTAAAAATATAAAAAATTTAGCCAGTCAATGTTGGTGTGCTGCTGTAATCCCA 10897
QY 4394 GCTACTCGGGAGGCTGAGGCAAGAGAAATGCTTTGAACCTGGGAGGCGAGGTTGCAAGTGA 4453
Db 10898 GCTACTC-AGAGGCTGAGGCGAGAGAAATCGCTTTGAACCCAGGAGGCGGAGGTTGCAAGTGA 10956
QY 4454 GCCGAGATCCACCCTGCACTCCAGCTGGGGCGACACAGCGAGACTTATCTCAAAAAA 4513
Db 10957 GCCGAGATCCACCCTGCACTCCAGCTTGGGTGACAGAGCGAGACTTAAATCTCAAAAAA 11016
QY 4514 AATAAATAAATAAATAA 4531
Db 11017 AACAAACAAACAAATGAA 11034

RESULT 32

US-11-112-908-57

; Sequence 57, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112,908

; PRIOR FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 57

; LENGTH: 161994

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-57

Query Match

Best Local Similarity 57.1%; Pred. No. 1.3e+02;

Matches 852; Conservative 1; Mismatches 553; Indels 85; Gaps 8;

QY 3107 TTTTGTGCTGTTTGTAGACAGGCTCTGCTCTGTCACCCAGGATGAGCACAGTGT 3166
Db 55272 TTTTGTGCTGTTTGTAGACAGGCTCTGCTCTGTCACCCAGGATGAGCACAGTGTGC 55331

QY 3167 GCAACCATAGTCTACTGAGGCTCAACCTCTGAGCTCAAGGGATCTGCTACCTCAGCC 3226
Db 55332 ACAATCTTGGCTCACTACAACTCCGCTCCAGGTTCAAGCAATATATCTCCCTCAGCT 55391
QY 3227 TCCCAAGTAGTGGGACTACGAGCGTGACACACACCGCTGGCTAAATTAATAAATTTT 3286
Db 55392 TCCCAAGTAGTGGGATTTACAGGCACACGCCACCATGCTGGCTAAATTTTGTATTTT 55451
QY 3287 TTGTAGACACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCTCTGGCTTCAAGCA 3346
Db 55452 TAGAAGAGATGGCGTTTCGCCATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAGGTG 55511
QY 3347 ATCTCTCACTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTCGCGC 3406
Db 55512 ATCCACCTCGCTCGTCTCAAAAGTACTGGGATTTACAGGCATGAGCCACCGCCGCGC 55571
QY 3407 TACTTATTTCTTTTCAATTCATCTTTCCAAATAGAAATGTAAGATCCACAGAACAGGATTA 3466
Db 55572 CAAGTGTCACTTTTCAATGCTTAGAAAAGTTCACCTGTATTTATTTTACCTTCAGCTTGTGTTG 55631
QY 3467 CTGCTATTTTCTCTCTTTTGTGGACGGAATCTCCTCTGTCAACAGGCTGGAGTGCAGTGTG 3526
Db 55632 TTTGTTGTTGTTTGGGACGGAATCTCCTCTGTCAACAGGCTGGAGTGCAGTGTG 55691
QY 3527 ----TTCAGCTCACTGCAACCTCTGCTCCCGGGTTCAAGYATTTCTCTGCTCAAGCT 3582
Db 55692 CGATTTCCGCTCACCGCAACCTCTGCTGCCAGGTTTCAAGCGATCTCTCTGCTCAGCT 55751
QY 3583 CTTGAGTAGTGGGAATTAAGCGTGCACACCATGCTTGGCTAAATTTTGTATTTT 3642
Db 55752 TTCCAGTAGTGGGATTTACAGGCATACACCCACACCCAGCTGATTTT--GTATTTTA 55809
QY 3643 GCAGAGATGGGTTTACCATGTTGCCCGAGGCTGCTCAAACTCTGACCTCAAGTGTAT 3702
Db 55810 GTAGAGATGGGTTTCACTGTTGGCCAGGTTGCTCTCGAACTCTGACCTCAAGTGTAT 55869
QY 3703 CTGCTGCTCAGTCTCCCAAGTGTGGAATTTATAGGCGTGAAGTCACTGTGCTCGGCG 3762
Db 55870 CGCGCCGCTTGGCTTCCCAAGTCTGGGATTAACAACATGAGCCACCTCTCCCGGCTA 55929
QY 3763 ATTACTGTCTATTTTCTTTTATGCTATATCCCAATC-----TAG 3803
Db 55930 CCTCCAGTTTGTGTTTGTGTTTAAATTTGAAAACATACATAGAAGTACAAAGAATAA 55989
QY 3804 AGCAGTGTGACATATAGTAGTCTCAATAAATTAATGATGAATGACACACCTAGATA 3863
Db 55990 AAAAAATATGACCATATATCTCCCAAGTTTAATCATGTTAACATTTTATTATGCT 56049
QY 3864 TAAACTTTCTTTTCTTTTAAACAATCTTGACAACTTTGACAGATTAATAAATACT 3923
Db 56050 TGTGAAGTTTAAATCAAAAAAGAAATAAATTGGACACCATGTTTCTATGCTATAATCT 56109
QY 3924 --TGCAATCTGCTTTTCTATATCACTTGTATGACTTTTTCATATGCTCTCAACCT 3981
Db 56110 CAGCCCTTTGAGAGGCCAATGACAGGAGTATCGCTTTGAGCCTAGAAAGTTTGAAGCAGCT 56169
QY 3982 T-----TATTTGTTACTGTTTTCATTTGTTACTATTTTAGTCACTGAATAATATGCTT 4036
Db 56170 GGGCAACAGTAAAGTCCATCTCTCAAAATAAATAAATAAATAAATAAATAAATAAATA 56229
QY 4037 ATTTGCTTATACATCTCTGCTCCACTTTTGAAGGCCAAATTTTACAAAT----- 4086
Db 56230 AGCTGGAAGTCCATCTTGTTCCTTGGCAAGCCAGCCACTTTTAAATGAATTTTTCAGCTG 56289
QY 4087 -----CTGATGAAGCTATGAACCC 4106
Db 56290 GGGCTTCTAGTTTGTGTTTATCTTCTACTACATAATAGTATTTGAGCTGCCAGGTGCAATG 56349
QY 4107 TCTCCCGCAGAGAAATACACACACACACACTCACACACAGTTTTTTTTTTAATGTTTG 4166
Db 56350 GCTCAGGCTGTATCTCCAGCACTTTGGAGGCTGAGGGGGAAGATGCTCGAGCCCAAG 56409
QY 4167 CAACTAAGACAAAGAAACCTGCAATAGAGATGTTTGTTCATATTAATTAATAAATAAATACTCA 4226

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Db 56410 GAGTTTGAGACCGCCTGGGCAACATGGCCAAACCCCTCTCTATATAAAAAACACAAAAAG 56469
Qy 4227 GTTGGGCACAGTGACTCAAGCCCTGTAAACACAGTACTTTTGGAGTCCAGGTTGGGTGGAT 4286
Db 56470 GCAGGAGCAGTGGCTCACGCCCTGTAAATCCATCACTTTTGGGAGCGGAGGGGGTGGAT 56529
Qy 4287 CACTTGAGGTGAGAAGTTTCAGAGACCAGCCCTGGTCAATATATGGTGAACCCCTATCTCTACTA 4346
Db 56530 CAC--AAGGTGAGAGATCGAGACCATCTCTGGCTTAACATGGTGAACCCCATCTCTACTA 56587
Qy 4347 AAAATA-CAAAAAATTAGCTGGGTGTAGTGTATGATGATGCTGTAGTCCAGCTACTCGGGAG 4405
Db 56588 AAAATATTAAAAATTAGCTGGCGTGTGGCAGGCGCTATAGTCCAGCTACTACAGGAA 56647
Qy 4406 GCTGAGCAGAGAAATTTGCTTGAACCTGGGAGGCGAGGTTGAGTGAGCCGAGATCCCA 4465
Db 56648 GCTGAGGAGAGAAATGGCGTGAACCTTGAACCGGAGCTTGCAGTGAGCCGAGATCAG 56707
Qy 4466 CCACTGCACCTCCAGCCTGGGCGCACAGCGAGAGCTCTATCTCAAAAAATA 4516
Db 56708 CCACTGCAITTCAGCCTGGGCAACAGATGAGACTCTACTCAAAAAATA 56758

RESULT 33
US-10-995-561-13251/c
; Sequence 13251, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13251
; LENGTH: 38023
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13251

Query Match 7.1%; Score 353.2; DB 10; Length 38023;
Best Local Similarity 52.0%; Pred. No. 4e+02;
Matches 1199; Conservative 20; Mismatches 968; Indels 117; Gaps 16;

Qy 2280 AAATCGCTTTTCAGGCCAGGCGCGGTGGCTCATCGCTGTAAATCCAGCAGCTTTTGGGAGGCC 2339
Db 32335 AAAAGAGTGGCAGCGCGGCACAGTGGCTCACGCCCTATAATCCTAGCAGCTTTTGGGAGGCC 32276
Qy 2340 GAGCGGGGGGATCACTTGAGGTGAGGTTGAGACCGAGCTGGGCCAAGCTGGTGAAC 2399
Db 32275 AAGCGAGGTGGATCACTGAAGTCAGGAGTTTCAGAGCTTCAGAGCTGGCCAACTGGTGAAC 32216
Qy 2400 CTTGCTCTACTAAAAATACAAAAATAGCCGGACATGGTGGCAGCGCTGTAAACCC 2459
Db 32215 TCTATCTCTACTAAAAATATAAACAATTAGCCAGGTGTGGTGGCAGGTGCTGTATATCC 32156
Qy 2460 AGCTACTTGGGAGACTGA-GTTGGAGGTTTCAGTGAGCCAAAGTTCGTGTCATCTGTCTCC 2518
Db 32155 AGCTACTCGGAGGCTGAGCAGGAGAAATCCCTTGAACCCAGGAGCGGAGGCTGCAGTG 32096
Qy 2519 AGCTGGGTAAACAGAGCACTGTCTCAAAAAAATAAATGCTTCAATAAATATATGA 2578
Db 32095 AGCCAAAGATCA-----TGCCACTGCACTCCAGCGTGGGTGACAGAGAGACTC 32047
Qy 2579 TAAAAGGACTTATATTTTTTCAAGCCATAGATCATTTCTCTCTGAAGCATCTTGGCGAAG 2638
Db 32046 CCATCTCAAAAAATTTTTTTTTTAAATGACAGGTTGAGCTGCTCACTTACTCTAATTT 31987
Qy 2639 TCATCCCCACCTGTTCTCTGAGAGTGGGCGAGGTGAGGCGTGACCTATTGCTCTGCACTTAC 2698
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Db 31986 CTATTTCTGGAGTGAATTTCTCTGGAGAGKCTAGGTAAAGACTGAAAAAGGCAVTTGTACGTCC 31927
Qy 2699 TCCTATCTCAGCTGTCCTCCACCTTTCCAGGTGCTGCCAGACATGACACATGACATGCTCTAYG 2758
Db 31926 ACCTCTCAT-----CTCACTTGGACAAGAACTCAGGAGAACTATTGAACTGAGGTG 31875
Qy 2759 ACCAGGCCAAG---AAGCTGGACAGCTGTAAATTTCTGTGTGACAMMCCGTACACCCACA 2815
Db 31874 ACAAAATTATGATCAATGTGGTGATCTGAGGTGATATAAAACACTGAGCTCTTTCCAGT 31815
Qy 2816 CCTATTCTATCTGCTGCTGCTCGGCAATCACCTGTAGCAGTAGGTATTATCCCTTCT 2875
Db 31814 CACAAACACTGCAAGGCGAGGTGTTTCTAAACAAGCCTTAAAGCTGATGTCGACATGCCCA 31755
Qy 2876 TGACCTATGAAATTTCTAGTTGTTCTCAGTAGGCCCGGGGGAATAATAGTAAACAACAGCC 2935
Db 31754 CAATTCCTTGTCACTCACAGCACATCCCGCTGCTCCATGCTAGACGAGCGAAGAG 31695
Qy 2936 ATGATTTAGTGTAAATTTTCTTGGTCTCGGCAGTGTCTCTTTTAATCCTCAAGAACACA 2995
Db 31694 CTGCAGGTGCGTATATGATGGAGGTGAGGAGACAGTGGCATGGAATGAATCAACTCAG 31635
Qy 2996 CTATGGGATAGGTAACAATATTCCTCACTTAA--CAGATAAGAAAACTGAGGCTCAGAAGG 3053
Db 31634 TTTGGGAGCAGGAGAACTTTATTGAGGTATGAATATATTCTACTTGAACCTGGAAGGA 31575
Qy 3054 CTGAGCTATTTGCCCAAGATCACAGCTGTGTAAGTGGTGACAGTTTGGGTTTTTTTTTG 3113
Db 31574 TAAAGTGGTATGAATTTTGGCTTATGGTAACTTTTGTAAAGCATCTTCTTTTCTTTT 31515
Qy 3114 TTGTTGTTTAGAGACAGAGGTCTTGTCT-TGTCAACCCAGGCATGAGCACAGTGGTGAACC 3172
Db 31514 TTTTGTGGTGAACACAGATTTCACTCTTGTCCCCAGGCTGAGTGAATGCGGTGATC 31455
Qy 3173 ATAGTCTAGCTGAGCCTCAACCTCTCTGAGCTCAAGGATCTGCTGACCTCAGCCTCCCAA 3232
Db 31454 TCGGCTCACTGCATCTCTGCTCCAGGTTCAAGCGATTTCTCGTACCTCAGCCTCCCA 31395
Qy 3233 GTAGCTGGGACTACGAGGCTGCACCACCGCTGGCTAAATTTAAAAAATTTTTTTGTAG 3292
Db 31394 GTAGCTGGGATTACAGGCATGTGCAGCATGCTTGGCTAAATTTTGTGA---TTTTTAGTAG 31338
Qy 3293 AGACTGGGTCTTACTACGTTGGCCAGGCTTGTCT-TAAACTCCTGGCTTCAAGCAATCTCT 3351
Db 31337 AGATGGGTTTACCGTGTGCCAAGGCTGATCTCAAACTCTCAACCTCAGTGTCTG 31278
Qy 3352 CTACTTTGGCATCCAAAGTCTGGGATTACAGGGGTGAGCCACATGTGCGGTACTTT 3411
Db 31277 CCGGCTCAGCCTCCAAAGTCTGGGATTACAGGCTTGAGCCACTGYCCCGGCTTTT 31218
Qy 3412 ATTTCTTTTACATTTCCATCTTTCCAATGAATGTAAAGTCCACAGACAGGATTACTGCC 3471
Db 31217 TTTTTTTTTTTTTTTTTTAAATTAITGAGACGGAGCTTGGCGCTG----- 31174
Qy 3472 TATTTTCTCTCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACCTCAACCTCCGTTCA 3531
Db 31173 -----TCAACGAGCTGGAGTGCACTGGCACTGTCTYGG 31140
Qy 3532 CTCATGCAACTCTGCTCCGGGTTCAAGYGATTTCTTCCCTCAAGCTCCTCCTGAGTAG 3591
Db 31139 CTCATGCAACTCTCCGCTCCGGGTTCAAGCGATTCTCTGCTCAGCCTCCCAAGTAG 31080
Qy 3592 CTGGAATTACAGCGTGCACCACTGCTTGGCTAAATTTTTTGTATTTTATAGCAGAGATG 3651
Db 31079 CTGGGATTACAGGCATGTGCCACCATGCCCAGCTAA-TTTTTGTATTTTATAGAGGTG 31021
Qy 3652 GGGTTTACCATTGTTGCCAGGCTGCTCAAACTCTCAAGCTCAAGTGAATCTGCTGCC 3711
Db 31020 AGGTTTCAAGATTTGGCAGGCTGCTTGAATCTCTGACCT--TGTCATCTCCACC 30963
Qy 3712 TCAGTCTCCCAAGTGTGGAAATTATAGCGGTGAGTCACTGTGCTGCGCCGATTAATGTC 3771
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Db 30962 TTGGCCTCCCAAAGTCTGGGTTTACAGGGYAGGCCACSAAGCGGCTGTTTATGCTCA 30903
Qy 3772 TATT-----TTCTTTTATGCTATATCCCGAGATCTAGAGCAG 3808
Db 30902 TCATGGCACTTAAGAGATGCTTAACAAACCTTTCTACAAATGTTCTCGAATTTTCAGAG 30843
Qy 3809 TGTCTGACATATAGTGGTCTCAATAAATAATTTGATGAATGCACAGCCTAGATATAAAG 3868
Db 30842 CTTATTGTATCTAGATCTGGTTCCTAAATCTTGATGATCATCAGAGCAAACTTGAAT 30783
Qy 3869 TTTCTTTTCTTTTAAACAAATCTTGAAACTTTTGACAGATAAATAACAATCTTGCAT 3928
Db 30782 GCTTTGGAAAGCYAGCCTCATACCACCTTCAGTTGGGAAGGGAGTACTGAGGTGTAC 30723
Qy 3929 TCTGCTTTTTCATCTATGCTTGTATGACTTTTTCATATTCGCTCAAACTTTATGTT 3988
Db 30722 CTTGGCAGGACAGTGAATGATGCT-GGTTCTTCTAGTTTGTCTATACCAAGAACTGC 30664
Qy 3989 TACTGTTTTTTCATTGTTACTATTTTGTAGTCACTGAAATAATATGGCTTAATTTGCTTATAC 4048
Db 30663 TATAACATGTTCTAAACACAGGCTATGAAAGCACTAGAGTTCTTGACCAAGCAATGCAG 30604
Qy 4049 ATCTCTCTGCTCCACTTTAGAGGCCAAATTTTAAATCTGATGAAGCTATGAACCTTC 4108
Db 30603 ACCAGTGGCATACAAATTTCAAATACTGTATMCAGGCCCTTGACTCCAGCCCAAACCAAG 30544
Qy 4109 TCCCCAGAGAAATACACACACACACACTCACACAGTTTTTTTTTTTAAATGTTTGA 4168
Db 30543 CTGGAGGGCATCCAGGGGGATGGTTTCCACACGGGGTAGCATCTTTGGTTATGTGAGATC 30484
Qy 4169 ACTAAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAAT----- 4213
Db 30483 ACCAAGACACCAACCTGTTTTATGAGTGAATCCTCAGCTTGTGCTGATTTGGCT 30424
Qy 4214 -TAAAAATAACTCAGTTGGGCACAGTGAACCTGTAAGCCCTGTAACACAGTACTTTGGAAGTC 4272
Db 30423 GATAAAAAATACAGGCAGGCCCGAGTGGCTCACRCCTGTAATCCCAACACTTTTGGGAGGC 30364
Qy 4273 CAAGTGGGTGGATCACTTGAAGTGAAGTTCGACACCAAGCCTGCTCAATATGTTGAA 4332
Db 30363 TGAGGCAGGACAGCACTCAGGCGCRGGAGTTTGAACACTAGCCTGCCAACATGGTGAA 30304
Qy 4333 CCTATCTCTAC-TAAAAATACAAAAAATAGCTGGGTGATGATGCATGCCCTGTAGTCC 4391
Db 30303 TCTGTATGTACTTAAAAATACAAAAATACCCAGGCATTTGAGTGCCTGTCTATCC 30244
Qy 4392 CAGCTACTCGGGAGGTGAGGCAGAGAAATGCTTGAACCTGGGAGGCAG-AGGTTGCA 4450
Db 30243 CAGCTACTCGAAAGGCTGAAAGCAGGAGAAATCGCTTGAATCTAGGAGGCTGCAGGTTGCA 30184
Qy 4451 TGAGCCGAGATCCACCACTGCACTCCAGCCTGGGCGACACAGCGAGACTTATCTCAA 4510
Db 30183 TGAGCTGAGAAAGCGCCCACTGCACTCAGCCYGGGAGAGCGGAATCTCACTCTGCTCAGTCA 30124
Qy 4511 AAAAAATAATAAAAAAAGGA 4534
Db 30123 CAACACACAAAAAATAGCA 30100
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RESULT 34

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US-10-995-561-13402
; Sequence 13402, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 13402
; LENGTH: 56054
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (56054)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13402
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Query Match 7.1%; Score 353.2; DB 10; Length 56054;
Best Local Similarity 52.0%; Pred. No. 3e+02;
Matches 1199; Conservative 20; Mismatches 968; Indels 117; Gaps 16;

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Qy 2280 AAATCGCTTTTCAGGCCAGCGCGGTGGCTCATGCTGTAATCCCGAGCACTTTGGGAGGCC 2339
Db 52209 AAAAAAGATGGCAGCGGCGCACAGTGGCTCATATACTTAGCACTTTTGGGAGGCC 52268
Qy 2340 GAGCGCGCGGATCACTTTGAGGTCAAGGATTCGACACAGCCTGGCCAAACATGGTGAAC 2399
Db 52269 AAGGCAGGTGGATCACTGAAAGTCAGGATTCMAGACAGCCTGGCCAAACATGGTGAAC 52328
Qy 2400 CCTGTCTCTACTAAAAAAATACAAAAATTAGCCGACATGGTGGCGAGCGCTGTAAACCC 2459
Db 52329 TCTATCTCTACTAAAAATATAAAACATTAGGCCAGGTGGTGGCAGGTGCTGTAAATCC 52388
Qy 2460 AGCTACTTTGGGAGACTGA-GTTGGAGGTTTCAGTCAGCAAGGTGCTGCTCACTGCTGTCC 2518
Db 52389 AGCTACTCGGGAGGCTGAGGCAGGAGAAATCCCTTGAACCCAGGAGCGGAGGCTGCAGTG 52448
Qy 2519 AGCCTGGGTAAACAGAGCAACTCTGTCTCAAAAAAATAAATGCTTTCAATAAATATATGA 2578
Db 52449 AGCCAAGATCA-----TGCCTACTGCACTCCAGCTGGGTGCACAGAGAGACTC 52497
Qy 2579 TAAAAAGACTTATATTTTTTCAAGCCATAGGATCAATTTCTCTGAAGCATCTTGGCGAAG 2638
Db 52498 CCATCTCAAAAWTTTTTTTTTAAATGCAGAGTTGGACTGCCTACCTATATCTCTAAATTT 52557
Qy 2639 TCATCCCCACCTGTTCTTGAGAGTGGGCGAGGTGAGGCTGACCTATTGCTCTGCACTTAC 2698
Db 52558 CTAATCTCGAGTGATTTCTCTGGAGAGKCTAGGTAAAGACTGAAAGGCAATGTTTACGTCC 52617
Qy 2699 TCCTATCTCAGCTGCCCTCCCACTTTCCAGGTGCTGCCACACATGACACATGCACTCTAYG 2758
Db 52618 ACCTGTCAAT-----CTCCTGGACAAGAAATCCAGGAGAACTATTGAACTCAGGTG 52669
Qy 2759 ACCAGGCCAAG---AAGCTGGACAGCTGTAAATTTCTGCTGGACAMMCGGTACACCCACA 2815
Db 52670 ACAAAGTTTATGATCAATCTGGTGTATCTGAGGTGATTTAAAAACACATGAGCTCTTTCC 52729
Qy 2816 CCTATTCTACTCTGCTCTGGCTCGGCAATCACCTGTAGCAGTAGGTTTATCCCTTCTCT 2875
Db 52730 CACAAACACTGCAAGGCAGGTGTTTCTAAACAAAGCCTTAAGCTGATGTGACATGCCCA 52789
Qy 2876 TGACCTATGAATTTCTAGTTGTTCTCAGTAGCGCCGGGGGAAATAATAGTAAACAACAGCC 2935
Db 52790 CNAATTCCTGTCTCACTCACCAGCACATCCCGCTGCTCATCTAGAGCAGGCAAGAG 52849
Qy 2936 ATGATTTTAGTGTAAATTTTGTGGTCTGGGCGAGTGTCTCTCTTAATCTCTAGAACACA 2995
Db 52850 CTGCAGGTGCGTATATGATGAGGTGAGGAGACAGTGGCATGGAATGAATCAACTCAG 52909
Qy 2996 CTATGGGATAGGTACAATATCTTCACTTAA--CAGATAAGAAACTGAGGCTCAGAGG 3053
Db 52910 TTTGGGAGCAGGGGAACTTTATTGAGGTATGAATATATTCTTCTTGAACCTGGAAGA 52969
Qy 3054 CTGAGCTATTTGCCCAAGATCACACAGCTTGTAAAGTGGTGACAGTTGGGTTTTTTTTT 3113
Db 52970 TAAAGTGGTATGAATTTGTGGCTTATGTTAACTTTGTTAAGCATCTTTCTTTCTTTT 53029
Qy 3114 TTGTTGTTTAGACAGAGGCTTGTGTC-TGTACCCAGGCATGAGACAGTGGTGAAC 3172
Db 53030 TTTTTTGGTGAGACACAGATTCACTTTGTGTCCTGAGTGGAGTGAATGGCGTGATC 53089
```


Db	38540	AGTGTATCCACCCGCTCTCGGCCTCCCAAGTGTGGGATTTACAGGCATCAGCACCGTGCC	38481
Qy	3403	CGGCTACTATTTCITTTACATTCATCTTTCCAAATAGATGTAAAGATCCACAGAACAGGG	3462
Db	38480	AGGCCA-----GCATTAAGCAATTTCTTAAAGCCCATGTAGTT	38444
Qy	3463	ATTACTGCCTATTTCITTCCTCTCTTTTGTAGACAGAGTCTCACTTCATCACCTCAACC	3522
Db	38443	ATTATTATTATTATTATTATTATTTTGTAGACGGAGTCTCACTCTGTCAACCGGCT	38384
Qy	3523	TCGGT-----TCAGTCACTGCACACCTCTGCCTCCCGGTTTCAAGYGATC	3568
Db	38383	GGAGTGGGTGGCGCGATCTCGGCTCACTGCACACCTCCGCTCCCGGCTCAGCGCATTC	38324
Qy	3569	TCTCTGCTTAAGCCTCTCGTAGTAGTGAATTAACAAGCTGCACACCATGCTTCGGCTAAT	3628
Db	38323	TCTCTGCTCAGCCTCCGAGTAGTTGGGACTACAGTCCCGCCACCAACACTGGCTAAT	38264
Qy	3629	TTTTTGTATTTTGTAGCAGAGATGGGGTTTTACCATGTTGCCCAGAGCTCGTCTCAAACTCC	3688
Db	38263	TTTTTGTATTTGTAGAGATGGGGTTTACCAATGTTAGCCAGAGATGGTCTTGAGCTCC	38204
Qy	3689	TGACCTCAAGTGATGCTCGCTCAAGTCTCCCAAAGTCTCGAAATATATAGCGCTGAGTC	3748
Db	38203	TGACCTC--GTGATCGCCTGCTCGGCCTCCCAAAGTCTGGGATTACAGCGGTAGGCC	38146
Qy	3749	ACTGTGCTGGCCGATTACTGTCTATTTCT-----TTATTGCTATATATCCCGAT	3799
Db	38145	ATCGCGCCCAAGCCTATTTATTTATTTTGTGGACAGAGTCTCATTTCTGTCAACAGG	38086
Qy	3800	CTAGAGCAGTGTCTGCATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGCCTA	3859
Db	38085	CTGGAGTACAGTGGTGTGATCACTGCTCACTGCAGCCTTGATCTTCCCGGGCTCAGGTGA	38026
Qy	3860	GATATAAACTTTCTTTTCTTTTAAAAACAATCTTG-----ACAACCTTTGCAGATA	3913
Db	38025	TCCTGCCACCTCTACCGCCCAAGTAGCTGGGAGTGTAGCGGCACACCACTACACCTAAT	37966
Qy	3914	AATACAATCTTGCAATTCCTGCTTTTTCACCTTATACCTTGTATGACTTTTTCATATTGCC	3973
Db	37965	TTTGTATGTTTTGTAGAGATGGGGTTTTTGCATGTTGCCCAGGCTGATCTCAAACTCC	37906
Qy	3974	TCAAACTTTATTGTTACTGTTTTTTTTCATTTGTTTACTATTATTTAGTCACTGAATAATATGGC	4033
Db	37905	TGGGTTCAAGTGATCCTCCGACCTTGGCCCTCCCAAAGTCTGGCATTCGAGGTGTAGGC	37846
Qy	4034	TTAATTTGCTTATACATCCTCTGCTCCACTT-----TAGAAGGCCAAATTTA	4081
Db	37845	ACCGCATGGGGTCCCATTTAGTTCTTAAATTTCTGTGTAGTAGGTATTATCCCTATTTTA	37786
Qy	4082	CAAACTGTATGA-----AAGCTATGAACCTCTCCCCAGAGAAATACACACACAC	4133
Db	37785	CACATGAGGACACTGAGACGCAAGTAAAGTAACTTGTCCATACGGGCTATTAAAGTACGTCA	37726
Qy	4134	ACACACTCACACACAGTTTTTTTTTAAATGTTTGTGCAACTAAGACAAGAACTGTGATAGA	4193
Db	37725	TGTGACTAGGTTTGTGTGACTCCAGAGCCTATGTTCCGCATTAATTTATCTGTTACATGT	37666
Qy	4194	GGATGTTTGTTCATATTAA--TTAAAAATAAATCAAGTTGGGCACAGTGACTCAAGCCTGTA	4252
Db	37665	TAATCTCAGAATGCATAAAGATAAATGGTCATGGGCTGGCGTGTGGCTCAGCGCTGTA	37606
Qy	4253	ACCACAGTACTTTGGGAAGTCCAAAGTGGGTGGATCACTTGAAGTGAGAAGTTTCGAGACCA	4312
Db	37605	ATCCAGCAATTTTGGGTGTCTGAGGCAGGCAGATCA--TGAGGTCAAGAGATTCGAGACCA	37548
Qy	4313	GCCTGGTCAATATGGTGAACCCCTATCTCTACTTAAATAACAAAAATTTAGCTGGGTGAG	4372
Db	37547	TCCTGGCCACATGGTGAACCCCGCTCTCTCTATAAATAACAAAAATTTAGCATG-----	37494
Qy	4373	TGATGCATTCCTGTAGTCCCAAGTACTCGGGAGGCTGAGGCACAGAAATTTGCTTGAACCT	4432

Db	37493	-----TGCCTGTAGTCCCGAGCTACTCGAGAAAGCTGAGGCAGCAGAAATCGCTTGAACCC	37444
QY	4433	GGGAGGCAGAGGTTGCAGTGCAGCGAGATCCCAACCACTGCACCTCCAGCGCTGGCGCACACA	4492
Db	37440	AGAGGTGAGGTTGCAGTGCAGCGAGATCGCACCACTGCACCTCCAGCT-GGTGACAGA	37382
QY	4493	CGGAGACTCTATCTCAAAAAATAAATAAATAAAGGATCGGAGAGAAACAAAACT	4552
Db	37381	GGGAGACTCTGCTCTCAAAAAAAGATGCTGGTGTACGATGGTGAGGACAAAGAATTCA	37322
QY	4553	AATAA 4557	
Db	37321	AATTA 37317	
RESULT 36			
US-11-112-908-37/c			
; Sequence 37, Application US/11112908			
; Publication No. US20050260659A1			
; GENERAL INFORMATION:			
; APPLICANT: Harris, Cole			
; APPLICANT: Davis, Lisa M.			
; TITLE OF INVENTION: Breast Cancer Biomarkers			
; FILE REFERENCE: 04-164-US			
; CURRENT APPLICATION NUMBER: US/11/112,908			
; CURRENT FILING DATE: 2005-04-22			
; PRIOR APPLICATION NUMBER: US 60/564,758			
; PRIOR FILING DATE: 2004-04-23			
; PRIOR APPLICATION NUMBER: US 60/575,978			
; PRIOR FILING DATE: 2004-06-01			
; PRIOR APPLICATION NUMBER: US 60/631,702			
; PRIOR FILING DATE: 2004-11-30			
; PRIOR APPLICATION NUMBER: US 60/633,826			
; PRIOR FILING DATE: 2004-12-07			
; NUMBER OF SEQ ID NOS: 511			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 37			
; LENGTH: 150481			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-112-908-37			
Query Match 7.0%; Score 352.2; DB 17; Length 150481;			
Best Local Similarity 53.4%; Pred. No. 1.5e+02;			
Matches 1217; Conservative 2; Mismatch 915; Indels 147; Gaps 17;			
QY	2278	AAAAATCGCTTTCAGGCCAGGCGGTGCTCATCGCTGTAATCCAGCACTTTG---GG	2334
Db	92808	AAATAAATCTTTTATAGCCAGGCATGATGGCTGACGCTTTGTAATCTCAGCACTTTAGGGAGG	92749
QY	2335	AGGCCAGGCGGCGGATCACATTGAGTTCAGAGATTCGAGACCACTGGCCAAACATGGT	2394
Db	92748	AGGCCAAGGCTGAGAGCTGCTTTGAGCCTTAGGCATTTCAAGACCACTTGGGCAACAAAGT	92689
QY	2395	GA-AACCCCTGCTCTACTAAAAATAACAAAAATTAGCCCGACATGGTGGCAGCGCCTGT	2453
Db	92688	GAGACCCCTGCTCTACAAAAAATTTAAAAAATTAGCCAGGCATGGTGGCATGCACCTAT	92629
QY	2454	AACCCAGCTACTTTGGGAGACTGAGTTGG-----AGTT 2487	
Db	92628	GGTCCCAGCTACTTTGGGAGGCTGAGCAGGAGGATTTGCTTGCAACCAGGAGCAAAAGTT	92569
QY	2488	TCAGTGAGCAAGGTCGTGTCCTACTGTCGCCAGCTGGGTAAACAGACAACTCTGCTCTCA	2547
Db	92568	GCAGTGAGCCATGATCGCACCACTGCACCTCCAGCCTGGCGAAGGTGAACCTCTCAAA	92509
QY	2548	AAAAAATAAATGCTTTTCAATAAATATATGATAAAAGGACTTATATTTTTTTCAAGCCATA	2607
Db	92508	AAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATGCTTTACTTCTATTGA	92449
QY	2608	GGATCATTTCTCCTGAAGCATCTTTGGCGAAGTCATCCCACTGTTCCTGAGAGTGGCA	2667
Db	92448	AAAGAAAAAATAATACATTAGGTGACCTGAAAAAATTTCTGGATTTCTTAGCTACTATTACGG	92389

; PRIOR FILING DATE: 2004-11-30									
; PRIOR APPLICATION NUMBER: US 60/633,826									
; NUMBER OF SEQ ID NOS: 511									
; SOFTWARE: PatentIn version 3.3									
; SEQ ID NO 59									
; LENGTH: 168656									
; TYPE: DNA									
; ORGANISM: Homo sapiens									
US-11-112-908-59									
Query Match 7.0%; Score 352.2; DB 17; Length 168656;									
Best Local Similarity 59.2%; Pred. No. 1.4e+02;									
Matches 871; Conservative 1; Mismatches 524; Indels 75; Gaps 13;									
Qy	3098	TTTGGGTTTTTTTTTTGTTTGTAGAGACAGGGTCTTGCTGTGCACCCAGGCATGAG	3157						
Db	132627	TTTTGTTTTTTTTTTTTTTTGGAGACGGAGTCTCACTCTGTGCGCCAGGCTGGAG	132568						
Qy	3158	CACAGTGGTGCACCATAGTCTACTCGAGCCTCAACCTCTAGCTCAAGGATCTGCTG	3217						
Db	132567	TGCAGTGGCACGATCTCGGCTCACTGCAAGCTCCACCTCCCGGGTTTCACGCCATCTCTCT	132508						
Qy	3218	ACCTCAGCCTCCCAAGTAGTGGGACTACGAGCGTGCACCCACACCGCCTGGCTAATAAA	3277						
Db	132507	GCCTCAGCCTCTCTAGTGTGGGACACACGACCCACACACGCCCGGCTAATTTTT	132448						
Qy	3278	AAAAATTTTTTTGTAGAGATGGGTCTTACTACTGTCGCCAGGCTGTCTTAAACTCCTGG	3337						
Db	132447	TGTA-TTTTTTAGTAGACAGGGTTTCACTGTCTTAGCCAGGATGGTCTCGATCTCTGA	132389						
Qy	3338	CTTCAGCAATCTCTACTCTTGCCATCCCAAGTCTGGATTACAGGGGTGAGCCACC	3397						
Db	132388	CCTCATG--ATCCACCACCTCGGCTCCCAAGTCTGGGATTACAGGCATGAGCCACC	132331						
Qy	3398	ATGTGGGGTACTTATTTCTTACATTCATCTTCCAAATAGAAATGAAGATCCACAGAA	3457						
Db	132330	GCGCCGGC-----CTTTGTGTGTTTTTTTTTAGATGGAGTCTCATCTGTGCACC	132280						
Qy	3458	CAGGGAATTAAGCTATTTTCTCTTTCTTTTGTGAGACAGAGTCTCACTCATCACT	3517						
Db	132279	CAGGCTTGAGTGAATGGTTCGACC-----	132255						
Qy	3518	CAACCTCCGTTACGCTCACTGCAACCTCTGCCCTCCGGGTTCAAGYATTCTCTGCCCTA	3577						
Db	132254	-----TCGGCTCACTTCAACCTTCACTCCCAAGTTCAAGGATCTCTCTGCCCTC	132205						
Qy	3578	AGCCTCCTGAGTAGCTGGAAATTACAAGCGTGCACACCATGCTTGGCTAATTTTTTGAT	3637						
Db	132204	AGCCTCCGAGTAGCTGGGACTACAGGCGATGCCACACACCTGGCTAA-TTTTTGCAAT	132146						
Qy	3638	TTTTAGCAGATGGGGTTTTACATGTTGCCAGGCTGTCTCAAACTCTCGACCTCAA	3697						
Db	132145	TTTTCTTAGACAGAGGGTTTTCAC--TGTTAGCCAGGCTGGTCTCGAACTCTCGACCTC--	132090						
Qy	3698	GTGATCTGCCTGCTCAGTCTCCCAAGTCTGGAATTATPAGCGTGAGTCACTGTCCT	3757						
Db	132089	GTGATCTGCCTGCTCAGCCTCCCAAGGGCTGGGATTACAGGCATGATCACCATGCCT	132030						
Qy	3758	GGCGGATTAAGTCTATTTCTTTATTTGCTATATCCCCAGATCTAGACAGTGTCTGACA	3817						
Db	132029	GGCTGAGTCTGCGTTCTTAATGCTCGCTGGTGACTTTTCCACCCTACCATATCCAATGT	131970						
Qy	3818	TATA-GTAGTGTCTCAATAAATATGATGAATGCACAGCTAGATATAAACTTTCTTTT	3876						
Db	131969	CACAGGGTCTTGCTCCGTCACCCAGGCTGGAATGCAATAGACAAATCATAGTGGTGTGA	131910						
Qy	3877	TCTTTTTTTAAACAATCTTTGACAACTTTTCAGAAATAAATACAAATC-----TTGCATTTCTG	3932						
Db	131909	ACTTGGNACTCCAGGTTCAAGCAATCTCGCCACAGCTTTCCAAATAGCTGTGACTACAG	131850						
Qy	3933	CTTTTTCATTTATCACCTTGTTATGACTTTTTTTCATATTTGCTCCAAACCTTTATTTGTTACT							

Query Match 7.0%; Score 352.2; DB 17; Length 170285;
Best Local Similarity 59.2%; Pred. No. 1.3e+02;
Matches 871; Conservative 1; Mismatches 524; Indels 75; Gaps 13;

Query Match				7.0%;	Score 351.6;	DB 10;	Length 27509;	
Best Local Similarity				53.5%;	Pred. No. 5.2e+02;			
Matches 1208;				Conservative	9;	Mismatches 878;	Indels 165;	Gaps 17;
Qy	2322	CGAGCACTTTGGAGGCCGAGGGGGCGGATCACTTTGAGGTTCAGAGTTTCAGACACGCC	2381					
Db	1	CCAGCACTTTGGAGGCCGAGGCGAGGTGGAACAC--GAGGTTCAGAGATTTCAGACCACTCC	58					
Qy	2382	TGSCCAACATGGTGAACCCCTGCTCTACTATAAAATAC-AAAAATTAGCGCGACATGGT	2440					
Db	59	TGGCTAACAGGTGAACCCCGCTCTCTACTATAAAATACAAAAAATTAGCGGGCGGGT	118					
Qy	2441	GGCCAGCGCTGTAAACCCAGCTACTTTGGGAGACT-----	2475					
Db	119	GGTGGGTGCTGTAGTCCCGACTACTCAGAGGCTGAAGCAGGAGATGGCAGGAACCGG	178					
Qy	2476	-GAGTTGGAGGTTTCAGTGAGCCAGGTGCTGTACTGCTGTCAGCGCTGGTAAACAGAG	2534					
Db	179	GGAGGCAGAGGTTGTAGTCAGCTGAGATCGCGCCATTGCACTCCAGCGCTGGCGACAGAG	238					
Qy	2535	C--AACTCTGCTCAAAAAAATAATGCTTTCAATAAATATATGATATAAAGACTTATA	2592					
Db	239	CGAAGATCCGCTTCGAAAAAATAAATAACACACACACAAAACTGTGTTAAT	298					
Qy	2593	TTTTTTTCAAGCCATAGGATCATTTCTCTGGAAGCATTTTGGCGAAGTCATCCCCACCTGT	2652					
Db	299	GCTTAACTACAAAAAATGATTAATCAGATAAATATATGCAATTTATTAGAGAACTGCATGTT	358					
Qy	2653	TCCTGAGAGTGGCAGGTGAGGGCTGACCTATTGCTCTGCACTTACTCTATCTCAGCTG	2712					
Db	359	GGTCAGTCCAGTCCCTGCGAGAGGAATTCAGCATGACCTCAITTCATCTGTGAAGACAG	418					
Qy	2713	TCCTTCCCACTTTCAGGTGCTGCCAGACACATGACAACTGCTAYGACCAGGCCAAGAG	2772					
Db	419	AGCAATCCCTTGTGTTTATTTTAAAGATGKATCTCACTCTGTGTGCCAGACTGGAGTG	478					
Qy	2773	CTGACAGCTGTAAATTTCTGCTGGACAMCCGTACACCCACCTATTCTATCATCTCGTC	2832					
Db	479	CAGTGGCATGATCTCAGCCCTCTGCCACCTCCACCTTCGGGGTTCAGAGATTCTCATGC	538					
Qy	2833	TCCTGGCTCGGCAATACCTGTAGCAGTAGGTTTATCCCTTCTTGACCTATGAAATTCAG	2892					
Db	539	CTCAGCCTCTGAGTAGCTGAGATTACAGGCTTGTGCCTCCRTGCCAGCTAAATTTTTT	598					
Qy	2893	TTGGTTCTCAGTAGGCGGGGGGAATATAGTAACACACAGCCATGATTTAGTCTTAAT	2952					
Db	599	ATTTTACTAGAGATGAGGTTTCACAGTTTGGGAGGCGG-----GTCTCAAAC	648					
Qy	2953	TTCTTGTTCTGGGAGTGTCTCTTTAATCTCTCAGAAACACACTATGGGATAGGTACAA	3012					
Db	649	TCCTGACCTCAAGTGATCCACCCACCTCGGCTCCCGAAGTCTGGGATGACAGGTGC--	706					
Qy	3013	TTATCTCACTTAACAGATAAGAAAACTGAGGCTCAGAGGCTGAGCTATTTCGCCAAGA	3072					
Db	707	-----CTGCTCAGCAACTGTTGTTTATAGACATACACATTTTATCTGCTCGTCCAGCA	757					
Qy	3073	TCACAGCTTGTAACTGGTGACAGTTTGGGTTTTTTTTTGTGTTTATAGACAGAGG	3132					
Db	758	TGGTCAGCCCTCCACTT-----TTTAAATTTTATTTTATTTATTTTATTTTATAGACAGAG	810					
Qy	3133	TCCTTGCTCTGTACACCGAGCATGAGCACAGTGGTGCACCATAGTGTCACTCGACCTCAA	3192					
Db	811	TCTCACTCTGTTGTCAGAGTTGGAGTCCAGTGGCGTGATTTCCGGCTCACTGCAACCTCTA	870					
Qy	3193	CCTCCTGAGCTCAAGGGATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACGAGCGT	3252					
Db	871	CTTCCAGGTTTCGASCAATTCCTGCGCTCAGCTTCCCGAGTAGCTGGGATTCAGAGGCC	930					
Qy	3253	GCACACACCGCTCGCTAAATTAATAAATTTTTTTGTAGAGATGGGTCTTACTACGTT	3312					
Db	931	CGCTTCCCAACACCTAGCTAAATTTTGTGA--TTTTTATAGTAGACAGAGGTTTTCCACATGTT	988					


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QY 3226 CTCCCAAGTAGCTGGGACTACGAGCGTGCACACACCGCTCGCTAATTAATAAATTTT 3285
D 177249 CTTCTAGTAGCTGGGATTACAGCGCCCGCCACCAAGCTCGCTAATTTTGTGTA--TTT 177306
QY 3286 TTTGTAGAGACTGGGTCTTACTACGTGTGGCCAGGCTTGTCTTAAACTCTGGCTCAAGC 3345
D 177307 TTAGTAGATACAGGGTTTCACCATATTTGCCAGTCTGTGTC-TCAACTCTGACCTCAAGT 177365
QY 3346 AATCCTCTACCTTGCATCCCAAGTGTGGGATTACAGGGGTGAGCCACCATGTGGG 3405
D 177366 GATCCACCCGCTTGGCCCTCCCAAGTGTGGGATTACAGGGGTGAGCCACCGCCTGG 177425
QY 3406 CTACTTATTTCTTACATTTCCATTTTCCAAATAGAAATGTAAGATCCACAGAAAGAGGATT 3465
D 177426 TCTATTTCTTTTCTTTT-----TTTGTGATGAGTCTTCTCCTCGCCAGGCTGG 177480
QY 3466 ACTGCCTATTTCTTCTCTTTCTTTTGTGAGACAGAGTCTCACTTCATCACTCAACCTCC 3525
D 177481 GGTGCAGAGGCACAATC----- 177497
QY 3526 GTTCAGCTCACTGCACACTCTGCCTCCGGGTTCAAGYATTCTCTGCTAAGCTCCT 3585
D 177498 --TCGGCTCACTGCACACTCCGCTCCAGGTTCAAGCGATTCTTCTGCTCAGCCTCCC 177555
QY 3586 GAGTAGCTGGAATTACAAGCGTGCACACCATGCTTGGCTAATTTTGTATTTTAGCA 3645
D 177556 AAGTAGCTGGGATTACAGTGTCCCGCCACACACCATCTGCTAATTTTGTATTTAGTA 177615
QY 3646 GAGATGGGTTTACCATGTTGCCAGGTGTCTCAAACTCTGACCTCAAGTGAATCTG 3705
D 177616 GAGACAGGATTTTCAACATGTTGCCAGGCTGATCTCAAACTCTGACCTCAGGTATTCG 177675
QY 3706 CTTGCTCAGTCTCCCAAGTGTGGAATATAGGCGTAGTCACTGTGCTGCGCGGATT 3765
D 177676 CCACCTCGCCCTCCCAAGTGTGGGATTACAGGTGTGAGCCACCGCCTGGCTGTAA 177735
QY 3766 ACTGTCTATTTCTTATTTGCTATATCCCGAGATCTAGACAGTGTCTGACATATAGTAG 3825
D 177736 TTGCTCTTAAAGAGAAACAGTCAAGTTGGATTGGGGCGACCTCAGGAGCTCATTTG 177795
QY 3826 GTGCTCA-----ATAAATAATGATGAATGACAGCTTAGATATAAATTTCTTTTTC 3878
D 177796 AACCTAATAATCTCTTAAAGTCTGTCTCGCGGGGCCAAGCACAGTGGCTCAAGC 177855
QY 3879 TTTTAAACATCTCTGACACTTTGCAGATATAATCAATCTTGCATTCTGCTTTT 3938
D 177856 TTGTAATCCAAATCTTTGAGAGGCCAAGCGAGGATCACTGGTGGCCAGGATTGA 177915
QY 3939 CACTTA-----TCACCTTGTATGACTTTTTCATATTGCTTCAAACTTTTATTGT 3988
D 177916 GACTAGCTGGGCAACACAGCAGACCCCATCTCTACAAAAAATAAATAATTTGT 177975
QY 3989 TACTGTTTTTCAATGTTACTATTTTGTACTGAATAATATGGCTTAATTTGCTTATAC 4048
D 177976 TAGCAGGTGTGGGGACATGCTGTGTCTGAGCTACTCGGAGCCCAATGTGGAGG 178035
QY 4049 ATCCTCTGCTCCACTTTTGAAGGCCAAATTTACAAATCTGATGAAGCTATGAACCTC 4108
D 178036 ATCC-CCTGAGCCAGGAGTTTGAGGCTGTGGTGGCCGTGATCACTCCCACTGCATC 178094
QY 4109 TCCCCAGAGAAATACACACACACACACTCACACAGTTTCTT-----TT 4157
D 178095 CAGCCTGGGCCACAGAGAGACTTCTATCTCCAGCCCAAGTGCCTTAGGTCAAGCTA 178154
QY 4158 TAATGTTTGAACATAAGACAGAAACCTGCATTAGAGGATGTTTGTTCATATAATTAATA 4217
D 178155 TAATCCAGCAGTTTGGCAGCAGAGTGGAGGATCACTTGAGCCTTACAAGTTCAAGAC 178214
QY 4218 AATAACTCAGTTGGGCACAGTACTCAAGCCTGTAAACAGTACTTTTGAAGTCCAAG 4277
D 178215 CAACCCGGGCTGGGCGGTGGCACACGCTGTGAATCCAGACACTTTTGGGAGGCGGAG 178274
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RESULT 45

US-11-121-086-24

; Sequence 24, Application US/11121086

; Publication No. US2005026459A1

; GENERAL INFORMATION:

; APPLICANT: POULSEN, TIM S.

; APPLICANT: NIELSEN, KIRSTEN V.

; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

; FILE REFERENCE: 09138-6000-00000

; CURRENT APPLICATION NUMBER: US/11/121,086

; CURRENT FILING DATE: 2005-05-04

; PRIOR APPLICATION NUMBER: 60/567,570

; PRIOR FILING DATE: 2004-05-04

; NUMBER OF SEQ ID NOS: 107

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 24

; LENGTH: 120096

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-121-086-24

Query Match

Best Local Similarity 7.0%; Score 350.2; DB 17; Length 120096;

Matches 849; Conservative 0; Mismatches 547; Indels 71; Gaps 10;

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QY 3091 GTGACAGTTGGTTTTTTTTTGTGTTGTTAGAGACA-GGGTCTTCTGTCTGTCAACCA 3149
D 34144 GTGATGGTCTGTTTCTTACTGTTTTTTTTCAGACAGGGGACTTTTCTGTGGCCCA 34203
QY 3150 GGCATGACACAGTGGTGCAACCATAGGTCACTGCAGGCTCAACCTCCTGAGCTCAAGG 3209
D 34204 GGTGGAGTGTAGTGGCAGCATCATAGTCTACTGCTGCTGATCTCTTAGGCTCAAGTG 34263
QY 3210 ATCTGCTGACCTCAGCCTCCCAAGTAGCTGGGACTACAGCGGTGCACCAACGCTGGC 3269
D 34264 ATCTCTCTGCTCAGCCTCCTGAGTAGTTAGGACTACAGAGACATGCCACTATGTCCAGC 34323
QY 3270 TAAATTAATAAATTTTTTTGTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAA 3329
D 34324 TAAATTTTAA---TTTTTTGTAAAAATGGGGTCTTGTCTATATTTGCCAGGGTGTCTGAA 34380
QY 3330 ACTCTGCTTCAAGCAATCTCTTACCTTGGCATCCCAAGTGTGGGATPACAGGGT 3389
D 34381 ACTCTGGGTTCAAGCAATCTCTGCTGCCCTCCCAAGGGCTGGGAATACAAATGT 34440
QY 3390 GAGCCACCATGTGGCGCTACTTATTTCTTATCATTTTCCATTTTCCAATAGAAATGAAGT 3449
D 34411 GAGCCACCAACCTTGGCCTGTTTTTTTGTGTTGTTGTTTGA----- 34486
QY 3450 CCACAGAACAGGATTACTGCTATTTTCTTCTTCTTTTGTAGACAGAGTCTCACTT 3509
D 34487 -----GACAGCGTTTCACTCTTGTGTTGCCAGGCTGGAGTGCAACGCGCACGCTC----- 34534
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QY 3510 CATCACTCAACCTCCGTTTCAGCTCACTGCAACCTCTGCTCCGGTTCAGAGATTCT 3569
Db 34535 -----TTGGCTCACTGCAACCTCCGTTTCAGCTCCGAGTTCAA--GATTCT 34574
QY 3570 CTTGCTTAAGCTCCTGAGTAGCTGGAATTTACAAGGGTGACACCATGCTTGGCTAAAT 3629
Db 34575 CTTGCTCAGCTTCCCAAGTAGCTGGATTACAGGTGCCCGCCACACGCCAAGCTAAT 34634
QY 3630 TTTTGTATTTTACAGAGATGGGTTTT-----ACCATGTTGCCAGGCTGGTCT 3680
Db 34635 TTTTGTATTTGTAGTAGATGGGTTTTCACCGTGTTCACCATGTTTCACAGGCTAGTCT 34694
QY 3681 CAACTCCTCAGCTCAAGTATCTGCTGCTCAGTCTCCAAAGTCTCGGAATTATAGG 3740
Db 34695 CAACTCCTCAGTATCTCACCCTGCTGGCTCCAAAGTCTCGGAATTACAGG 34754
QY 3741 CGTGAGTCACTGCTGCGCGGATTTACTGTCTATTTTCTTTATTTGCTATATCCAGATC 3800
Db 34755 CGTGAGTCACTGCTGCGCGCTGTTGTTGTTTAAATAAACACAGCTTTACTGAGATCTCA 34814
QY 3801 TAGAGAGTGTGTGACATATAGTAGGTGCTCAATAATAATTAATGATGAATGCACAGCTAG 3860
Db 34815 TTCACAAATAATTTACCCATTTTAAGTTTCACTTTGTAGCTACAACCATCACCA----- 34868
QY 3861 ATATAAATTTCTTTTCTTTTAAACAATCTTGACAACCTTTGCAGATAATAACAA 3920
Db 34869 AAACCAATTTTAGAACATTTTCACTACCCCAATAAGAAATCTGTACTCAAGGCCAGGCA 34928
QY 3921 TCTTGCACTCTGCTTTTCACTTATCACCTTGTATG-----ACTTTTCTATATGCTCAA 3977
Db 34929 TTTGGCTCAAGCTATAATCCAGCCTTTTGGAGGCCAAGAGGAAATCACTTGAG 34988
QY 3978 ACCTTATTTGTTACTGTTTCTTCACTGTTACTATTTTAGTCACTGAATTAATATGGCTTAA 4037
Db 34989 GCTGGGAGTTTGAGACAGCCTGAGCCACATAGTGAGACACCCCGTTTCTACAAAAAAT 35048
QY 4038 TTTGCTTATACATCTCTCTCCCTCTTCTAGAGGCCAAATTTACAAATCTGATGAAGC 4097
Db 35049 TTAATAATTTGAGGGAGTGGTGACACCTGTGGTCTAGCCACTCAGAAAGCTGAGGTG 35108
QY 4098 TATGAACCTCTCCCCAGAGAAATACACACACA--CACACACTCACACACAGTTTTTTTT 4156
Db 35109 GGAGGATCATCTGCTCCAGGAGTGTGGGCTACAGTGAATTTACTGAACCACTGCAC 35168
QY 4157 TTAATGTTGCAACTAAGACAAAGAACCTGCTGATAGAGGATGTTGTTCAATTAATTA 4216
Db 35169 TCCAGCCTTAGTGACAGAACAGACCTCATCTCTAAAGACAAATTTAAAAAGTCAAAAGT 35228
QY 4217 AAATAACTCAGTTGGGCACAGTGACTCAAGCCTGTAACCACTGTTTGGAGTCCAAG 4276
Db 35229 TAAATAATTTAGCCGGTGAGTGGCTTATGCCCTCTAATCTATCTATTTTGGCAAGCAAG 35288
QY 4277 GTGGGTGGATCACTTTGAGGTGAGAGTTTCAGACCAAGCCTGCTCAATATGGTGAACCC- 4335
Db 35289 GCAGCGGATCACCTGAGCTCAGAGTTTCAGACCAAGCCTGGCCAAACAGGCCAACCCCA 35348
QY 4336 -TATCTCTACTAAATAACAAAAATTTAGCTGGGTGTAGTATGATGCTGCTGAGTCCAG 4394
Db 35349 TCTCTACTGAAATAAATACTAAATAATTTGCTGGATGTTGGTGGCCGACACCTGTAAATCCAG 35408
QY 4395 CTACTCGGAGGCTGAGGCAAGAGATTGCTTGAACCTGGAGGCGAGAGTTTGCAGTGAG 4454
Db 35409 CTACTTCGAGGCTGAGGCACTGGAATTTGCTTGAACCTGGAGGCGAGAGTTTGCAGTTAG 35468
QY 4455 CCGAGATCCCACTGCTCCTCCAGCTGGGCGACACAGCAGAGCTCTATCTCAAAAAAA 4514
Db 35469 CTGAGATCGTCCACTGGAATCTCAGACTAGGCGACAGAGTGAGACCTTCTCAAAAGAA 35528
QY 4515 TAAATAAATAAATAAAGGATCGAGA 4541
Db 35529 AGAAAAAATAAATAAAGAACCTCTGA 35555

RESULT 46
US-10-330-773-698/c
; Sequence 698, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FaetSEQ for Windows Version 4.0
; SEQ ID NO 698
; LENGTH: 178024
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(178024)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-698

Query Match 7.0%; Score 348.4; DB 11; Length 178024;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 862; Conservative 1; Mismatches 452; Indels 163; Gaps 8;

QY 3104 TTTTGTGTTGTTGTTTGTAGAGACAGGCTCTGTCTGTACCCAGGATGAGCACAGT 3163
Db 129644 TTTTGTGTTGTTGTTTGTAGAGACAGTCTCAATCTGTACCCAGGCTGGAGTGCA 129585
QY 3164 GGTGCAACATAGGTCACTGAGCCTCAACCTCTGAGTCAAGGATCTGCTGACCTCA 3223
Db 129584 GCGTGATCTCAGCTCAACGCAACCTCCGCTCCAGGTTTAAAGGATTTCTCTGCTCA 129525
QY 3224 GCCTCCCAAGTAGCTGGGACTACAGCGGTGACACCAACGCTGCTGCTAAATAAAAAAT 3283
Db 129524 GCCTCCGAGTAGCTGGGATTTACAGGCATGTGCCATCATGCTAGCTAATTTTGTGTA--T 129467
QY 3284 TTTTGTGAGACTGGGCTTTACTAGTTGGCCAGGCTTGTCTTAAACTCTCTGGCTTCAA 3343
Db 129466 TTTTGTGAGACTGGGCTTTGCGCATGTTGGCCAGGCTGCTCAAAATTTCTTGACCTCAG 129407
QY 3344 GCAATCCTCCTACCTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGC 3403
Db 129406 GTGATCCGCTGCTCCGCTTCCCAAGTGTGGCATTTACAGGCTTGAGTACACAGCT 129347
QY 3404 GGCTACTTATTTCTTTTACATTTCCATCTTTC--CAATAGAAATGTAAGATCCACAGAACAGG 3461
Db 129346 GGCCAGCTTTTTCATTTCTCTCAAAAGCCATCATTTGAGCTTTTTCATCCGAGCTTTTAG 129287
QY 3462 GATTAAGCTTAATTTTCTCTTTCT-----TTTTTGAGACAGAGTCTCATTTCTAT 3512
Db 129286 AATTTAGAACTATTTCTTTCTGATTTTTTTGTTGTTTTTGAGACAGAGTCTCGCTCTGT 129227
QY 3513 CACCTCAACCTCCGTTCA-----GCTCACTGCAACCTCTGCTCCCGGTT 3558
Db 129226 CACTCAGACTGGAGTGCAGTGTGCTGGCTCACTGCAATCCCTGCTCTCTGAGTT 129167
QY 3559 CAAAGTATTTCTCTGCTTAAGCTCTCTGAGTAGCTGGAAATTAACAAGCGTGCACCACTAG 3618
Db 129166 CCAGCAATTTCTGCTGCTCAGCTCCCGAGTAGCTGGGACTACAGGGGCATACCAACCA 129107
QY 3619 CTTGGCTAATTTTGTATTTTACAGAGATGGGTTTTTACCATTGTTGCCCAGGCTGT 3678
Db 129106 CCCAGCTAA--TTTTTGTATTTTAGTAGAGATGTGGTTTTTACCATTGTTGCCCAGGCTGT 129048
QY 3679 CTCAAACTCCTGACCTCAAGTATCTGCTGCTCAGTCTCCCAAGTCTCCGAATTTATA 3738
Db 129047 CTTGAACCTCTGGCATCAAGTATCCACCGCTCGGCTCCCAAGTCTCCGGGATTACA 128988
QY 3739 GCGTGAGTCACTGCTGCTGGCGGATTAATGTTATTTTCTTTT--ATTGCTATATCCCA 3796

Db	128987	AATGTGAGCAGCTGTGCCAGCCAGCAGCATAACTTTTATGTGTAATATTTGTGCTTCA	128928
Qy	3797	GATCTAGAGCAGTGTCTGACATATAGTGTGCTCAATAAATAATGATGAATGCACAGC	3856
Db	128927	AATTAACAGTAAAGCCTATGCTGGTGTCTAGTTATATTTTTTTTGAGAAATAGTGTCTC	128868
Qy	3857	CTAGATATAAACTTTCTTTTCTTTTAAACAACTTTGCAAACTTTGCGAGAATAAAT	3916
Db	128867	TAGGAATTCAAATGGAGAACACTGCCTAAA-----GCAGTATTTCTCAACCAGAG	128818
Qy	3917	ACAACTTGTGATTTCTGCTTTTTCACATATACCTTGTGTATGACTTTTTCATATTTGCTCA	3976
Db	128817	AAGCTTTTGGCCTCCAGAGGACATGTGACAATGTGTGGAGACATTTTTTGTGATTTGCACAA	128758
Qy	3977	AACCTTTATTTGTTACTGTTTTTTTCAATGTTTACTATTTTGTAGTCACTCAATAATATGCTTA	4036
Db	128757	CTCGGGAGTGCTACTGGCCTCTGCTGGGTAGGCCAGATGCTGCTAAACA-----	128705
Qy	4037	ATTGTCTTATACATCTCTCTGCTCCACTTTTGAAGGCCAAATTTTACAAATCTGATGAAAG	4096
Db	128704	-----	128705
Qy	4097	CTATGAACCTCTCTCCAGAGAAATACACACACACACACTCACACAGTTTTTTTT	4156
Db	128704	-----TTCT	128701
Qy	4157	TTAATCTTTGCTAACTAAGACAGAACCTGCATTAGAGGATGTTTGTTCATATTAATAA	4216
Db	128700	GAAATGCCCCCAACAAGAAAATGATCTGGCCTGAGATATGTCAAAAGTGTGAAGGAA	128641
Qy	4217	AAATAACTCAGTTGGGCACAGTCAAGCCTGTAAACCACAGTACTTTTGGAGTCCAAG	4276
Db	128640	CCCTGTTTGGCCGGGTGAGTGGTTTCAACCTGTAATCTTAACACTTTTGGGAGGCTGAG	128581
Qy	4277	GTGGGTGGATCACTTGAGTGAAGATTTCAGACCAGCCTGCTCAATATGTTGAACCTT	4336
Db	128580	CGCGGCGGATTACCTGAGTTCAGAGTTCGAGACCAGCCTGGCCCAATATGTTGAACCC	128521
Qy	4337	ATCTCTACTAAATAACAAAATTAGCTGGTGTAGTGTGATGATGCTGCTAGTCCAGCT	4396
Db	128520	GTCTCTGCTAAATAACAGAAATTAGCTGGCGTGTGTGGCGGCTGTAGTCCAGCT	128461
Qy	4397	ACTCGGGAGGCTGAGGCAAGAGAAATTTGTAACCTGGGAGGCGAGAGTTGCGAGTGAGCC	4456
Db	128460	ACTCAGAGGCTGAGGCGAGAGATCGCTTGAACCCGGGAGGTGGAGTTGCGAGTGACCC	128401
Qy	4457	GAGATCCCACCTGCACTCCAGCCTGGGCGACACAGGAGACTTATCTCAAAAAATA	4516
Db	128400	AAGATCACGCCACTGCACTGCAGCCTGGGCAACAGAGCGAGATTCCATCTCAAAAAAGAA	128341
Qy	4517	ATAAATAAATAAAGGATCGGAGAGAAACAAACTAA	4554
Db	128340	AAAAAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAA	128303
RESULT 47			
US-11-121-086-57/c			
; Sequence 57, Application US/11121086			
; Publication No. US20050266459A1			
; GENERAL INFORMATION:			
; APPLICANT: POULSEN, TIM S.			
; APPLICANT: NIELSEN, KIRSTEN V.			
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES			
; FILE REFERENCE: 09138.6000-00000			
; CURRENT APPLICATION NUMBER: US/11/121,086			
; PRIOR FILING DATE: 2005-05-04			
; PRIOR APPLICATION NUMBER: 60/567,570			
; PRIOR FILING DATE: 2004-05-04			
; NUMBER OF SEQ ID NOS: 107			
; SOFTWARE: PatentIn version 3.3			
; SEQ ID NO 57			
; LENGTH: 155989			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-121-086-57			
Query Match			
Best Local Similarity 54.0%; Pred. No. 1.6e+02;			
Matches 1241; Conservative 4; Mismatches 871; Indels 183; Gaps 19;			
Qy	2276	TTAAAAATCGCTTTTCAGGCCAGGCGCGTCTATGCTCTGTAATCCCGACACTTTGGGA	2335
Db	59130	TTGCAATTCACATCGAGCCAGCGTGTGCTCAGCTGTATCCCGACACTTTGGGA	59071
Qy	2336	GGCCAGCGGCGGATCACTTGTAGGTGAGAGTTCAGACAGCCTGCCCAACATGGTG	2395
Db	59070	GGCTGAGGCGAGCAGTCACTTGAATCAGGAATCAAGACCAGCCTGCCCAACATGGTG	59011
Qy	2396	AAACCTCTCTCTACTAAATAATACAAAATTTAGCCGACATGTTGCGAGCGCCTGTAA	2455
Db	59010	AAACCCCTCTCTAGT-AAAAATACAAAATAGCCGACATGTTGCGACATGCTCTATAA	58952
Qy	2456	CCCCAGCTACTTGGGAGACT-----GAGTTGGAGGTTTTCAGT	2492
Db	58951	TCCCAGGTACTCAGAGAGGCTGAGCGAGAAATTCCTTGAACCTGGGAGGTGGAGTTGCAGT	58892
Qy	2493	GAGCCAGGTCTGTCTCTGCTCCAGCCTGGGTA-ACAGAGCAACTCTGTCTCAAAA	2551
Db	58891	AAGCCAGATCGTGCCACTGCACCTCCAGCCTGGGAGCAGAGTGAGACTCCATCTCAAAA	58832
Qy	2552	AAAAAATGCTTTCATTAATATATGATAAAGGACTTA-----TATTTTTT	2598
Db	58831	AACAACAAAAAACAATGCACATGCAAGTAGGTAAACAGAGAAATTCAAAACTCTTTTA	58772
Qy	2599	CAAGCCATAGGATCATTTCTCTGAAGCATCTTGGCGAAGTCATCCCACTGTTCTCTGA	2658
Db	58771	ACAGACTTAGAACCAAAATACCAATTTATTAATTTGCGAGAGTAATGACATGGAATACCAT	58712
Qy	2659	GAGTGGCGAGTGAGGGCTGACCTATGCTCTGCACTTACTCTATCTCAGCTGCTCCTC	2718
Db	58711	TAAATTTTC---GTTAGTAAGGGTTATTTTATGAAAAGCTAATGTTTTTGCACGTTATA	58656
Qy	2719	CACTTTTCCAGGTGCTGCCAGACATGACACTCTATGACCACTTATTCATCTCGTCTCGG	2777
Db	58655	ATTTTGCACACAATGCTAAAAAATATTTTGAATATGACTTATTAACCACTTTAGTTAAGT	58596
Qy	2778	CAGCTGTAAATTTCTGCTGGACAMCCGTACACCCACACCTTATTCATCTCGTCTCGG	2837
Db	58595	TTTCCATGATTTTCACTTTGATACATTTCCCATGGGTCTTCATCACATTTCTCTTAG	58536
Qy	2838	CTCGCAATCACTGTAGCAGTGGTTTATCCCTTCTTGCCTATGAAATTTCTAGTTGGT	2897
Db	58535	CAGTCTATCCCATAGGAATATAATGCAAGCCATATTAATTTTAAATTTTCTTTCTTT	58476
Qy	2898	TCTCAGTAGGCGGGGAAATAATAGTAAACAGCCATGATTTAGTTGTTAATTTCTTT	2957
Db	58475	CTTTTTTTTTTTTGTAGATGGAGTCTCCCTCTGTGCGCCCAAGCTGGCATGCGAGTGCAC	58416
Qy	2958	GGTCTCTGGG-CAGTCTCTCTTTTAAATCTCAGAACACACATATGGGATAGGTACAATAT	3016
Db	58415	GATCTTGGCTACTGCAACCTCCGCTCTGCGGTCAAACTTTAAATTTCTAGTAGCCA	58356
Qy	3017	CCTCATTTAACAGATAAGAAAACTGAGGCTCAGAGGCTGAGCTATTTGCCCAAGATCAC	3076
Db	58355	TATTAATAAGTTTTCTTTAAAGGTTAATTAATTTGATATTTTATTTTAAACCAATAGAT	58296
Qy	3077	ACAGCTTGTAGTGTGACAGTTTGGGTTT---TTTTTGTGTTGTTAGACAGGGT	3133
Db	58295	ACATAATATGATTTCAACACGTAATCACTTAGAAAAAATAATGTTTTTGTAGATAAAAT	58236
Qy	3134	CTTGTCTCTGTCACCCAGGATGAGCAGTGTGTCACCACTAGGTGCTGACGCTCAAC	3193
Db	58235	CTCAGTTTGTGCTCCAGGTTGGCGTACAGTGGTACAAATACAGCTCACTGCACTCTCAA	58176
Qy	3194	CTCCTGAGCTCAAGGGATCTGCTGACCTCCAGCTCCCAAGTAGCTGGGACTACGAGCGTG	3253

Qy	3584	CTGAGTAGCTGGAAATTAAAGCGTGCACCAACCATGCTTGGCTAAATTTTTTGTATTTTTTAG	3643
Db	1018	CAAAGTAGCTGGGATTACAGGCATGCAACCAACCATATCGAGCTAA- TTTTGTGTATTTTTTAG	960
Qy	3644	CAGAGATGGGGTTTTACCATGTTGCCAGCGTGTCTCAAACTCCTGACCTCAAGTGATC	3703
Db	959	TAGAGATGGGGTTTTACCATGTTGGCAGGCTGTCTCAAACCTCCTCACCTCAAGTAAATC	900
Qy	3704	TGCCTGCCTCAGTCTCCCAAAGTGTCTGGAATTA- TAGGCGGTGAGTCACTGTGCTCGGCC-	3761
Db	899	CGCCGCGCTGGCGCTCCCAAAGTGTCTGGGATTACAAGCGGTGACCCACCGGGCTGGCCC	840
Qy	3762	-----GATTACTGTCTATTTCTTTATTGCTATATCCCGAGATCTAGAGCAGTGTCT	3813
Db	839	TGTGTGTTGTTTATGTATGTTCTTATGTGTTATATTTACAAATAAACTAAATATATA	780
Qy	3814	GACATATAGTAGGTGCTCAATAAATAATTTGATGAATGCACAGCGCTAGATATAAATTTCT	3873
Db	779	AACAAAGATAACTGATAGCTATGCACAAAGGTATTTAAATTTCAACCTCACAAATAATT	720
Qy	3874	TTTTTCTTTTTTAAACAACTCTGACAACTTTGCAGAAATAAATACAATCTTGCAATCTGC	3933
Db	719	TTTTTTTTTTGAGACAGATCTACTCTGTTTACCAGGCTGGAGTGCAGTGGCACCACT	660
Qy	3934	TTTTTCACTTATCAC---CTTGTTATGACTTTTTTCATATTGCTCAAACTTTATTGTT	3989
Db	659	TGGTTCACCTGCAGCTTGACCTCCAGGCCCAAGCGATCTTCTACCTCAGCCTCCTGAG	600
Qy	3990	ACTGTTTTTTTCATTGTTACTATTTTTAGTCAAGTAATAATGCGTTAAATTTGCTTATACA	4049
Db	599	TAGCTGGGACTACAGGCACACTCCACACACCCCACTAAATTTTTTGTATTTTTTGGTAAAGA	540
Qy	4050	TCCTCTGCTCCACTTTAGAGAGGCCAAATTTTACAAATCTGATGAAGCTATGAACCTCT	4109
Db	539	TGGGGTTTACCATTGTTGGCCAGGCTGGTCTCGAA--CTTCTGGGATCAAGGAATCTCTCC	482
Qy	4110	CCCAGAGAAATACACA-----	4133
Db	481	AACCTTGGCTTTCCAAAGTGTGTTATTACAGGCGTGAGCCACTGTACCCGGCCAGAAT	422
Qy	4134	ACACACTCACACACAGTTTTTTTTTAATGTTGCAACTAGACAAAGAACTGCATTAGA	4193
Db	421	AGTTTCTTCTCCTTAGCTAGAGACCTCTGCAGAAATGCTGGGAGATCTTTTGGAGAG	362
Qy	4194	GGATGTTTGTTCATATTAATTTAAAAATAAATCACTTGGGCACAGTGACTCAAGCTGTAA	4253
Db	361	GGGAGATTTTTTTAAATAAAAAATTTAATACTTGGAGGGCGTGGTGGCTTACCCCTGTAA	302
Qy	4254	CCACAGTACTTTGGAAGTCCAAAGTGGGTGGATCATTTGAGGTGAGAAGTTTCGAGACCAG	4313
Db	301	TCCCAGACATTTTGGAGGCCAAGCGCAGACAGATCA--GGAAGTCAGAGATTTGAGACCAC	244
Qy	4314	CCTGGTCAATATGTTGAAACCCCTATCTCTACTAAAAATAC-----AAAAATTAGCTGGGTG	4369
Db	243	CCTGGCTAACACGCTGAAACCCCATCTCTACTAAAAAAATAACAAAAATTAGCTGGCA	184
Qy	4370	TAGTGATGCATGCTGTAGTCCCAAGCTACTCTGGGAGGCTAGGCAAGAGAAATTCCTTGAA	4429
Db	183	TCGTGGCGGGCGCTGTAGTCCCAAGTACTCTGGGAGGCTGAGTCAGGAGACTTGGCGTGA	124
Qy	4430	CCTGGGAGGCAGAGGTTGCAGTAGGCGAGATCCACACTGCACTCCAGCTGGGCGAC	4489
Db	123	CCTGGGAGGCGAGCTTGCAGTGAGCGCAGCATCGGGCCACTGCACTCAGCCTGGGCGAC	64
Qy	4490	ACAGCAGACTCTTATCTCAAAAAAATAAATAATA	4524
Db	63	ACAGCAGACTTCGTCTCAAAAAAATAAATAAATAA	29

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; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13231
; LENGTH: 52192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13231

```

[illegible]

QY 3021 ACTTAACAGATAAGAAACCTGAGGCTCAGAAGGCTGAGCTATTGTGCCAAGATCACACAG 3080
Db CTTTGAGAACCAACCCATTGGCCTTCCAGTCCCTCCCTAGACTTTATGTCTGGTGC 14716
QY 3081 CTTGTAAGTGGTGACAGTTGGGTTTTTTTTTGTGTTGTTTA--GAGACAGGGTCTTGC 3138
Db CTTCTGCCCTTCCCTATTCTTCTTTTGTGTTGGTGGGAGGAGGGGGGACAGAGTCTCGT 14776
QY 3139 TCTGTCAACCCAGGCATGACACAGTGGTGCAACCATAGTCTCACTGCGAGCTCAACTCTCT 3198
Db TCTGTCCGCCAGGCTGGAGTGAGTGGCGTGATCTCAGCTCACTGAGCATCTGGCTCCC 14836
QY 3199 GAGCTCAAGGGGATCTGCTGACCTCAGCCTCCCAAGTAGTGGGACTACAGAGGCTGACCA 3258
Db AGGTTCAAGTGATGCTCTCCCTCAGCCTCCCAATTTAGCGAGGACTACAGGCGGTGCCA 14896
QY 3259 CACGCGCTGGCTAAATTAATAAATAATTTTTTTGTAGAGACTGGGTCTTACTAGTGTGGCCAG 3318
Db CCACGCCAGCTTATTTTGTGA--TTTTTTCTAGAGACAGGGTTTCATCATGTGGCCAG 14954
QY 3319 GCTTGTCTTAAGTCTCGGCTCAAGCAATCCTCCTACCTTGGCATCCCAAGTGTGGG 3378
Db GCTGGTCTCGAAGCTCCCAACTTCAAGTGATCTGCGTGACTCGGCTCTCAAGTGTGGG 15014
QY 3379 ATTACAGGGGTGAGCCACCATGTGCGGTACTT-----ATTCTTTACATTCATCTTTC 3433
Db ATTACAGGCGTGAGCCACCTTGCCCGGCCCTTGCCCGGCCCTTCCTATTCTTTTAT 15074
QY 3434 CAATAGAATGTAAGATCCACAGAACAGGGAATTAAGCCCTATTCTCTCTTTCTTTTGG 3493
Db CCTCAAAAACCTCCCTGCCAAGCGGCTGAGCAGGACCATCTCTCTTTTTTTTTTTTTT 15134
QY 3494 AGACAGAGTCTCATCTCATCACTCAACT-----CCGTTCAAGTCACTG 3538
Db AGACAAAGTCTTGCTCTTGTCACCCAGGCTGAGTGAGTGAGTGCGGAGATCTCAGCTCACTG 15194
QY 3539 CAACCTCTGCCTCCCGGTTCAAGYATTTCTCTGCTTAAGCTCTCCTGAGTAGCTGGAAT 3598
Db TAACTCCACCTCCAGGTTTCAAGTATCTCTGCTCAGCTCTGAGTAGCTGGAT 15254
QY 3599 TACAAGGTGACACCACTGCTTGGCTAATTTTTTGTATTTTTTAGCAGAGTGGGTTTT 3658
Db TACAGGCACATGCAACACCGCTGGCTAA--TTTTTGTATTTTTTAGTAGACAGGGTTTC 15313
QY 3659 ACCATGTTCCAGGCTGCTCAAACTCCTGACCTCAAGTGATCTGCTGCTCAGTCT 3718
Db ACCATGTTTGGCAGGCTGGTCTCAAACTCCTGACCTCAGATGATCGCCTGCTCAGCTT 15373
QY 3719 CCCAAAGTGTGGAATTTATAGGCGTGAGTCACTGTGCTGGCGGATTAAGTCTATT 3775
Db CCCAAAGTGTAGGATTTACAGGCGTGAGCCACACCCCGCCCATCATCCCTTTT 15430

RESULT 53
US-10-276-233A-6/c
; Sequence 6, Application US/10276233A
; Publication No. US20050260572A1
; GENERAL INFORMATION:
; APPLICANT: DNA Chip Research Inc.
; APPLICANT: Hitachi Software Engineering Co., Ltd.
; TITLE OF INVENTION: A method of predicting cancer condition
; FILE REFERENCE: PH-1533-PCT
; CURRENT APPLICATION NUMBER: US/10/276,233A
; CURRENT FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: JP 2001-73063
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: JP 2001-108503
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: JP 2001-234807
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6

; LENGTH: 79528
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-276-233A-6
Query Match 6.9%; Score 344.4; DB 10; Length 79528;
Best Local Similarity 65.3%; Pred. No. 2.8e+02;
Matches 546; Conservative 0; Mismatches 271; Indels 19; Gaps 2;
QY 301 TTTATTTCTTTTTCAGACAGGGTCTGTCTATATACCCAGGCTGGAGTTCAGTGCA 360
Db 48966 TTTTCTTTTTCCTGAGACAGTCTCACTTTGTCGCCAGGCTGGAATCGATGGCG 48907
QY 361 TGATCATAGCTCACACAGCTTCCAACTCGTGGGCTCAAGTGATCCTCCACCTTACTCA 420
Db 48906 TGAATCATCTCACTGTAGCTCCGCCCTCCGGCTTCAACCAATTCCTCTACTCGGCT 48847
QY 421 ACTAAGTAGTGTAG-----GCCAATCTCCATTTATTTTATTTTAA 465
Db 48846 CCTAAGTAGTGGTGTACAGTGACACACACACAGCTAGATGGCTGGGTTTTT 48787
QY 466 TTTTATTTTATTTTACTTTATTTTATTTTGTAGACGGGCTCACTGTGCCCGAGC 525
Db 48786 TTGTTGGTTTTTGTGTTTTTCTGAGACAGGCTCTCACTCTGTCAACCGAGC 48727
QY 526 TGGAGTGGGCTGGCGTGATCTCAGATCACTCAACCTCCATCTCCTGGGTTCAAAATAAT 585
Db 48726 TGGAGTGAGTGGCGGATTTGGCTTACTGCNACTCCATGTCTCTGGGTTCAAGTAT 48667
QY 586 CTCTTGGCTCAGCTCTCTCAAGTAGTGGGACTTTAGTCTCAAGTAGTGCGCACACACC 645
Db 48666 CTCCTACCTCAGCTCCAGAGTAGTGGGATTTACAGGCAATGTGCACACACACCGGTAAT 48607
QY 646 ACCATGCCAGTAATTTTTTGTGTTTT-----TTTTGTAGACACAGGTTTTTCA 701
Db 48606 TTTTGTGATTTTGTAGTAGAGTGGGTTTTACCATGTGTGTCAGGCTGGTTTTGA 48547
QY 702 GTTGCCAGGCTGGGTGACCTCCCTTTTATAGTTCTCTCATCTGCTCTATTCTTCCC 761
Db 48546 CTGGCTCAAGTGATCCAGCTGCTCGGCTCCCAAGTGTGGGATTTACAGACGTGAG 48487
QY 762 TTCTAATCAGTATCCAGTTTCTCTTACTTATCAATTTATTTATTTATTTATTTG 821
Db 48486 CATCATGCCAGCAATGGCTGTGTTTTTTTGTGTGTTTTGTTGTTTTGTTTTG 48427
QY 822 AGACAGAGTCTGCTTTGTCGCCAAGGCTGGAGTACAGTGGTGGCATCTCGGCTCACTGC 881
Db 48426 AGACGAGTCTCACTCTGTCAACCCAGGCTGGAGTGGAGTGGCGCATCTCTCTCACTGC 48367
QY 882 AAGCTCCACCTGCTGGGTTACGCCATTTCTCCGCTCAGCCTCCCGAGTAGCTGGGACT 941
Db 48366 AAGCTCCACCTCCAGGTTACGCCATTTACCCGCTCAGCCTCCCGAGTAGCTGGGACT 48307
QY 942 AAAGCGCTGCCACACCGCCCGCTAATTTTTTTTGTATTTTTTAATAAGACGGGTTTC 1001
Db 48306 ACAGGACCTGCCACACCGCCCGCTAATTTTTTGTATTTTTTAGTAGAGATGGGTTTC 48247
QY 1002 ATCGTGTAGCAGAGTGGTCTCGATCTCATGACCTTGTGATCCGCTCGCTCGGCTCC 1061
Db 48246 ACCATGTTAGCAGAGTGGTCTCGATCTCCTGACCTTGTGATCTCGCTCGCTCGGCTCC 48187
QY 1062 CAAAGTGTGGGATTTACAGGATAGCCACCGTCCCGGCTTTATCACAATTTATTA 1117
Db 48186 CAGAGTGTGGGATTTATAGGCATAGACCCAGCCAGCCATGGCTGTTTTTA 48131

RESULT 54
US-10-330-773-278
; Sequence 278, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro

; TITLE OF INVENTION: Novel Compositions and Methods in Cancer

; FILE REFERENCE: 529452001300

; CURRENT APPLICATION NUMBER: US/10/330, 773

; CURRENT FILING DATE: 2002-12-27

; NUMBER OF SEQ ID NOS: 981

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 278

; LENGTH: 127722

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)-(127722)

; OTHER INFORMATION: n = A, T, C or G

US-10-330-773-278

Query Match 6.9%; Score 344.4; DB 11; Length 127722;
Best Local Similarity 57.4%; Pred. No. 1.9e+02;
Matches 833; Conservative 1; Mismatches 547; Indels 71; Gaps 9;

QY	3107	TTTTTTGTTGTTT	TAGACAGAGGTTCTGTCTGTCA	CCCCAGGCA	TGAGCAGTGGT	3166
DB	5161	TTTTTTTTTTTTT	TTGAAATGGAGTTTCACTCTTGT	TGCCAGGCTGCGTGCAGTGGC	5220	
QY	3167	GCAACCATAGTGT	CACTGCAGCCTCAACCTCTGAGCT	CAAGGATCTGTGACCTCAGCC	3226	
DB	5221	ATGATCTGGCTCA	CTAATAATGTTGGCTCTCTGGTTC	AAGCATTTTCTGGCTCAGCC	5280	
QY	3227	TCCCAAGTAGTCT	GGGACTACGAGCGTGCACACACG	CCCTGGCTAAATAAAAAATTTTT	3286	
DB	5281	TCCTGAGTAGT	AGGATTACAGGGCTTCCACACAC	CTGGCTAATTTTTTGTGTA--TTTT	5338	
QY	3287	TTGTAGAGCTGGT	CTTACTAGTGTGGCCAGGCTTGTCT	TAACTCTCTGGCTTCAAGCA	3346	
DB	5339	TAGTAGAGACGGG	TTTTCACAGGTTGGCCAGGCTGGT	CTTGAACCTCTGACCTCAGGTG	5398	
QY	3347	ATCTCTCTACTT	GGCATCCCAAGTGTGGGATTACAG	GGGTGAGCCACCATGTGCGGC	3406	
DB	5399	ATCCACTGACTCA	GCCTCCCAAGTGTGGAAATTAAGG	TGTGAGCCATCACACCCGA	5458	
QY	3407	TACTTATTTCTT	TACATTCATCTTTTCCAAATAGAA	TGTAAAGTCCACAGAACAGGATTA	3466	
DB	5459	CTTTTAACTCTT	TTTTTTTGA-----	-----	5479	
QY	3467	CTGCCTATTTCT	CTCTCTTTTGTAGACAGAGTCTCA	CTTCATCACTCAACCTCCG	3526	
DB	5480	---GACAGAGT	CTCGCTCTGTGCCCCAGGCTGAG	TGCAGTGATGATC-----	5526	
QY	3527	TTCAGCTCACTG	CAACCTCTGCTCCCGGTTCAAGY	GATTCTCCTGCTTAAGCCTCCTG	3586	
DB	5527	-TCGGCTCACTG	CNAACCTCTGCTCCAGGTTCAGG	GGATTCTCCTGCTCAGCCTCCCA	5585	
QY	3587	AGTAGCTGGAAT	TACAAAGCTGCACCACTATGTTG	GCTAAATTTTGTATTTTTTAGCAG	3646	
DB	5586	AGTAGCTGGACT	ACAGCGCCGCCACCACTGCTTTT	TTTGTATTTTTTAGTAG	5645	
QY	3647	AGATGGGTTTAC	CAATGTTGCCAGGCTGGTCTCAAC	CTCTGACTCAAGTATCTGC	3706	
DB	5646	AGACGGGTTTCA	CGGTTTAGCCAGGATGCTCGATC	TCTCCGACCTC--GTGATCCAT	5703	
QY	3707	CTGCCTCAGTCT	CCAAAGTGTGGAATATAGCGTG	AGTCACTGTGCTGCGCCGATTA	3766	
DB	5704	CTGCCTGGCTCC	CAAGTGTAGGATACAGAGTGAGC	CACTGGCCCGGCTTAATC	5763	
QY	3767	CTGTCTATTTCT	TATATGCTATATCCAGATCTTAG	AGCAGTGTCTGACATAT-AGTAG	3825	
DB	5764	ATTTTTAAGTGT	ATAGTTCAAGTGTATAGTACAA	CCACCACCGCCATCCATCTCCAGAA	5823	
QY	3826	GTGCTCAATAAT	TATGATGACAGCCTAGATATAA	CTTTCTTTCTTTT	3885	
DB	5824	CTTTTCACTTCC	CAACTGAACTCTATCCCCGTTAA	TATCAAGTCCCAATCCCCC	5883	
QY	3886	AAAACAATCTT	GCACAACTTTTGCAGAAATAACA	ATCTTGTCAATTTCTTCACTTAT	3945	

DB	5884	TCCCCGCGCCCT	GGCACCCACCA	TTCACCTTCTCTCTATGAGTCTGACTACTCCAG	5943
QY	3946	CACCTTGTATG	ACT-TTTTCATAT	TGCTCAAACTTTATTTGTTACTGTTTTTTCATTTG	4004
DB	5944	GACCCTCATAT	GAGTGAATCCT	TACAGTATTTATGCAATTTGTGCTCCTCATTTCAITTT	6003
QY	4005	TTACTATTTT	AGTCACTGAATA	TATGCTTAATTTGCTTTATACATCTCTCTGCTCCACT	4064
DB	6004	AGCATAGTAT	----CCTCAAGG	TTCATGTTTAAACAGGTGTGAGGACTCCCTCT	6059
QY	4065	TTAGAAGGCC	CAAAATTTTACAAAT	CTCATGAAAGCTATGAACCTCTCTCCCGAGAGAAATACA	4124
DB	6060	TTTTAAGGCT	GGATCATCTTCT	TATTTGTGGATAGACGTCATTTTGTCTTATTTCAITTCATC	6119
QY	4125	CACACACACAC	ACTCACACAGT	TTTTTTTTTAAATGTTTGCACATTAAGACAAGAAC	4184
DB	6120	AGCTGATAAC	ATCAGGTTGCCCTCC	ACATTTTGGCTATTGTGAATAATGCTGTATATAACAT	6179
QY	4185	TGCATTAGAG	GATGTTTGTTCATATTA	TAAATAACTCAGTTGGGCACAGTGACTCA	4244
DB	6180	TGGTGTACAG	ATATCTCTCAATCT-----	CTGCTTTTGGCGGGCATGTGGCTCA	6232
QY	4245	AGCCTGTAA	CCACAGTACTTTG	GAAGTCCAAGTGGTGGATCACTTGAGGTGAGAAGTT	4304
DB	6233	CGCCTGTAAT	CCAGCACTTTGG	GAGGCTGAGGCAAGTGGATCACCTGAGGTGAGGAGTT	6292
QY	4305	CGAGACAGCT	GTGTCATATGTTG	AAACCTCTCTCTACTAAAAATACAAAAATAGCT	4364
DB	6293	CAAGACCACT	GTGGCCACCATG	TGTAACCCCGCTCTCTACTAAAAATTTAAAAATTTAGCC	6352
QY	4365	GGGTCTAGT	GTGATGCTCTAGT	CCAGCTACTCGGAGGCTGAGGCAAGAGATTC	4424
DB	6353	AGCATGTTGT	GTGGCACTCTGTAAT	CCCACTATTTTGGAGGCTGACACAGAGATCAC	6412
QY	4425	TTGAACCTCT	GGGAGGAGGTTG	CAGTGAAGCCAGATCCCACTGCACTCCAGCTGG	4484
DB	6413	TTGAACCCAG	GAGGACAGGTTG	CAGTGAAGCCAGATCACGCCACTGCACTTAGCCTGG	6472
QY	4485	GGGACA-CAG	CAGACTCTATCTCA	AAAAATAAATAAATAAAGATCGGAGAGA	4543
DB	6473	ACAATAAGAG	GGAATCCATCTCA	AAAAAAGCAAAACAAACACAAAAAAC	6532
QY	4544	AAACAAACT	TAAT 4555		
DB	6533	AAACAAAAA	TAAT 6544		

RESULT 55

US-10-995-561-13341
; Sequence 13341, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13341
; LENGTH: 28693
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13341

Query Match 6.9%; Score 344; DB 10; Length 28693;
Best Local Similarity 50.1%; Pred. No. 5.9e+02;
Matches 1599; Conservative 15; Mismatches 1355; Indels 221; Gaps 23;

QY 752 TTCTTCCCTTTCTAATGCAGTATCCAGTTTCTTACTTATCACATTTATTTATTTCTTT 811


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QY 2911 GGGGAAATAATAGTAACACGCCATGATTTAGTCTTAATTTCTTGTGTTCTGGCACT 2970
Db 2965 CTCAAACCTGTGCTCAGCTCTGCTCCAGATACCCAACTTGTTGTGTGTTCTCTCT 26024
QY 2971 GTCTCCTTTAATCCTCAGAACAACTACTGGGATAGGTAC----- 3010
Db 26025 CTCTTTCAAATTTGAGAAATTTTCTCAATCTGTCTGGACCATGGCAGCAGCTCCTCT 26084
QY 3011 -----AATTATCTCACTTAACAGATAAGAAACTGAGGCTCAGAAAGCT 3055
Db 26085 AAGAAATTTGCTCTTAATTTCTCCATATTTTAATTTCTATCTACATGGCAGTAAGAAACA 26144
QY 3056 GAGCTAATTTGCCCAAGATCACAGCTTGTAAGTGGTGACAGTTTGGGTTTCTTTTGT 3115
Db 26145 CAGATCTAATTTGTCTAATTTCCGTTTGTGTGTTGTTGTTTGTGTTTGTGTTT 26204
QY 3116 G-----TTGTTTAGAGCAGGGTCTTGCTCTGTCCACCCAGGCATGAGCAGAGTGGTC 3168
Db 26205 GTTTTGTGTTTGTGAGACAGAGTCTCTCTGTCCACCCAGGCTGGAGTGCGAGTAGTCT 26264
QY 3169 AACCATAGTCACTGAGCCTCAACCTCTGAGCTCAAGGGATCTGCTGACCTCAGCCTC 3228
Db 26265 GAACTTAGCTCACTGCAACCTCTGCCTCACAGGTTTCAAGCAATTTCTCTGCCTCAACCTC 26324
QY 3229 CCAAGTAGCTGGGACTACGAGCGTGACACCAACCGCTGGCTAATTTAAAAAATTTTTT 3288
Db 26325 CCAGTAGCTGGGATTTACAGGCATGTGCCACACGCCCGGCTAATTTTGTGA-TTTT 26383
QY 3289 GTAGAGACTGGGTCTTACTACGTTGGCCAGGCTTGCTTTAACTCTCGCTTCAAGCAAT 3348
Db 26384 GTAGAGTCGGGGTTTCAACATGTTGTCAGGCTGGTCTTGAGCTCTGACCTCAAGTGAT 26443
QY 3349 CTTCTTACCTTGGCATCCCAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGGG---- 3405
Db 26444 CTACCCGCTTGGCCTCACAAAGTGTGGGATTTACAGGGGTGAGCCACCAACCGCTGGACT 26503
QY 3406 -----CTACTTATTTCTTACATTCATCTTTTCAATAGATGTAAGATCCACAG 3455
Db 26504 GTTTTAAATTTCTCATTGAGTTAATTCAGAACTCTCAAAATGACATTCAGGCTTG 26563
QY 3456 AACAGGG-----ATTACTGCCTATTTTCTCT 3483
Db 26564 CACAATGTGGCCCCCAACCTAAATTTCTAATTTAAATTTTAAATTTTAAATTTTAA 26623
QY 3484 TTCTTTTGTGAGACAGATCTCACTTCATCACTCACTCAACCTCCGT-----TC 3529
Db 26624 TTTTATTTTGTGAGATGGAGTCTCACTCTGTCAACCCAGGCTGGAGTAAAGTGGTGGATCTC 26683
QY 3530 AGCTCACTGCAACTCTGCTCCCGGTTTCAAGYGATTTCTCTGCTTAAGCCTCCTGAGT 3589
Db 26684 TGTCTCACTGCAACTCACTCTCTGGGTTCAAGTATTTCTTACCTCAGCCTCCCACT 26743
QY 3590 AGCTGGAATTTAAGCGTGACACCACTGCTGGCTAAATTTTGTGTTTGTATTTTAGCAGAGA 3649
Db 26744 AGCTGGGATTTGACGATGTCACCTCTGGGTTCAAGTATTTCTTACCTCAGCCTCCCACT 26802
QY 3650 TGGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCTGACCTCAAGTATCTGCTG 3709
Db 26803 CGGGGTTTCAACATGTTGGTTCAGGCTGGTCTTGAATCTCTGACCTCA--TGATCTGCTCT 26860
QY 3710 CCTCAGTCTCCCAAGTGTGGAAATTTATAGGCGTGAGTCACTGTGCTGGCCGATTA 3769
Db 26861 CCTTGGCTCCCAAGTGTGGGATTTGCCGGCTGAGCCACTGTGCCCGGCCCTCAAT 26920
QY 3770 TCTATTTTCT 3779
Db 26921 TTTATTTTCT 26930
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RESULT 56

US-09-925-065A-667240/c

; Sequence 667240, Application US/09925065A

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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 667240
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-667240
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Query Match 6.9%; Score 343; DB 7; Length 1561;
Best Local Similarity 58.5%; Pred. No. Se+03;
Matches 863; Conservative 2; Mismatches 497; Indels 113; Gaps 11;

QY 3105 TTTTGTGTTGTTGTTTGTAGACAGAGGTTCTGTCTC-TGTCAACCCAGGATGAGCACAGT 3163
Db 1445 TTTTGTGTTTGTGTTTGTAGACGGAGTTTCGTCTCTTGTGCCCCAGGCTGAGTACAAT 1386
QY 3164 GGTGCAACCATAGTCACTGACAGCCTCAACCTCTCTGAGCTCAAGGGATCTGCTGACCTCA 3223
Db 1385 GCGTGATCTCAGCTCAAAACAACTCTACCTCCAGATTCAGAGGATTTCTCTGCTCTCA 1326
QY 3224 GCCTCCCAAGTAGCTGGGACTACGAGCGTGCACACACGCTGCTAATTAATAAAATTT 3283
Db 1325 GCCTCAAAGTAGCTGGGATTTCACTCATGAACACCATGCCGCTAATTTGTGA---C 1269
QY 3284 TTTTGTGAGACTGGGTCTTACTACGTTGGCCAGGCTTGTCTTAAACTCTCTGGCTCAA 3343
Db 1268 TTTTAGTAGGATGGGTTTCTCCATGTTGTCAGGCTGGTCTCGAACTCTGACTCAA 1209
QY 3344 GCAATCTCTTACCTTGGCATCCCAAAGTGTGGGATTTACAGGGGTGAGCCACCATGTGC 3403
Db 1208 GGGATCTCGCCGCTCGGCTCCCAAAGTGTGGGATTTACAGGCGTGAGCCACACACC 1149
QY 3404 GCCTACTTATTTCTTTTACATTCCTATTTTCCAATAGATGTAAGATCCACAGAACAGGA 3463
Db 1148 AGCTATATTTTCTTTTCTTTTGTAGACAGTCTGACTCCGTTGGCCAG----- 1097
QY 3464 TTACTGCCTATTTTCTCTCTTTTGTGACAGAGTCTCATCTTCATCCTCAACCT 3523
Db 1096 -----GCTGGAGTGAGTAGCGC 1079
QY 3524 CGTTTCACTCACTCAACCTCTGCTCCGGGTTCAAGYGATTTCTCTGCTCAAGCCTC 3583
Db 1078 GATCTTGGTTTCACTTAATCTTCTGCTCCAGGTTTCAAGCGATTTCTCTGCTCAGCCTC 1019
QY 3584 CTGAGTACTGGAATTTACAAGCGTGCCACACCATGCTTGGCTAAATTTTGTGTTTGTAG 3643
Db 1018 CCAAGTAGCTGGATTTACAGGCATGCACCAATCCGACTAA-TTTTGTGTTTGTAG 960
QY 3644 CAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTCAAGTATC 3703
Db 959 TAGAGATGGGTTTCAACCATGTTGGCCAGGCTGGTCTCAAACTCTCTACCTCAAGTAAATC 900
QY 3704 TGCCTGCCTCAGTCTCCCAAAGTGTGGAAATTA-TAGGCGTGAGTCACTGTGCTCGGCC- 3761
Db 899 CGYCCGCTCGGCTCTCCCAAAGTGTGGGATTTACAAGCGGTGACCCACCGGCGCTGGGCC 840
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QY 3762 -----GATTACTGTCTATTCTTTATTTGCTATATCCCGAGTCTAGAGCAGTGCT 3813
Db 839 TGTGTGTTGTTTATGTATGTTCTATATGTTGTTATTTTCAATAAATAATATTA 780
QY 3814 GACATATAGTAGGTCTCAATAAATAATGATGAATGCACAGCTAGATATAAATTTCT 3873
Db 779 AACAAAGAATAACTGATAGTATGCAAAAGGATTTTAAATTTTCAACCTCACAATAAT 720
QY 3874 TTTTCTTTTAAACAACTTGCAACTTTGCAGAAATAATACAACTTTCATCTGTC 3933
Db 719 TTTTCTTTTAAACAACTTGCAACTTTGCAGAAATAATACAACTTTCATCTGTC 660
QY 3934 TTTTCTTTTAAACAACTTGCAACTTTGCAGAAATAATACAACTTTCATCTGTC 3989
Db 659 TGTGTTCACTGCAGCTTGACCTCCAGGCCCAAGCGATCTTCTACCTCAGCTCCTGAG 600
QY 3990 ACTGTTTTTTCATGTTTACTATTTTATGTCACCTGAATAATATGCTTTTATACA 4049
Db 599 TAGCTGGGACTACAGGCACACTCCACACACCCACCTAATTTTGTATTTTGGTAAAGA 540
QY 4050 TCCTCTGCTCCACTTTAGAGCCCAATTTACAACTCTGATCAAGCTATGAACCTCT 4109
Db 539 TGGGGTTTCAACATGTTGGCCAGGCTGGTCTCGAA--CTTCTGGGATCAAGGAATCCTCC 482
QY 4110 CCCCAGAGAAATACACA-----CACACAC 4133
Db 481 AACCTTGGCTTCCAAAGTCTGGTATTACAGCGGTGAGCCACTGTACCGGCCAAGAT 422
QY 4134 ACACACTCACACAGATTTTTTTTTTAAATGTTTGCAACTAAGACAAAGAACTGCAATGA 4193
Db 421 AGTTTCTTCTCTTACCTAGGTAGACACCTCTGCAGAAATGCTGGGAGATCTTTGGAGAG 362
QY 4194 GGATGTTTGTTCATATTAATAAATAACTAGTTGGGCACAGTCAAGCCCTGTAA 4253
Db 361 GGAGAGATTTTTTAAATAAATAAATTTAATACTTGGAGGGGCGTGGTGGCTTACCCCTGTAA 302
QY 4254 CCACAGTACTTTGGAAGTCAAGGTGGGTGGTCACTTCCAGGTGAGAAGTTCGAGACCAG 4313
Db 301 TCCAGCAGCTTTGGGAGGCCAGGCGGACAGATCA--GGAGTCAAGGAGATTTGAGACCAC 244
QY 4314 CTGGTCAATATGTTGAACCCCTATCTCTACTAAATAATAC-----AAAAATAGCTGGGTG 4369
Db 243 CTGGCTAAACAGGTGAACCCCTATCTCTACTAAATAAATAAATAAATAAATAAATAAATA 184
QY 4370 TAGTGATGATGCTTGTAGTCCAGTACTCTGGGAGGCTGAGGCAAGAGAAATGCTTGA 4429
Db 183 TCGTGGCGGGCGCTTGTAGTCCAGCTACTCTGGGAGGCTGAGTCAAGGAGCTGGCGTGAA 124
QY 4430 CTGGGAGGCGAGAGTTGCAAGTGGAGCGGAGATCCCACTGCACTCCAGCCTGGGCGAC 4489
Db 123 CTGGGAGGCGAGCTTGCAGTGAGCGGACATCGGCGCACTGCATCCAGCCTGGGCGAC 64
QY 4490 ACAGCAGACTCTATCTCAAAAAATAAATAAATA 4524
Db 63 ACAGCAGACTCTCTCTCAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 29
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RESULT 57

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US-09-925-065A-667242/c
; Sequence 667242, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
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; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 667242
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-667242
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```
Query Match 6.9%; Score 343; DB 7; Length 1561;
Best Local Similarity 58.5%; Pred. No. Se+03;
Matches 863; Conservative 2; Mismatches 497; Indels 113; Gaps 11;

QY 3105 TTTTGTGTTGTTGTTTGTAGACAGGGTCTTTGCTC-TGTACCCAGGAGCATGAGCAGT 3163
Db 1445 TTTTGTGTTTGTGTTTGTAGACAGGGTCTTTGCTC-TGTACCCAGGAGCATGAGCAGT 1386
QY 3164 GGTGCAACATAGTCACTGCGAGCTCAACCTCTGAGCTCAAGGATCTGCTGACCTCA 3223
Db 1385 GCGGTGATCTCAGCTCAAAACAAACCTCTACCTCCAGATTCAGCGATTTCTCTGCTCA 1326
QY 3224 GCCTCCCAAGTAGCTGGGACTACGAGCTGCAACACACGCTGCTAATTAATAAATAAT 3283
Db 1325 GCCTCCAAAGTAGTGGGATTTAGTATGACACACATGCCGCTAATTTTGTGTA--C 1269
QY 3284 TTTTGTGTTGTTGTTGTTTGTAGACAGGGTCTTTGCTC-TGTACCCAGGAGCATGAGCAGT 3343
Db 1268 TTTTGTGTTGTTGTTGTTTGTAGACAGGGTCTTTGCTC-TGTACCCAGGAGCATGAGCAGT 1209
QY 3344 GCAATCTCTACCTGTCATCCCAAGTGTGGGATTTACAGGCTGAGCCAGCAGTGC 3403
Db 1208 GGGATCTCCCGCTCCCGCTCCCAAGTGTGGGATTTACAGGCTGAGCCAGCAGTGC 1149
QY 3404 GGTACTATTATTCTTTTACATTCATCTTTTCAATAGAATGTAAGATCCACAGAACAGGA 3463
Db 1148 AGCTATATATTTTCTTTTCTTTTGTAGACAGTCTGACTCCGTTGCCAG----- 1097
QY 3464 TTACTGCTATTTTCTCTCTTTTGTAGACAGAGTCTCATCTTCATCATCACTCAACCT 3523
Db 1096 -----GCTGGAGTGCAGTAGCGC 1079
QY 3524 CGTTCACTCACTCAACCTCTGCTCCCGGTTCAAGYATTTCTCTGCTGCTAGCCTC 3583
Db 1078 GATCTTGGTTCACTGTAATCTTCTGCTCCAGGTTCAAGCGATTTCTCTGCTCAGCCTC 1019
QY 3584 CTGAGTAGCTGGAATTAACAAGGCTGCACACCATGCTTTGGCTAAATTTTGTATTTTGTAG 3643
Db 1018 CCAAGTAGCTGGATTAACAGGATGACACCAACATCCGACTAA-TTTTGTATTTTGTAG 960
QY 3644 CAGAGATGGGTTTACCATGTTGCCAGGCTGGTCTCAAACTCTCTGACCTCAAGTATC 3703
Db 959 TAGAGATGGGTTTCAACCATGTTGGCCAGGCTGGTCTCAAACTCTCTCACTCAAGTATC 900
QY 3704 TGCCTGCTCAGTCTCCCAAGTGTGGAATTA-TAGGCGTGAAGTCACTGTGCTGCGCC- 3761
Db 899 CGCCCGCTCGGCTCCCAAGTGTGGAATTAACAGGCTGACCCACCGGCTCGGCCC 840
QY 3762 -----GATTACTGTTCTATTTTCTTTATGCTATATCTCCAGATCTAGAGCAGTGTCT 3813
Db 839 TGTGTTGTTTATGTTATGTTTCTATATGTTTATATTTTCAATAAATAATTAATA 780
QY 3814 GACATATAGTAGGTCTCAATAAATAATGATGAATGCACAGCCTAGATATAAATTTCT 3873
Db 779 AACAAAGAATAACTGATAGTATGCAAAAGGATTTTAAATTTTCAACCTCACAATAAT 720
QY 3874 TTTTCTTTTAAACAACTTTGCAACTTTGCAGAAATAATACAACTTTCATCTGTC 3933
Db 719 TTTTCTTTTAAACAACTTTGCAACTTTGCAGAAATAATACAACTTTCATCTGTC 660
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QY 4176 CAAGAAACCTGCATTAGAGGATGTTGTTTCATATT----- 4210
DB 25892 GCAGAAACCTACTTTAAATTTTTCAAATAATGCTCTATTATACCTTAATTTCTATCACC 25951
QY 4211 -----AATTAATAAATACTAGTTGGGCACAGTCAAGCTGTAAACACAGT 4260
DB 25952 AATCATTTAAATAAATACTTTCTTGGCCAGGCGGTGGCTCAGCCTATAATCCAGC 26011
QY 4261 ACTTTGGAGTCCAAGTGGTGGATCACTTGAAGTGAGAGTTGAGACACAGCTGGTC 4320
DB 26012 ACTTTGGAGGAGGAGGCGGTGGATCAC--GAGGTCAAGAGTTCAAGACACAGCTGGCC 26069
QY 4321 AATATGCTGAACCCCTATCTTACTAAAAATAACAAAAATAGCTGGTGTAGTGATCAT 4380
DB 26070 AGATGGTGAACCCCGTCTTACTAAAAATAACAAAAATAGCCAGGACAGTGGCAGAT 26129
QY 4381 GCGTGTAGTCCAGCTACTCGGAGAGCTGAGGCAAGAGAAATGCTTTGAACCTGGGAGG-- 4438
DB 26130 GCGTGTAAATCCAGCTACTTGGAGGCTGAGGAGGAGAAATGCTTTGAACCTGCGGGGG 26189
QY 4439 --CAGAGGTGCGAGTGGAGAGTCCACCACTGCACTCCAGCTGGGGGACACAGCA 4496
DB 26190 TACGGAGGTGCGAGTGGAGCAAGATCATGCCACTGCCTCCAGTTCGGCAACAGAGTGA 26249
QY 4497 GACTGTATCTCAAAAAATAAATAAA 4522
DB 26250 GACTGCTCAAAAAATAAATAA 26275

RESULT 59
US-11-121-086-27
; Sequence 27, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121, 086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 153142
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-27

Query Match 6.8%; Score 341.2; DB 17; Length 153142;
Best Local Similarity 58.1%; Pred. No. 1.8e+02;
Matches 850; Conservative 1; Mismatches 529; Indels 82; Gaps 11;

QY 3098 TTGGGTTTTTTTTTCTGTTGTTTAGACAGGGTCTTGCTCTGTCACCCAGGATGAG 3157
DB 101687 TTTTGTGTTTTTTTTTTTTTTTGGACGGAGTCTCGCTTTGTCGCCAGGCTGGAG 101746
QY 3158 CACAGTGGTGCAACATAGTCACTGCAGCCTCAACCTCTGAGTCAAGGGATCTGTG 3217
DB 101747 TGCAGTGGCGGGATCTCGGCTCACTGCAAGCTCCGCTCCCGGTTTCAGCCATCTCCT 101806
QY 3218 ACCTAGCCTCCCAAGTAGTGGAGTACAGGGTGCAACACACCCCTGGCTTAATAA 3277
DB 101807 GCCTAGCCTCCCAAGTAGTGGAGTACAGGGTCCCGCCCTATACCCGGTAATTTT 101866
QY 3278 AAAATTTTTTTGAGAGCTGGGTCTTACTACGTGGCAGGCTTGTCTTAAACTCTCG 3337
DB 101867 TTGTATTTTGTAGAGACGGGTTTTTCAACGGTTTTAGCCGGATGTCGATCTCTGA 101926
QY 3338 CTTTCAAGCAATCTCTTACCTTGGCATCCCAAGTCTGGGATTAACAGGGGTGAGCCACC 3397

DB 101927 CUTC--GTGATCCGCCCGCTCGGCTCCCAAGAGTGTGGGATTACAGCGGTGAGCCACC 101984
QY 3398 ATGTCGCGCTACTTATTCTTTTACATTCATCTTTTCCAAATAGAATGTAAAGTATCCACAGAA 3457
DB 101985 GCGCCGCGCTGTTTTTTTTTT----- 102006
QY 3458 CAGGGATTACTGCCTATTCTTCTCTCTTTTGTGAGACAGAGTCTCAGTTTCATCAGCT 3517
DB 102007 -----TTTTTTTGTGAGACTGAGTCTGCACTGCGCCAGGCTGGAGTGAG 102052
QY 3518 CAACCTCCGTTAGCTCACTGCAACCTCTGCTCCGCGGTTCAGYGAATTCCTTCGCTTA 3577
DB 102053 TGGCGCGATCTCGGCTCACTGCAACCTCTCCAGCTTCACAGGTTCAAGCAATTCCTTCGCTC 102112
QY 3578 AGCCTCTGAGTAGTGGAAATTTACAAGCGTGCACCAACCATGCTTGGCTAA----- 3627
DB 102113 AGCTCTCTGAGTAGTGAATTTACAGTGCCACCAAGTGGCCAGCTAACTTTTTTTTT 102172
QY 3628 -TTTTTGTATTTTGTAGCAGAGA--TGGGTTTTTACCATGTTGCCCAGGCTGGTCTCAAC 3685
DB 102173 TTTTTTGTATTTTGTAGAGACGGGGTTTCAACATGTTGGTCAGGCTGGTCTCGAAC 102232
QY 3686 TCCTGACCTCAAGTGAATCTGCTGCTCAGTCTCCCAAGTCTGGAATTAAGGCTGA 3745
DB 102233 TCCTGACCTC--GTGATCCGCCCGCTTGGCCCTCCCAAGTGAATGGGATTCAGGCGTGA 102290
QY 3746 GTCAGTGTGCTGCGCGGATTTACTGTCTATTTTCTTTTATTTGCTATATCCCAGATCTAGAG 3805
DB 102291 GCCACGTCGCCAGC-----TTTTTTTTTTTTTTTATAGACGGGGTCTTACTATGTTG 102346
QY 3806 CAGTGTCTGACATATAGTAGTGTCTCAATAATAATTTGATGAATGCACAGCTAGATATA 3865
DB 102347 CCCAGGCTGGACTCTCAAACTCTCTGGCTCAAGGAATCTTCTACACAGCTTCTGAGT 102406
QY 3866 AACTTCTCTTTTCTTTTTTAAACAATCTTGACAACCTTTGCAGATAATAACATCTTG 3925
DB 102407 AGCTGGGCTACAAGCCCTGCCCACAGTACCTGGCTGTTT--TTGTTTTTTTATAATTTG 102465
QY 3926 CATCTGCTTTTCTACTTATCACCTTGTATGACTTTTTTTCATATTGCTCAAACTTTAT 3985
DB 102466 GTAAATATAACAACATGCGCGGTGTGGTCTCAGCCTGTAAATCTCAACACTCT-- 102523
QY 3986 TGTACTGTTTTTTCTATTTTACTGTTAGTCACTGAATAATATGGCTTAATTTGCTTA 4045
DB 102524 --GGGAGGTGAGGTGGGAGGATTTACTTTGAACCCAGGAGTTCAAGACCACTGCTGGCAAC 102581
QY 4046 TACATCTCTGCTCCACTTTTAGAAGGCCAAATTTTCAAAATCTGATGAAGTATGAACC 4105
DB 102582 TTGGCAAAACTGTGTTTCTACAAAAATAAAAAATATTAGCTGGGCGAGCGCAGTGG 102641
QY 4106 CTCTCCCGAGAGAAATACACACACACACACTCACACAGTTTTTTTTTAAATGTTT 4165
DB 102642 CTCATGCTGCAATCCCAGCACTTTGGGAGGTGAGGTGGATGGATCACTGAGAGTCA 102701
QY 4166 GCAACT--AAGACAAGAAACCTGCAATTAGAGGATGTTTGTTCATATTAATTAATAAATAA 4222
DB 102702 GGAGTTTGAGACCACTCTGGCCCAACATGTTGAAACCTGTCTCTTTAAAAATAACAAAAA 102761
QY 4223 CTCAGTTGGGCACAGTGAATCAAGCTGTAAACCAAGTACTTTTGAAGTCCAGAGTGGGT 4282
DB 102762 ATGAGCCAGCATGTTGCTGCTCAGCTGTAATCCAGCACTTTGAGAGGCCAAGCAGGT 102821
QY 4283 GGATCACTTGGAGTGAAGTTTCAGACACAGCTGCTCAATATGTTGAACCTATCTCT 4342
DB 102822 GGATCACTGAGTCAAGAGTTCAAGACCAACCTGGCCAACTTTGTGAACCCCTCTCT 102881
QY 4343 ACTAAAAATAC--AAAAATTAGCTGGGTGTAGTGAATGCTGTAGTCCAGCTACTCG 4401
DB 102882 ACTAAAAATACAAAAAATTAGCTGGGCATGTTGGCAGCGCTTATAATTTCCAGCTACTAA 102941
QY 4402 GGAGCTGAGGCAAGAGAAATGCTTTGAACCTGGGAGGAGGAGTTGCAAGTGGAGCCAGAT 4461
DB 102942 GGAGCTGAGGCGGAGAAATCGCTTTGAACCCGGGAGGAGGTTGCAAGTGAAGTCAAGAT 103001

